METHODS AND COMPOSITIONS FOR MODULATING A GENOME

RELATED APPLICATIONS

This application claims priority to U.S. Serial No.: 63/241,953 filed September 8, 2021 and 63/373,444 filed August 24, 2022, the entire contents of each of which is incorporated herein by reference.

SEQUENCE LISTING

The instant application contains a Sequence Listing which has been submitted electronically in XML format and is hereby incorporated by reference in its entirety. Said XML copy, created on October 27, 2022, is named V2065-7023WO_SL.xml and is 20,090,757 bytes in size.

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.

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*. In particular, the invention features compositions, systems and methods for inserting, altering, or deleting sequences of interest in a host genome.

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

1. A gene modifying polypeptide comprising:

a DNA binding domain (DBD) that binds to a target nucleic acid sequence and

a reverse transcriptase (RT) domain of Table 1, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto (e.g., to a sequence as listed for the RT domain in Table 6);

wherein the DBD is heterologous to the RT domain (e.g., a Cas domain, e.g., a Cas nickase domain, e.g., a Cas9 nickase domain); optionally 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 1 as the RT domain, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

2. The gene modifying polypeptide of embodiment 1, wherein the RT domain has a sequence with at least 90% identity to the RT domain of Table 1.

3. The gene modifying polypeptide of any of the preceding embodiments, wherein the RT domain has a sequence with at least 95% identity to the RT domain of Table 1.

4. The gene modifying polypeptide of any of the preceding embodiments, wherein the RT domain has a sequence with at least 98% identity to the RT domain of Table 1.

5. The gene modifying polypeptide of any of the preceding embodiments, wherein the RT domain has a sequence with at least 99% identity to the RT domain of Table 1.

6. The gene modifying polypeptide of any of the preceding embodiments, wherein the RT domain has a sequence with 100% identity to the RT domain of Table 1.

7. The gene modifying polypeptide of any of the preceding embodiments, wherein the linker has a sequence with at least 90% identity to the linker sequence from the same row of Table 1 as the RT domain.

8. The gene modifying polypeptide of any of the preceding embodiments, wherein the linker has a sequence with at least 95% identity to the linker sequence from the same row of Table 1 as the RT domain.

9. The gene modifying polypeptide of any of the preceding embodiments, wherein the linker has a sequence with at least 97% identity to the linker sequence from the same row of Table 1 as the RT domain.

10. The gene modifying polypeptide of any of the preceding embodiments, wherein the linker has a sequence with 100% identity to the linker sequence from the same row of Table 1 as the RT domain.

11. The gene modifying polypeptide of any of the preceding embodiments, wherein the RT domain comprises a mutation as listed in Table 2.

12. The gene modifying polypeptide of any of the preceding embodiments, wherein the Cas domain comprises a sequence of Table 7 or 8, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 98%, or 99% identity thereto.

13. The gene modifying polypeptide of any of the preceding embodiments, wherein the Cas domain is a Cas nickase domain.

14. The gene modifying polypeptide of any of the preceding embodiments, wherein the Cas domain is a Cas9 nickase domain.

15. The gene modifying polypeptide of any of the preceding embodiments, wherein the Cas domain comprises an N863A mutation.

16. The gene modifying polypeptide of any of the preceding embodiments, which comprises an NLS, e.g., wherein the gene modifying polypeptide comprises two NLSs.

17. The gene modifying polypeptide of any of the preceding embodiments, which comprises an NLS N-terminal of the Cas9 domain.

18. The gene modifying polypeptide of any of the preceding embodiments, which comprises an NLS C-terminal of the RT domain.

19. The gene modifying polypeptide of any of the preceding embodiments, which comprises a first NLS which is N-terminal of the Cas9 domain and a second NLS which is C-terminal of the RT domain.

20. The gene modifying polypeptide of any of the preceding embodiments, which 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.

21. The gene modifying polypeptide of any of the preceding embodiments, which 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.

22. The gene modifying polypeptide of any of the preceding embodiments, which comprises a GG amino acid sequence between the Cas domain and the linker.

23. The gene modifying polypeptide of any of the preceding embodiments, which comprises an AG amino acid sequence between the RT domain and the second NLS.

24. The gene modifying polypeptide of any of the preceding embodiments, which comprises a GG amino acid sequence between the linker and the RT domain.

25. The gene modifying polypeptide of any of the preceding embodiments, which 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.

26. The gene modifying polypeptide of any of the preceding embodiments, which comprises an amino acid sequence with at least 90% identity to any of SEQ ID NOs: 1-3332 in the sequence listing.

27. The gene modifying polypeptide of any of the preceding embodiments, which comprises an amino acid sequence with at least 95% identity to any of SEQ ID NOs: 1-3332 in the sequence listing.

28. The gene modifying polypeptide of any of the preceding embodiments, which comprises an amino acid sequence with at least 98% identity to any of SEQ ID NOs: 1-3332 in the sequence listing.

29. The gene modifying polypeptide of any of the preceding embodiments, which comprises an amino acid sequence with at least 99% identity to any of SEQ ID NOs: 1-3332 in the sequence listing.

30. The gene modifying polypeptide of any of the preceding embodiments, which comprises an amino acid sequence with 100% identity to any of SEQ ID NOs: 1-3332 in the sequence listing.

31. The gene modifying polypeptide of any of the preceding embodiments, which produces an increase in converted GFP+ of at least 10%, 20%, 30%, 40%, 50%, 60%, 70%, 75%, 80%, 85%, 90%, 95%, 100%, 125%, 150%, 175%, 200%, 250%, 300%, 400%, 500%, 600%, 700%, 800%, 900%, 1000%, 1500%, 2000%, or 2500% relative to unsorted input cells in an assay of Example 2 using HEK cells (e.g., HEK293T cells) and g4 guide RNA.

32. The gene modifying polypeptide of any of the preceding embodiments, which produces an increase in converted GFP+ of at least 10%, 20%, 30%, 40%, 50%, 60%, 70%, 75%, 80%, 85%, 90%, 95%, 100%, 125%, 150%, 175%, 200%, 250%, 300%, 400%, 500%, 600%, 700%, 800%, 900%, 1000%, 1500%, 2000%, or 2500% relative to unsorted input cells in an assay of Example 2 using U2-OS cells and g4 guide RNA.

33. The gene modifying polypeptide of any of the preceding embodiments, which produces an increase in converted GFP+ of at least 10%, 20%, 30%, 40%, 50%, 60%, 70%, 75%, 80%, 85%, 90%, 95%, 100%, 125%, 150%, 175%, 200%, 250%, 300%, 400%, 500%, 600%, 700%, 800%, 900%, 1000%, 1500%, 2000%, or 2500% relative to unsorted input cells in an assay of Example 2 using HEK cells (e.g., HEK293T cells) and g10 guide RNA.

34. The gene modifying polypeptide of any of the preceding embodiments, which has an activity that is at least 50%, 60%, 70%, 80%, or 90% of the activity of a gene modifying polypeptide comprising, in an N-terminal to C-terminal direction:

a) an NLS and Cas domain sequence of SEQ ID NO: 4000;

b) a linker having the sequence EAAAKGSS (SEQ ID NO: 5152);

c) an RT domain having the sequence of PERV_Q4VFZ2_3mutA_WS; and

d) an NLS sequence of SEQ ID NO: 4001,

in an assay of Example 1 using HEK cells and g4 guide RNA.

35. The gene modifying polypeptide of any of the preceding embodiments, which has an activity that is at least 10%, 20%, 30%, 40%, 50%, 60%, 70%, 75%, 80%, 85%, 90%, 95%, 100%, 125%, 150%, 175%, 200%, 250%, 300%, 400%, 500%, 600%, 700%, 800%, 900%, 1000%, 1500%, 2000%, or 2500% greater than the activity of a gene modifying polypeptide comprising a sequence of SEQ ID NO: 4002 in an assay of Example 1, e.g., using HEK cells and g4 guide RNA.

36. A nucleic acid (e.g., DNA or RNA, e.g., mRNA) encoding the gene modifying polypeptide of any of the preceding embodiments.

37. A cell comprising the gene modifying polypeptide of any of embodiments 1-35 or the nucleic acid of embodiment 36.

38. A system comprising:

i) the gene modifying polypeptide of any of embodiments 1-35, and

ii) a template RNA that comprises:

a) a gRNA spacer that is complementary to a portion a target nucleic acid sequence;

b) a gRNA scaffold that binds the Cas domain of the gene modifying polypeptide;

c) a heterologous object sequence; and

d) a primer binding site sequence (PBS sequence).

39. A method for modifying a target nucleic acid in a cell (e.g., a human cell), the method comprising contacting the cell with the system of embodiment 38, or nucleic acid encoding the same, thereby modifying the target nucleic acid.

40. A gene modifying polypeptide comprising:

a Cas domain (e.g., a Cas nickase domain, e.g., a Cas9 nickase domain);

a reverse transcriptase (RT) domain comprising the RT domain of a reference gene modifying polypeptide having the sequence of any one of SEQ ID NOs: 1-7743, 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 comprises the linker of said reference gene modifying polypeptide, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

41. The gene modifying polypeptide of embodiment 40, wherein the reference gene modifying polypeptide has the amino acid sequence of a SEQ ID NO as listed in Table 1.

42. The gene modifying polypeptide of embodiment 40, wherein the reference gene modifying polypeptide has the amino acid sequence of a SEQ ID NO as listed in Table A1.

43. The gene modifying polypeptide of embodiment 40, wherein the reference gene modifying polypeptide has the amino acid sequence of a SEQ ID NO as listed in Table A5.

44. The gene modifying polypeptide of embodiment 40, wherein the reference gene modifying polypeptide has the amino acid sequence of a SEQ ID NO as listed in Table D1.

45. The gene modifying polypeptide of embodiment 40, wherein the reference gene modifying polypeptide has the amino acid sequence of a SEQ ID NO as listed in Table D2.

46. The gene modifying polypeptide of embodiment 40, wherein the reference gene modifying polypeptide has the amino acid sequence of a SEQ ID NO as listed in Table D3.

47. The gene modifying polypeptide of embodiment 40, wherein the reference gene modifying polypeptide has the amino acid sequence of a SEQ ID NO as listed in Table D4.

48. The gene modifying polypeptide of embodiment 40, wherein the reference gene modifying polypeptide has the amino acid sequence of a SEQ ID NO as listed in Table D5.

49. The gene modifying polypeptide of embodiment 40, wherein the reference gene modifying polypeptide has the amino acid sequence of a SEQ ID NO as listed in Table D6.

50. The gene modifying polypeptide of embodiment 40, wherein the reference gene modifying polypeptide has the amino acid sequence of a SEQ ID NO as listed in Table D7.

51. The gene modifying polypeptide of embodiment 40, wherein the reference gene modifying polypeptide has the amino acid sequence of a SEQ ID NO as listed in Table D8.

52. The gene modifying polypeptide of embodiment 40, wherein the reference gene modifying polypeptide has the amino acid sequence of a SEQ ID NO as listed in Table D9.

53. The gene modifying polypeptide of embodiment 40, wherein the reference gene modifying polypeptide has the amino acid sequence of a SEQ ID NO as listed in Table D10.

54. The gene modifying polypeptide of embodiment 40, wherein the reference gene modifying polypeptide has the amino acid sequence of a SEQ ID NO as listed in Table D11.

55. The gene modifying polypeptide of embodiment 40, wherein the reference gene modifying polypeptide has the amino acid sequence of a SEQ ID NO as listed in Table D12.

56. The gene modifying polypeptide of embodiment 40, wherein the reference gene modifying polypeptide has the amino acid sequence of a SEQ ID NO as listed in Table T1.

57. The gene modifying polypeptide of embodiment 40, wherein the reference gene modifying polypeptide has the amino acid sequence of a SEQ ID NO as listed in Table T2.

58. The gene modifying polypeptide of embodiment 40, wherein the reference gene modifying polypeptide is an AVIRE polypeptide (e.g., as described herein), and wherein the linker comprises an amino acid sequence as listed in Figure 11.

59. A gene modifying polypeptide comprising:

a Cas domain (e.g., a Cas nickase domain, e.g., a Cas9 nickase domain);

a reverse transcriptase (RT) domain of Table 1, 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 1 as the RT domain, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

60. A gene modifying polypeptide comprising:

a Cas domain (e.g., a Cas nickase domain, e.g., a Cas9 nickase domain);

a reverse transcriptase (RT) domain of Table A1, 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 comprises a sequence from the same row of Table A1 as the RT domain, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

61. A gene modifying polypeptide comprising:

a Cas domain (e.g., a Cas nickase domain, e.g., a Cas9 nickase domain);

a reverse transcriptase (RT) domain of Table A5, 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 comprises a sequence from the same row of Table D1 as the RT domain, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

62. A gene modifying polypeptide comprising:

a Cas domain (e.g., a Cas nickase domain, e.g., a Cas9 nickase domain);

a reverse transcriptase (RT) domain of Table T1, 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 comprises a sequence from the same row of Table D1 as the RT domain, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

63. A gene modifying polypeptide comprising:

a Cas domain (e.g., a Cas nickase domain, e.g., a Cas9 nickase domain);

a reverse transcriptase (RT) domain of Table T2, 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 comprises a sequence from the same row of Table D1 as the RT domain, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

64. A gene modifying polypeptide comprising:

a Cas domain (e.g., a Cas nickase domain, e.g., a Cas9 nickase domain);

a reverse transcriptase (RT) domain of Table D1, 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 comprises a sequence from the same row of Table D1 as the RT domain, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

65. A gene modifying polypeptide comprising:

a Cas domain (e.g., a Cas nickase domain, e.g., a Cas9 nickase domain);

a reverse transcriptase (RT) domain of Table D2, 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 comprises a sequence from the same row of Table D2 as the RT domain, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

66. A gene modifying polypeptide comprising:

a Cas domain (e.g., a Cas nickase domain, e.g., a Cas9 nickase domain);

a reverse transcriptase (RT) domain of Table D3, 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 comprises a sequence from the same row of Table D3 as the RT domain, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

67. A gene modifying polypeptide comprising:

a Cas domain (e.g., a Cas nickase domain, e.g., a Cas9 nickase domain);

a reverse transcriptase (RT) domain of Table D4, 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 comprises a sequence from the same row of Table D4 as the RT domain, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

68. A gene modifying polypeptide comprising:

a Cas domain (e.g., a Cas nickase domain, e.g., a Cas9 nickase domain);

a reverse transcriptase (RT) domain of Table D5, 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 comprises a sequence from the same row of Table D5 as the RT domain, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

69. A gene modifying polypeptide comprising:

a Cas domain (e.g., a Cas nickase domain, e.g., a Cas9 nickase domain);

a reverse transcriptase (RT) domain of Table D6, 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 comprises a sequence from the same row of Table D6 as the RT domain, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

70. A gene modifying polypeptide comprising:

a Cas domain (e.g., a Cas nickase domain, e.g., a Cas9 nickase domain);

a reverse transcriptase (RT) domain of Table D7, 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 comprises a sequence from the same row of Table D7 as the RT domain, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

71. A gene modifying polypeptide comprising:

a Cas domain (e.g., a Cas nickase domain, e.g., a Cas9 nickase domain);

a reverse transcriptase (RT) domain of Table D8, 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 comprises a sequence from the same row of Table D8 as the RT domain, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

72. A gene modifying polypeptide comprising:

a Cas domain (e.g., a Cas nickase domain, e.g., a Cas9 nickase domain);

a reverse transcriptase (RT) domain of Table D9, 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 comprises a sequence from the same row of Table D9 as the RT domain, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

73. A gene modifying polypeptide comprising:

a Cas domain (e.g., a Cas nickase domain, e.g., a Cas9 nickase domain);

a reverse transcriptase (RT) domain of Table D10, 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 comprises a sequence from the same row of Table D10 as the RT domain, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

74. A gene modifying polypeptide comprising:

a Cas domain (e.g., a Cas nickase domain, e.g., a Cas9 nickase domain);

a reverse transcriptase (RT) domain of Table D11, 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 comprises a sequence from the same row of Table D11 as the RT domain, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

75. A gene modifying polypeptide comprising:

a Cas domain (e.g., a Cas nickase domain, e.g., a Cas9 nickase domain);

a reverse transcriptase (RT) domain of Table D12, 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 comprises a sequence from the same row of Table D12 as the RT domain, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

76. A gene modifying polypeptide comprising:

a Cas domain (e.g., a Cas nickase domain, e.g., a Cas9 nickase domain);

a reverse transcriptase (RT) domain of Table T1, 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 comprises a sequence from the same row of Table T1 as the RT domain, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

77. A gene modifying polypeptide comprising:

a Cas domain (e.g., a Cas nickase domain, e.g., a Cas9 nickase domain);

a reverse transcriptase (RT) domain of Table T2, 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 comprises a sequence from the same row of Table T2 as the RT domain, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

78. A gene modifying polypeptide comprising:

a Cas domain (e.g., a Cas nickase domain, e.g., a Cas9 nickase domain);

an AVIRE reverse transcriptase (RT) domain (e.g., as described herein), 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 comprises a sequence as listed in Figure 11, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

79. The gene modifying polypeptide of any one of embodiments 1-78, wherein the RT domain comprises an amino acid sequence of an AVIRE RT domain (e.g., as described in Table 6), or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, 99%, or 100% identity thereto.

80. The gene modifying polypeptide of any one of embodiments 1-78, wherein the RT domain comprises an amino acid sequence of an BAEVM RT domain (e.g., as described in Table 6), or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, 99%, or 100% identity thereto.

81. The gene modifying polypeptide of any one of embodiments 1-78, wherein the RT domain comprises an amino acid sequence of an FFV RT domain (e.g., as described in Table 6), or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, 99%, or 100% identity thereto.

82. The gene modifying polypeptide of any one of embodiments 1-78, wherein the RT domain comprises an amino acid sequence of an FLV RT domain (e.g., as described in Table 6), or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, 99%, or 100% identity thereto.

83. The gene modifying polypeptide of any one of embodiments 1-78, wherein the RT domain comprises an amino acid sequence of an FOAMV RT domain (e.g., as described in Table 6), or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, 99%, or 100% identity thereto.

84. The gene modifying polypeptide of any one of embodiments 1-78, wherein the RT domain comprises an amino acid sequence of an GALV RT domain (e.g., as described in Table 6), or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, 99%, or 100% identity thereto.

85. The gene modifying polypeptide of any one of embodiments 1-78, wherein the RT domain comprises an amino acid sequence of an KORV RT domain (e.g., as described in Table 6), or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, 99%, or 100% identity thereto.

86. The gene modifying polypeptide of any one of embodiments 1-78, wherein the RT domain comprises an amino acid sequence of an MLVAV RT domain (e.g., as described in Table 6), or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, 99%, or 100% identity thereto.

87. The gene modifying polypeptide of any one of embodiments 1-78, wherein the RT domain comprises an amino acid sequence of an MLVBM RT domain (e.g., as described in Table 6), or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, 99%, or 100% identity thereto.

88. The gene modifying polypeptide of any one of embodiments 1-78, wherein the RT domain comprises an amino acid sequence of an MLVCB RT domain (e.g., as described in Table 6), or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, 99%, or 100% identity thereto.

89. The gene modifying polypeptide of any one of embodiments 1-78, wherein the RT domain comprises an amino acid sequence of an MLVFF RT domain (e.g., as described in Table 6), or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, 99%, or 100% identity thereto.

90. The gene modifying polypeptide of any one of embodiments 1-78, wherein the RT domain comprises an amino acid sequence of an MLVMS RT domain (e.g., as described in Table 6), or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, 99%, or 100% identity thereto.

91. The gene modifying polypeptide of any one of embodiments 1-78, wherein the RT domain comprises an amino acid sequence of an PERV RT domain (e.g., as described in Table 6), or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, 99%, or 100% identity thereto.

92. The gene modifying polypeptide of any one of embodiments 1-78, wherein the RT domain comprises an amino acid sequence of an SFV1 RT domain (e.g., as described in Table 6), or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, 99%, or 100% identity thereto.

93. The gene modifying polypeptide of any one of embodiments 1-78, wherein the RT domain comprises an amino acid sequence of an SFV3L RT domain (e.g., as described in Table 6), or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, 99%, or 100% identity thereto.

94. The gene modifying polypeptide of any one of embodiments 1-78, wherein the RT domain comprises an amino acid sequence of an WMSV RT domain (e.g., as described in Table 6), or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, 99%, or 100% identity thereto.

95. The gene modifying polypeptide of any one of embodiments 1-78, wherein the RT domain comprises an amino acid sequence of an XMRV6 RT domain (e.g., as described in Table 6), or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, 99%, or 100% identity thereto.

96. The gene modifying polypeptide of any one of embodiments 1-78, wherein the RT domain comprises an amino acid sequence of an MLVAV, MLVBM, BAEVM, FLV, FOAMV, GALV, KORV, AVIRE, MLVCB, MLVFF, MLVMS, SFV3L, WMSV, or XMRV6 RT domain (e.g., as described in Table 6), or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, 99%, or 100% identity thereto.

97. The gene modifying polypeptide of any one of embodiments 1-78, wherein the RT domain comprises an amino acid sequence of a gammaretroviral RT domain, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, 99%, or 100% identity thereto.

98. The gene modifying polypeptide of embodiment 97, wherein the RT domain comprises an amino acid sequence of an GALV, MLVAV, MLVBM, BAEVM, FLV, AVIRE, KORV, MLVCB, MLVFF, WMSV, XMRV6, MLVMS, and PERV RT domain (e.g., as described in Table 6), or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, 99%, or 100% identity thereto.

99. The gene modifying polypeptide of any embodiment 40, wherein the RT domain comprises an amino acid sequence of an RT domain as listed in any one of Tables 1, A1, A5, D1-D12, T1, or T2, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

100. The gene modifying polypeptide of embodiment 40, wherein the linker comprises an amino acid sequence of a linker as listed in any one of Tables 1, A1, A5, D1-D12, T1, or T2, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

101. The gene modifying polypeptide of embodiment 40,

wherein the RT domain comprises an amino acid sequence of an RT domain as listed in any one of Tables 1, A1, A5, D1-D12, T1, or T2, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto; and

wherein the linker comprises an amino acid sequence of a linker as listed the same row of Table 1, A1, A5, D1-D12, T1, or T2, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

102. The gene modifying polypeptide of embodiment 40, wherein the RT domain comprises one or more (e.g., at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20) amino acid substitutions at a residue corresponding to position 200, 603, 330, 524, 562, 583, 51, 67, 67, 197, 204, 302, 309, 313, 435, 454, 594, 671, 69, or 653 of an MLVMS RT domain sequence as described herein (e.g., as listed in Table 6), e.g., an MLVMS_reference sequence, e.g., SEQ ID NO: 8137, relative to a wildtype sequence of the RT domain.

103. The gene modifying polypeptide of embodiment 40, wherein the RT domain comprises an RT domain comprising an amino acid sequence of an MLVMS RT domain sequence as described herein (e.g., as listed in Table 6), e.g., an MLVMS_reference sequence, e.g., SEQ ID NO: 8137, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

104. The gene modifying polypeptide of embodiment 40, wherein the RT domain comprises one or more (e.g., at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20) amino acid substitutions at a residue corresponding to position 200, 603, 330, 524, 562, 583, 51, 67, 67, 197, 204, 302, 309, 313, 435, 454, 594, 671, 69, or 653 of an MLVMS RT domain sequence as described herein (e.g., as listed in Table 6), e.g., an MLVMS_P03355 sequence, e.g., SEQ ID NO: 8070, relative to a wildtype sequence of the RT domain.

105. The gene modifying polypeptide of embodiment 40, wherein the RT domain comprises an RT domain comprising an amino acid sequence of an MLVMS RT domain sequence as described herein (e.g., as listed in Table 6), e.g., an MLVMS_P03355 sequence, e.g., SEQ ID NO: 8070, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

106. The gene modifying polypeptide of embodiment 40, wherein the RT domain comprises an RT domain comprising an amino acid sequence of an AVIRE RT domain sequence as described herein (e.g., as listed in Table 6), e.g., an AVIRE_P03360 sequence, e.g., SEQ ID NO: 8001, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

107. The gene modifying polypeptide of embodiment 40, wherein the RT domain comprises an RT domain comprising an amino acid sequence of an BAEVM RT domain sequence as described herein (e.g., as listed in Table 6), e.g., an BAEVM_P10272 sequence, e.g., SEQ ID NO: 8004, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

108. The gene modifying polypeptide of embodiment 40, wherein the RT domain comprises an RT domain comprising an amino acid sequence of an BLVAU RT domain sequence as described herein (e.g., as listed in Table 6), e.g., an BLVAU_P25059 sequence, e.g., SEQ ID NO: 8007, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

109. The gene modifying polypeptide of embodiment 40, wherein the RT domain comprises an RT domain comprising an amino acid sequence of an BLVJ RT domain sequence as described herein (e.g., as listed in Table 6), e.g., an BLVJ_P03361 sequence, e.g., SEQ ID NO: 8009, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

110. The gene modifying polypeptide of embodiment 40, wherein the RT domain comprises an RT domain comprising an amino acid sequence of an FFV RT domain sequence as described herein (e.g., as listed in Table 6), e.g., an FFV_O93209 sequence, e.g., SEQ ID NO: 8012, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

111. The gene modifying polypeptide of embodiment 40, wherein the RT domain comprises an RT domain comprising an amino acid sequence of an FLV RT domain sequence as described herein (e.g., as listed in Table 6), e.g., an FLV_P10273 sequence, e.g., SEQ ID NO: 8019, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

112. The gene modifying polypeptide of embodiment 40, wherein the RT domain comprises an RT domain comprising an amino acid sequence of an FOAMV RT domain sequence as described herein (e.g., as listed in Table 6), e.g., an FOAMV_P14350

sequence, e.g., SEQ ID NO: 8021, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

113. The gene modifying polypeptide of embodiment 40, wherein the RT domain comprises an RT domain comprising an amino acid sequence of an GALV RT domain sequence as described herein (e.g., as listed in Table 6), e.g., an GALV_P21414 sequence, e.g., SEQ ID NO: 8027, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

114. The gene modifying polypeptide of embodiment 40, wherein the RT domain comprises an RT domain comprising an amino acid sequence of an HTL1A RT domain sequence as described herein (e.g., as listed in Table 6), e.g., an HTL1A_P03362 sequence, e.g., SEQ ID NO: 8030, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

115. The gene modifying polypeptide of embodiment 40, wherein the RT domain comprises an RT domain comprising an amino acid sequence of an HTL1C RT domain sequence as described herein (e.g., as listed in Table 6), e.g., an HTL1C_P14078 sequence, e.g., SEQ ID NO: 8033, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

116. The gene modifying polypeptide of embodiment 40, wherein the RT domain comprises an RT domain comprising an amino acid sequence of an HTL32 RT domain sequence as described herein (e.g., as listed in Table 6), e.g., an HTL32_Q0R5R2 sequence, e.g., SEQ ID NO: 8038, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

117. The gene modifying polypeptide of embodiment 40, wherein the RT domain comprises an RT domain comprising an amino acid sequence of an HTL3P RT domain sequence as described herein (e.g., as listed in Table 6), e.g., an HTL3P_Q4U0X6 sequence, e.g., SEQ ID NO: 8041, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

118. The gene modifying polypeptide of embodiment 40, wherein the RT domain comprises an RT domain comprising an amino acid sequence of an JSRV RT domain sequence as described herein (e.g., as listed in Table 6), e.g., an JSRV_P31623 sequence, e.g., SEQ ID NO: 8045, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

119. The gene modifying polypeptide of embodiment 40, wherein the RT domain comprises an RT domain comprising an amino acid sequence of an KORV RT domain sequence as described herein (e.g., as listed in Table 6), e.g., an KORV_Q9TTC1 sequence, e.g., SEQ ID NO: 8047, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

120. The gene modifying polypeptide of embodiment 40, wherein the RT domain comprises an RT domain comprising an amino acid sequence of an MLVAV RT domain sequence as described herein (e.g., as listed in Table 6), e.g., an MLVAV_P03356 sequence, e.g., SEQ ID NO: 8053, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

121. The gene modifying polypeptide of embodiment 40, wherein the RT domain comprises an RT domain comprising an amino acid sequence of an MLVBM RT domain sequence as described herein (e.g., as listed in Table 6), e.g., an MLVBM_Q7SVK7 sequence, e.g., SEQ ID NO: 8056, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

122. The gene modifying polypeptide of embodiment 40, wherein the RT domain comprises an RT domain comprising an amino acid sequence of an MLVCB RT domain sequence as described herein (e.g., as listed in Table 6), e.g., an MLVCB_P08361 sequence, e.g., SEQ ID NO: 8062, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

123. The gene modifying polypeptide of embodiment 40, wherein the RT domain comprises an RT domain comprising an amino acid sequence of an MLVF5 RT domain sequence as described herein (e.g., as listed in Table 6), e.g., an MLVF5_P26810 sequence, e.g., SEQ ID NO: 8065, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

124. The gene modifying polypeptide of embodiment 40, wherein the RT domain comprises an RT domain comprising an amino acid sequence of an MLVRD RT domain sequence as described herein (e.g., as listed in Table 6), e.g., an MLVRD_P11227 sequence, e.g., SEQ ID NO: 8078, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

125. The gene modifying polypeptide of embodiment 40, wherein the RT domain comprises an RT domain comprising an amino acid sequence of an MMTVB RT domain sequence as described herein (e.g., as listed in Table 6), e.g., an MMTVB_P03365 sequence, e.g., SEQ ID NO: 8080, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

126. The gene modifying polypeptide of embodiment 40, wherein the RT domain comprises an RT domain comprising an amino acid sequence of an MPMV RT domain sequence as described herein (e.g., as listed in Table 6), e.g., an MPMV_P07572 sequence, e.g., SEQ ID NO: 8097, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

127. The gene modifying polypeptide of embodiment 40, wherein the RT domain comprises an RT domain comprising an amino acid sequence of an PERV RT domain sequence as described herein (e.g., as listed in Table 6), e.g., an PERV_Q4VFZ2 sequence, e.g., SEQ ID NO: 8099, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

128. The gene modifying polypeptide of embodiment 40, wherein the RT domain comprises an RT domain comprising an amino acid sequence of an SFV1 RT domain sequence as described herein (e.g., as listed in Table 6), e.g., an SFV1_P23074 sequence, e.g., SEQ ID NO: 8105, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

129. The gene modifying polypeptide of embodiment 40, wherein the RT domain comprises an RT domain comprising an amino acid sequence of an SFV3L RT domain sequence as described herein (e.g., as listed in Table 6), e.g., an SFV3L_P27401

sequence, e.g., SEQ ID NO: 8111, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

130. The gene modifying polypeptide of embodiment 40, wherein the RT domain comprises an RT domain comprising an amino acid sequence of an SFVCP RT domain sequence as described herein (e.g., as listed in Table 6), e.g., an SFVCP_Q87040 sequence, e.g., SEQ ID NO: 8117, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

131. The gene modifying polypeptide of embodiment 40, wherein the RT domain comprises an RT domain comprising an amino acid sequence of an SMRV RT domain sequence as described herein (e.g., as listed in Table 6), e.g., an SMRVH_P03364 sequence, e.g., SEQ ID NO: 8123, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

132. The gene modifying polypeptide of embodiment 40, wherein the RT domain comprises an RT domain comprising an amino acid sequence of an SRV2 RT domain sequence as described herein (e.g., as listed in Table 6), e.g., an SRV2_P51517 sequence, e.g., SEQ ID NO: 8126, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

133. The gene modifying polypeptide of embodiment 40, wherein the RT domain comprises an RT domain comprising an amino acid sequence of an WDSV RT domain sequence as described herein (e.g., as listed in Table 6), e.g., an WDSV_O92815 sequence, e.g., SEQ ID NO: 8128, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

134. The gene modifying polypeptide of embodiment 40, wherein the RT domain comprises an RT domain comprising an amino acid sequence of an WMSV RT domain sequence as described herein (e.g., as listed in Table 6), e.g., an WMSV_P03359 sequence, e.g., SEQ ID NO: 8131, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

135. The gene modifying polypeptide of embodiment 40, wherein the RT domain comprises an RT domain comprising an amino acid sequence of an XMRV6 RT domain sequence as described herein (e.g., as listed in Table 6), e.g., an XMRV6_A1Z651 sequence, e.g., SEQ ID NO: 8134, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

136. The gene modifying polypeptide of any one of embodiments 40-135, wherein the RT domain comprises:

a) the amino acid asparagine (N) at position 200 of SEQ ID NO: 8137 or at a corresponding position in a homologous RT domain;

b) the amino acid tryptophan (W) at position 603 of SEQ ID NO: 8137 or at a corresponding position in a homologous RT domain;

c) the amino acid proline (P) at position 330 of SEQ ID NO: 8137 or at a corresponding position in a homologous RT domain;

d) the amino acid glycine (G) at position 524 of SEQ ID NO: 8137 or at a corresponding position in a homologous RT domain;

e) the amino acid glutamine (Q) at position 562 of SEQ ID NO: 8137 or at a corresponding position in a homologous RT domain;

f) the amino acid asparagine (N) at position 583 of SEQ ID NO: 8137 or at a corresponding position in a homologous RT domain;

g) the amino acid leucine (L) at position 51 of SEQ ID NO: 8137 or at a corresponding position in a homologous RT domain;

h) the amino acid arginine (R) at position 67 of SEQ ID NO: 8137 or at a corresponding position in a homologous RT domain;

i) the amino acid lysine (K) at position 67 of SEQ ID NO: 8137 or at a corresponding position in a homologous RT domain;

j) the amino acid alanine (A) at position 197 of SEQ ID NO: 8137 or at a corresponding position in a homologous RT domain;

k) the amino acid arginine (R) at position 204 of SEQ ID NO: 8137 or at a corresponding position in a homologous RT domain;

l) the amino acid lysine (K) at position 302 of SEQ ID NO: 8137 or at a corresponding position in a homologous RT domain;

m) the amino acid asparagine (N) at position 309 of SEQ ID NO: 8137 or at a corresponding position in a homologous RT domain;

n) the amino acid phenylalanine (F) at position 313 of SEQ ID NO: 8137 or at a corresponding position in a homologous RT domain;

o) the amino acid glycine (G) at position 435 of SEQ ID NO: 8137 or at a corresponding position in a homologous RT domain;

p) the amino acid lysine (K) at position 454 of SEQ ID NO: 8137 or at a corresponding position in a homologous RT domain;

q) the amino acid glutamine (Q) at position 594 of SEQ ID NO: 8137 or at a corresponding position in a homologous RT domain;

r) the amino acid proline (P) at position 671 of SEQ ID NO: 8137 or at a corresponding position in a homologous RT domain;

s) the amino acid lysine (K) at position 69 of SEQ ID NO: 8137 or at a corresponding position in a homologous RT domain; or

t) the amino acid asparagine (N) at position 653 of SEQ ID NO: 8137 or at a corresponding position in a homologous RT domain.

137. The gene modifying polypeptide of embodiment 40, wherein the RT domain has a sequence with at least 90% identity to the RT domain of the reference gene modifying polypeptide.

138. The gene modifying polypeptide of any of the preceding embodiments, wherein the RT domain has a sequence with at least 95% identity to the RT domain of the reference gene modifying polypeptide.

139. The gene modifying polypeptide of any of the preceding embodiments, wherein the RT domain has a sequence with at least 98% identity to the RT domain of the reference gene modifying polypeptide.

140. The gene modifying polypeptide of any of the preceding embodiments, wherein the RT domain has a sequence with at least 99% identity to the RT domain of the reference gene modifying polypeptide.

141. The gene modifying polypeptide of any of the preceding embodiments, wherein the RT domain has a sequence with 100% identity to the RT domain of the reference gene modifying polypeptide.

142. The gene modifying polypeptide of any of the preceding embodiments, wherein the linker has a sequence with at least 90% identity to the linker sequence from the reference gene modifying polypeptide.

143. The gene modifying polypeptide of any of the preceding embodiments, wherein the linker has a sequence with at least 95% identity to the linker sequence from the reference gene modifying polypeptide.

144. The gene modifying polypeptide of any of the preceding embodiments, wherein the linker has a sequence with at least 97% identity to the linker sequence from the reference gene modifying polypeptide.

145. The gene modifying polypeptide of any of the preceding embodiments, wherein the linker has a sequence with 100% identity to the linker sequence from the reference gene modifying polypeptide.

146. The gene modifying polypeptide of any of the preceding embodiments, wherein the linker has an amino acid sequence with at least 80%, 85%, 90%, 95%, 97%, or 100% identity to SEQ ID NO: 11,041.

147. The gene modifying polypeptide of any of the preceding embodiments, wherein the RT domain comprises a mutation as listed in Table 2.

148. The gene modifying polypeptide of any of the preceding embodiments, wherein the RT domain comprises one or more (e.g., 1, 2, 3, 4, 5, or 6) mutations as listed in any single row of Table 2.

149. The gene modifying polypeptide of any of the preceding embodiments, wherein the RT domain comprises all of the mutations listed in any single row of Table 2.

150. The gene modifying polypeptide of any of the preceding embodiments, wherein the Cas domain comprises a sequence of Table 7 or 8, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 98%, or 99% identity thereto.

151. The gene modifying polypeptide of any of the preceding embodiments, wherein the Cas domain comprises the amino acid sequence of a Cas domain comprised in the amino acid sequence of the reference gene modifying polypeptide, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 98%, or 99% identity thereto.

152. The gene modifying polypeptide of any of the preceding embodiments, wherein the Cas domain does not comprise the amino acid sequence of a Cas domain comprised in the amino acid sequence of the reference gene modifying polypeptide, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 98%, or 99% identity thereto.

153. The gene modifying polypeptide of any of the preceding embodiments, wherein the Cas domain is a Cas nickase domain.

154. The gene modifying polypeptide of any of the preceding embodiments, wherein the Cas domain is a Cas9 nickase domain.

155. The gene modifying polypeptide of any of the preceding embodiments, wherein the Cas domain comprises an N863A mutation.

156. The gene modifying polypeptide of any of the preceding embodiments, which comprises an NLS, e.g., wherein the gene modifying polypeptide comprises two NLSs.

157. The gene modifying polypeptide of any of the preceding embodiments, which comprises an NLS N-terminal of the Cas9 domain.

158. The gene modifying polypeptide of any of the preceding embodiments, which comprises an NLS C-terminal of the RT domain.

159. The gene modifying polypeptide of any of the preceding embodiments, which comprises a first NLS which is N-terminal of the Cas9 domain and a second NLS which is C-terminal of the RT domain.

160. The gene modifying polypeptide of any of the preceding embodiments, which 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.

161. The gene modifying polypeptide of any of the preceding embodiments, which 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.

162. The gene modifying polypeptide of any of the preceding embodiments, which comprises a GG amino acid sequence between the Cas domain and the linker.

163. The gene modifying polypeptide of any of the preceding embodiments, which comprises an AG amino acid sequence between the RT domain and the second NLS.

164. The gene modifying polypeptide of any of the preceding embodiments, which comprises a GG amino acid sequence between the linker and the RT domain.

165. The gene modifying polypeptide of any of the preceding embodiments, which produces an increase in converted GFP+ of at least 10%, 20%, 30%, 40%, 50%, 60%, 70%, 75%, 80%, 85%, 90%, 95%, 100%, 125%, 150%, 175%, 200%, 250%, 300%, 400%, 500%, 600%, 700%, 800%, 900%, 1000%, 1500%, 2000%, or 2500% relative to unsorted input cells in an assay of Example 2 using HEK cells and g4 guide RNA.

166. A gene modifying polypeptide comprising:

a Cas domain (e.g., a Cas nickase domain, e.g., a Cas9 nickase domain);

a reverse transcriptase (RT) domain comprising an amino acid sequence of an RT domain provided in any one of SEQ ID NOs: 1-7743, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto; and

a linker disposed between the RT domain and the Cas domain comprising an amino acid sequence of a linker as listed in Table 10, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto,

wherein the amino acid sequences of the RT domain and the linker are provided in the same amino acid sequence of any one of SEQ ID NOs: 1-7743,

which produces an increase in converted GFP+ of at least 10%, 20%, 30%, 40%, 50%, 60%, 70%, 75%, 80%, 85%, 90%, 95%, 100%, 125%, 150%, 175%, 200%, 250%, 300%, 400%, 500%, 600%, 700%, 800%, 900%, 1000%, 1500%, 2000%, or 2500% relative to unsorted input cells in an assay of Example 2 using HEK cells and g4 guide RNA.

167. The gene modifying polypeptide of any of the preceding embodiments, which has an activity that is at least 50%, 60%, 70%, 80%, or 90% of the activity of a reference gene modifying polypeptide comprising, in an N-terminal to C-terminal direction:

a) an NLS and Cas domain sequence of SEQ ID NO: 4000;

b) a linker having the sequence EAAAKGSS (SEQ ID NO: 5152);

c) an RT domain having the sequence of PERV_Q4VFZ2_3mutA_WS; and

d) an NLS sequence of SEQ ID NO: 4001,

in an assay of Example 1 using HEK cells and g4 guide RNA.

168. The gene modifying polypeptide of any of the preceding embodiments, which has an activity that is at least 10%, 20%, 30%, 40%, 50%, 60%, 70%, 75%, 80%, 85%, 90%, 95%, 100%, 125%, 150%, 175%, 200%, 250%, 300%, 400%, 500%, 600%, 700%, 800%, 900%, 1000%, 1500%, 2000%, or 2500% greater than the activity of a reference gene modifying polypeptide comprising a sequence of SEQ ID NO: 4002, e.g., in an assay of Example 1 using HEK cells and g4 guide RNA.

169. A nucleic acid (e.g., DNA or RNA, e.g., mRNA) encoding the gene modifying polypeptide of any of the preceding embodiments.

170. A cell comprising the gene modifying polypeptide of any of embodiments 40-68 or the nucleic acid of embodiment 169.

171. A system comprising:

i) the gene modifying polypeptide of any of embodiments 40-68, and

ii) a template RNA that comprises:

a) a gRNA spacer that is complementary to a portion a target nucleic acid sequence;

b) a gRNA scaffold that binds the Cas domain of the gene modifying polypeptide;

c) a heterologous object sequence; and

d) a primer binding site sequence (PBS sequence).

172. A method for modifying a target nucleic acid in a cell (e.g., a human cell), the method comprising contacting the cell with the system of embodiment 171, or nucleic acid encoding the same, thereby modifying the target nucleic acid.

173. A gene modifying polypeptide comprising:

a Cas domain (e.g., a Cas nickase domain, e.g., a Cas9 nickase domain);

a reverse transcriptase (RT) domain having one or more (e.g., at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20) amino acid substitutions at a residue corresponding to (e.g., at a residue at a homologous position relative to) position 200, 603, 330, 524, 562, 583, 51, 67, 67, 197, 204, 302, 309, 313, 435, 454, 594, 671, 69, or 653 of an MLVMS RT domain sequence as described herein (e.g., as listed in Table 6), e.g., an MLVMS_reference sequence, e.g., SEQ ID NO: 8137 relative to a wildtype sequence of the RT domain, 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 1 as the RT domain, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

174. A gene modifying polypeptide comprising:

a reverse transcriptase (RT) domain of an AVIRE RT, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto;

a Cas nickase domain, wherein the RT domain is C-terminal of the Cas domain; and

a linker disposed between the Cas nickase domain and the RT domain, wherein the linker comprises an amino acid sequence as listed in Table 10, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto.

175. A gene modifying polypeptide comprising:

a reverse transcriptase (RT) domain comprising the RT domain of a reference gene modifying polypeptide having sequence of any one of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 9, 10, 12, 13, 14, 6076, 6143, 6200, 6254, 6274, 6315, 6328, 6337, 6403, 6420, 6440, 6513, 6552, 6613, 6671, 6822, 6840, 6884, 6907, 6970, 7025, 7052, 7078, 7243, 7253, 7318, 7379, 7486, 7524, 7668, 7680, 7720, 1137, 1138, 1139, 1140, 1141, 1142, 1143, 1144, 1145, 1146, 1147, 1148, 1149, 1150, 1151, 1152, 1153, 1154, 1155, 1156, 1157, 1158, 1159, 1160, 1161, 1162, 1163, 1164, 1165, 1166, 1167, 6015, 6029, 6045, 6077, 6129, 6144, 6164, 6201, 6227, 6244, 6250, 6264, 6289, 6304, 6316, 6384, 6421, 6441, 6492, 6514, 6530, 6569, 6584, 6621, 6651, 6659, 6683, 6703, 6727, 6732, 6745, 6755, 6784, 6817, 6823, 6841, 6871, 6885, 6898, 6908, 6933, 6971, 7009, 7018, 7045, 7053, 7068, 7079, 7096, 7104, 7122, 7151, 7163, 7181, 7244, 7273, 7319, 7336, 7380, 7402, 7462, 7487, 7525, 7569, 7626, 7689, 7707, 7721, 1371, 1372, 1373, 1374, 1375, 1376, 1377, 1378, 1379, 1380, 1381, 1382, 1383, 1384, 1385, 1386, 1387, 1388, 1389, 1390, 1391, 1392, 1393, 1394, 1395, 1396, 1397, 1398, 1399, 1400, 1401, 1402, 1403, 1404, 1405, 1406, 1407, 1408, 1409, 1410, 1411, 1412, 1413, 1414, 1415, 1416, 1417, 1418, 1419, 1420, 1421, 1422, 1423, 1424, 1425, 1426, 1427, 1428, 1429, 1430, 1431, 1432, 1433, 1434, 1435, 1436, 1437, 1439, 1440, 1441, 1442, 1443, 1444, 1445, 1446, 1447, 6001, 6030, 6078, 6108, 6130, 6165, 6265, 6275, 6305, 6329, 6370, 6385, 6404, 6531, 6585, 6622, 6652, 6733, 6756, 6765, 6798, 6824, 6972, 7046, 7054, 7069, 7080, 7105, 7123, 7143, 7152, 7204, 7320, 7351, 7381, 7403, 7438, 7488, 7500, 7526, 7588, 7612, 7627 or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto;

a Cas nickase domain, wherein the RT domain is C-terminal of the Cas domain; and

a linker disposed between the Cas nickase domain and the RT domain, wherein the linker comprises the linker of said reference gene modifying polypeptide, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

176. A gene modifying polypeptide comprising:

a reverse transcriptase (RT) domain having the sequence of SEQ ID NO: 8001, 8002, or 8003, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto;

a Cas nickase domain, wherein the RT domain is C-terminal of the Cas nickase domain; and

a linker disposed between the RT domain and the Cas nickase domain, wherein the linker comprises an amino acid sequence of the linker of any of SEQ ID NOS: a reference gene modifying polypeptide having sequence of any one of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 9, 10, 12, 13, 14, 6076, 6143, 6200, 6254, 6274, 6315, 6328, 6337, 6403, 6420, 6440, 6513, 6552, 6613, 6671, 6822, 6840, 6884, 6907, 6970, 7025, 7052, 7078, 7243, 7253, 7318, 7379, 7486, 7524, 7668, 7680, 7720, 1137, 1138, 1139, 1140, 1141, 1142, 1143, 1144, 1145, 1146, 1147, 1148, 1149, 1150, 1151, 1152, 1153, 1154, 1155, 1156, 1157, 1158, 1159, 1160, 1161, 1162, 1163, 1164, 1165, 1166, 1167, 6015, 6029, 6045, 6077, 6129, 6144, 6164, 6201, 6227, 6244, 6250, 6264, 6289, 6304, 6316, 6384, 6421, 6441, 6492, 6514, 6530, 6569, 6584, 6621, 6651, 6659, 6683, 6703, 6727, 6732, 6745, 6755, 6784, 6817, 6823, 6841, 6871, 6885, 6898, 6908, 6933, 6971, 7009, 7018, 7045, 7053, 7068, 7079, 7096, 7104, 7122, 7151, 7163, 7181, 7244, 7273, 7319, 7336, 7380, 7402, 7462, 7487, 7525, 7569, 7626, 7689, 7707, 7721, 1371, 1372, 1373, 1374, 1375, 1376, 1377, 1378, 1379, 1380, 1381, 1382, 1383, 1384, 1385, 1386, 1387, 1388, 1389, 1390, 1391, 1392, 1393, 1394, 1395, 1396, 1397, 1398, 1399, 1400, 1401, 1402, 1403, 1404, 1405, 1406, 1407, 1408, 1409, 1410, 1411, 1412, 1413, 1414, 1415, 1416, 1417, 1418, 1419, 1420, 1421, 1422, 1423, 1424, 1425, 1426, 1427, 1428, 1429, 1430, 1431, 1432, 1433, 1434, 1435, 1436, 1437, 1439, 1440, 1441, 1442, 1443, 1444, 1445, 1446, 1447, 6001, 6030, 6078, 6108, 6130, 6165, 6265, 6275, 6305, 6329, 6370, 6385, 6404, 6531, 6585, 6622, 6652, 6733, 6756, 6765, 6798, 6824, 6972, 7046, 7054, 7069, 7080, 7105, 7123, 7143, 7152, 7204, 7320, 7351, 7381, 7403, 7438, 7488, 7500, 7526, 7588, 7612, 7627, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

177. The gene modifying polypeptide of any of embodiments 174-176, wherein the RT domain comprises a mutation at one or more of positions 8, 51, 67, 69, 197, 200, 204, 302, 306, 309, 313, 330, 436, 455, 526, 564, 585, 596, 605, 655, 673 relative to a reference RT domain having sequence of SEQ ID NO:8001.

178. The gene modifying polypeptide of any of embodiments 174-177, wherein the RT domain comprises one or more of the following mutations: Q51L, T67R, E67K, E69K, T197A, D200N, N204R, E302K, Y309N, W313F, G330P, T436G, N455K, D526G, E564Q, D585N, H596Q, L605W, D655N, L673P

179. The gene modifying polypeptide of embodiment 178, wherein the RT domain comprises the following mutations: (a) D200N, G330P, and L605W or (b) D200N, G330P, L605W, T306K, and W313F.

180. The gene modifying polypeptide of any of embodiments 174-179, said polypeptide comprising a linker having a sequence of any one of SEQ ID NO: 11,041 - 11,050.

181. A gene modifying polypeptide comprising:

a reverse transcriptase (RT) domain having the sequence of SEQ ID NO: 8,003, or a sequence having at least 95% identity thereto;

a Cas nickase domain, wherein the RT domain is C-terminal of the Cas nickase domain; and

a linker disposed between the RT domain and the Cas nickase domain, wherein the linker comprises an amino acid sequence according to SEQ ID NO: 5217 or 15,401.

182. A gene modifying polypeptide comprising:

a reverse transcriptase (RT) domain having the sequence of SEQ ID NO: 8,020, or a sequence having at least 95% identity thereto;

a Cas nickase domain, wherein the RT domain is C-terminal of the Cas nickase domain; and

a linker disposed between the RT domain and the Cas nickase domain, wherein the linker comprises an amino acid sequence according to SEQ ID NO: 5217 or 15,402.

183. A gene modifying polypeptide comprising:

a reverse transcriptase (RT) domain having the sequence of SEQ ID NO: 8,074, or a sequence having at least 95% identity thereto;

a Cas nickase domain, wherein the RT domain is C-terminal of the Cas nickase domain; and

a linker disposed between the RT domain and the Cas nickase domain, wherein the linker comprises an amino acid sequence according to SEQ ID NO: 15,403.

184. A gene modifying polypeptide comprising:

a reverse transcriptase (RT) domain having the sequence of SEQ ID NO: 8,113, or a sequence having at least 95% identity thereto;

a Cas nickase domain, wherein the RT domain is C-terminal of the Cas nickase domain; and

a linker disposed between the RT domain and the Cas nickase domain, wherein the linker comprises an amino acid sequence according to SEQ ID NO: 15,404.

185. A gene modifying polypeptide comprising:

a reverse transcriptase (RT) domain comprising the RT domain of a reference gene modifying polypeptide having the sequence of any one of SEQ ID NOs: 1-7743,; and

a Cas nickase domain, wherein the RT domain is C-terminal of the Cas nickase domain; and

a linker disposed between the RT domain and the Cas nickase domain, wherein the linker comprises the linker of said reference gene modifying polypeptide.

186. The gene modifying polypeptide of any of embodiments 174-185, which comprises a nuclear localization signal (NLS).

187. The gene modifying polypeptide of any of embodiments 174-186, which comprises a first NLS which is N-terminal of the Cas nickase domain.

188. The gene modifying polypeptide of any of embodiments 174-187, which comprises an NLS which is C-terminal of the RT domain.

189. The gene modifying polypeptide of any of embodiments 174-188, which comprises a first NLS which is N-terminal of the Cas nickase domain and a second NLS which is C-terminal of the RT domain.

190. The gene modifying polypeptide of any of embodiments 174-189, which comprises a first NLS which is N-terminal of the Cas nickase domain, wherein the first NLS comprises an amino acid sequence of PAAKRVKLD (SEQ ID NO: 11,095).

191. The gene modifying polypeptide of any of embodiments 174-190, which comprises an NLS which is C-terminal of the RT domain and has an amino acid sequence of KRTADGSEFE (SEQ ID NO: 4650).

192. The gene modifying polypeptide of any of embodiments 174-191, which comprises an NLS which is C-terminal of the RT domain and has an amino acid sequence of KRTADGSEFESPKKKAKVE (SEQ ID NO: 4651).

193. The gene modifying polypeptide of any of embodiments 174-192, which comprises a sequence of SEQ ID NO: 4000 which comprises the first NLS and the Cas nickase domain.

194. The gene modifying polypeptide of any of embodiments 174-193, which comprises a sequence of SEQ ID NO: 4001 which comprises the second NLS.

195. The gene modifying polypeptide of any of embodiments 174-194, which comprises a GG amino acid sequence between the Cas nickase domain and the linker.

196. The gene modifying polypeptide of any of embodiments 174-195, which comprises an AG amino acid sequence between the RT domain and the second NLS.

197. The gene modifying polypeptide of any of embodiments 174-196, which comprises a GG amino acid sequence between the linker and the RT domain.

198. The gene modifying polypeptide of any of embodiments 174-197, wherein the Cas nickase domain comprises a Cas9 nickase domain.

199. The gene modifying polypeptide of any of embodiments 174-198, wherein the Cas nickase domain comprises an N863A mutation.

200. The gene modifying polypeptide of any of embodiments 174-199, wherein the Cas nickase comprises a sequence of SEQ ID NO: 11,096.

201. The gene modifying polypeptide of any of embodiments 174-200, wherein the Cas nickase comprises a sequence of any of SEQ ID NO: 9,001-9,037, 11,096, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

202. The gene modifying polypeptide of any of embodiments 174-201, which comprises a methionine at the N-terminal position of the RT domain.

203. The gene modifying polypeptide of any of embodiments 174-202, which does not comprises a methionine at the N-terminal position of the RT domain.

204. The gene modifying polypeptide of any of embodiments 174-203, which comprises an amino acid sequence according to any of SEQ ID NOs: 1372, 1373, or 1410 or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto.

205. The gene modifying polypeptide of any of embodiments 174-204, which comprises an amino acid sequence according to SEQ ID NO: 2784 or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto.

206. The gene modifying polypeptide of any of embodiments 174-205, which comprises an amino acid sequence according to SEQ ID NO: 647 or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto.

207. The gene modifying polypeptide of any of embodiments 174-206, which comprises an amino acid sequence according to SEQ ID NO: 1197 or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto.

208. A nucleic acid molecule encoding the gene modifying polypeptide of any of embodiments 174-207.

209. The nucleic acid molecule of embodiment 208, which comprises RNA.

210. The nucleic acid molecule of embodiment 209, which comprises mRNA.

211. A cell comprising the gene modifying polypeptide of any of embodiments 174-207.

212. A cell comprising the nucleic acid molecule of any of embodiments 208-210.

213. A system comprising:

i) the gene modifying polypeptide of any of embodiments 174-207, or a nucleic acid molecule encoding the gene modifying polypeptide, and

ii) a template RNA that comprises:

a) a gRNA spacer that is complementary to a portion a target nucleic acid sequence;

b) a gRNA scaffold that binds the Cas nickase domain of the gene modifying polypeptide;

c) a heterologous object sequence; and

d) a primer binding site sequence.

214. A lipid nanoparticle formulation comprising the gene modifying polypeptide of any of embodiments 174-207, the nucleic acid of any of embodiments 208-210, or the system of embodiment 213.

215. A method for modifying a target nucleic acid molecule in a cell, the method comprising contacting the cell with the system of embodiment 213, thereby modifying the target nucleic acid molecule.

216. A method of using the gene modifying polypeptide of any of embodiments 174-207, the nucleic acid of any of embodiments 208-210, or the system of embodiment 213, to modify a target genome by target-primed reverse transcription, the method comprising contacting the target genome with the gene modifying polypeptide, nucleic acid, or system, thereby modifying the target nucleic acid molecule.

In one aspect, the disclosure relates to a system for modifying DNA, 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 a human gene, (ii) a gRNA scaffold that binds the polypeptide, (iii) a heterologous object sequence comprising a mutation region, 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.

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.

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.

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.

FIGS. 2A-2B provide schematics of a gene modifying polypeptide candidate for a screening library and a description of the screening methodology. FIG. 2A is a schematic of the gene modifying polypeptide candidate, a fusion polypeptide comprising a nuclear localization signal (NLS), a *S. pyogenes* (Spy) Cas9 nickase containing an N863A mutation (Cas9n), a peptide linker selected from Table 10 (Linker), and a reverse transcriptase domain of retroviral origin selected from Table 6 (RT). FIG. 2B provides a schematic of the screen conducted with the pooled elements from the library of gene modifying polypeptide candidates.

FIG. 3 provides a schematic of an assay for detecting gene editing, including the target reporter gene (BFP) in the test cell line and the three outcomes in the assay depending on whether there is no edit, an imperfect edit, or a perfect edit of a C to a T, resulting in expression and detecting of GFP rather than BFP.

FIGS. 4A-4C are a series of graphs depicting editing activity of two exemplary gene modifying polypeptides, MLVMS and MMTVB. FIG. 4A shows the editing activity of the two exemplary gene modifying polypeptides as assessed by percent of

total cells converted to GFP-positive. FIG. 4B shows the editing activity of the two exemplary gene modifying polypeptides in the screen of Examples 2 and 3. FIG. 4C shows violin plots of the editing activities of all the exemplary gene modifying polypeptides comprising RT domains of the MLVMS RT family and of the MMTVB RT family.

FIGS. 5A-5G provide violin plots showing enrichment of exemplary gene modifying polypeptides grouped by RT family. FIG. 5A shows violin plots of enrichment after HEK293T cells were treated with the gene modifying polypeptide and exemplary template RNA g4. FIG. 5B shows violin plots of enrichment after U2OS cells were treated with the gene modifying polypeptide and exemplary template RNA g4. FIG. 5C shows violin plots of enrichment after HEK293T cells were treated with the gene modifying polypeptide and exemplary template RNA g10. FIG. 5D shows violin plots of enrichment after U2OS cells were treated with the gene modifying polypeptide and exemplary template RNA g10. FIG. 5E shows data for an additional replicate of the data presented in FIG. 5A, where HEK293T cells were treated with the gene modifying polypeptide and exemplary template RNA g4. FIG. 5F shows data for a further additional replicate of the data presented in FIG. 5A, where HEK293T cells were treated with the gene modifying polypeptide and exemplary template RNA g4. FIG. 5G shows violin plots combining the data of FIGs. 5A, 5E, and 5F, where HEK293T cells were treated with the gene modifying polypeptide and exemplary template RNA g4.

FIG. 6 shows a graph of enrichment of exemplary gene modifying polypeptides when editing activity was tested in HEK293T cells (X-axis) or in U2OS cells (Y-axis). A linear regression line is plotted based upon the scatter plot data.

FIG. 7 shows a graph of enrichment of exemplary gene modifying polypeptides when editing activity was tested with exemplary template RNA g4 (X-axis) or with exemplary template RNA g10 (Y-axis). A linear regression line is plotted based upon the scatter plot data.

FIGS. 8A-8F provide violin plots showing enrichment of exemplary gene modifying polypeptides grouped by RT family (FIG. 8A MLVAV, FIG. 8B MLVBM, FIG. 8C BAEVM, FIG. 8D FLV, FIG. 8E, FOAMV, FIG. 8F GALV), where the wild-type RT family gene modifying polypeptide is given at left, followed at right by gene modifying polypeptides comprising an increasing number of substitution mutations.

FIGS. 9A-9H provide violin plots showing enrichment of exemplary gene modifying polypeptides grouped by RT family (FIG. 9A KORV, FIG. 9B AVIRE, FIG. 9C MLVCB, FIG. 9D MLVFF, FIG. 9E MLVMS, FIG. 9F SFV3L, FIG. 9G WMSV, FIG. 9H XMRV6), where the wild-type RT family gene modifying polypeptide is given at left, followed at right by gene modifying polypeptides comprising an increasing number of substitution mutations. For KORV and SFV3L RT families, variants deleting/disabling the protease domain of the RT domain were also evaluated.

FIGS. 10A-10C provide violin plots showing enrichment of exemplary gene modifying polypeptides grouped by RT family (FIG. 10A PERV, FIG. 10B SFV1, FIG. 10C FFV), where the wild-type RT family gene modifying polypeptide is given at left, followed at right by gene modifying polypeptides comprising an increasing number of substitution mutations. For SFV1 and FFV RT families, variants deleting/disabling the protease domain of the RT domain were also evaluated.

FIG. 11 provides box and whisker graphs of enrichment of a selection of exemplary gene modifying polypeptides grouped by linker, where the square dotted line indicates the average enrichment of gene modifying polypeptides comprising the top performing linker and the dashed dotted lines indicate the standard error of the mean around said average enrichment. Figure discloses SEQ ID NOS 5217, 5130, 5006, 5129, 5128, 5124, 5112, 5220, 5136, 5219, 5118, 5143-5144, 5116, 5114-5115, 5117 and 5138, respectively, in order of appearance.

FIGS. 12A-12D show graphs of editing activity of exemplary gene modifying polypeptides when editing is targeted to a genomic landing pad BFP gene in U2OS cells (FIG. 12A), when editing is targeted to HEK3 in U2OS cells (FIG. 12B), when editing is targeted to murine Fah in primary murine hepatocytes (FIG. 12C), and when editing is targeted to murine Fah in the liver of Fah5981SB model mice (FIG. 12D).

FIG. 13 shows a graph of enrichment of a selection of exemplary gene modifying polypeptides after being provided to cells as a plasmid (DNA) or as mRNA.

FIG. 14 is a graph showing the Z-scores of a library of gene modifying polypeptide candidates in each of three conditions.

FIG. 15 is a diagram showing a workflow for arrayed screening of gene modifying polypeptides using flow cytometry.

FIG. 16 is a series of graphs showing the percentage of cells undergoing to a successful rewriting event and exhibiting GFP fluorescence after introduction of a gene modifying polypeptide and a plasmid according to the workflow shown in FIG. 15.

FIG. 17 is a series of graphs showing the result of testing of arrayed lead candidates compared to the results from screening pooled RT candidates.

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.

A "genomic safe harbor site" (GSH site) is a site in a host genome that is able to accommodate the integration of new genetic material, e.g., such that the inserted genetic element does not cause significant alterations of the host genome posing a risk to the host cell or organism. A GSH site generally meets 1, 2, 3, 4, 5, 6, 7, 8 or 9 of the following criteria: (i) is located >300kb from a cancer-related gene; (ii) is >300kb from a miRNA/other functional small RNA; (iii) is >50kb from a 5´ gene end; (iv) is >50kb from a replication origin; (v) is >50kb away from any ultraconservered element; (vi) has low transcriptional activity (i.e. no mRNA +/- 25 kb); (vii) is not in a copy number variable region; (viii) is in open chromatin; and/or (ix) is unique, with 1 copy in the human genome. Examples of GSH sites in the human genome that meet some or all of these criteria include (i) the adeno-associated virus site 1 (AAVS1), a naturally occurring site of integration of AAV virus on chromosome 19; (ii) the chemokine (C-C motif) receptor 5 (CCR5) gene, a chemokine receptor gene known as an HIV-1 coreceptor; (iii) the human ortholog of the mouse Rosa26 locus; (iv) the ribosomal DNA ("rDNA") locus. Additional GSH sites are known and described, e.g., in Pellenz et al. epub August 20, 2018 (https://doi.org/10.1101/396390).

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 a 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:," "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, *infra*), backbones (see, for example, Table 14, *infra*), and modified caps (see, for example, Table 15, *infra*). 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.

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 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, a deletion, an insertion, e.g., a coding sequence, a regulatory sequence, or a gene expression unit.

The disclosure also provides methods for treating disease 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 disease 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′, GTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGGACCGAG TCGGTCC (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) comprises nCAS9, e.g., comprising the 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 function 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 an aspect, the disclosure provides a gene modifying polypeptide comprising:

a DNA binding domain (DBD) that binds to a target nucleic acid sequence,

the RT domain of an AVIRE RT, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto, and

a linker disposed between the DBD and the RT domain (e.g., a linker comprising an amino acid sequence as listed in Table 10, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto);

wherein the DBD is heterologous to the RT domain (e.g., a Cas domain, e.g., a Cas nickase domain, e.g., a Cas9 nickase domain); optionally wherein the RT domain is C-terminal of the Cas domain.

In an aspect, the disclosure provides a gene modifying polypeptide comprising:

a DNA binding domain (DBD) that binds to a target nucleic acid sequence,

the RT domain of an BAEVM RT, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto, and

a linker disposed between the DBD and the RT domain (e.g., a linker comprising an amino acid sequence as listed in Table 10, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto);

wherein the DBD is heterologous to the RT domain (e.g., a Cas domain, e.g., a Cas nickase domain, e.g., a Cas9 nickase domain); optionally wherein the RT domain is C-terminal of the Cas domain.

In an aspect, the disclosure provides a gene modifying polypeptide comprising:

a DNA binding domain (DBD) that binds to a target nucleic acid sequence,

the RT domain of an FFV RT, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto, and

a linker disposed between the DBD and the RT domain (e.g., a linker comprising an amino acid sequence as listed in Table 10, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto);

wherein the DBD is heterologous to the RT domain (e.g., a Cas domain, e.g., a Cas nickase domain, e.g., a Cas9 nickase domain); optionally wherein the RT domain is C-terminal of the Cas domain.

In an aspect, the disclosure provides a gene modifying polypeptide comprising:

a DNA binding domain (DBD) that binds to a target nucleic acid sequence,

the RT domain of an FLV RT, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto, and

a linker disposed between the DBD and the RT domain (e.g., a linker comprising an amino acid sequence as listed in Table 10, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto);

wherein the DBD is heterologous to the RT domain (e.g., a Cas domain, e.g., a Cas nickase domain, e.g., a Cas9 nickase domain); optionally wherein the RT domain is C-terminal of the Cas domain.

In an aspect, the disclosure provides a gene modifying polypeptide comprising:

a DNA binding domain (DBD) that binds to a target nucleic acid sequence,

the RT domain of an FOAMV RT, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto, and

a linker disposed between the DBD and the RT domain (e.g., a linker comprising an amino acid sequence as listed in Table 10, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto);

wherein the DBD is heterologous to the RT domain (e.g., a Cas domain, e.g., a Cas nickase domain, e.g., a Cas9 nickase domain); optionally wherein the RT domain is C-terminal of the Cas domain.

In an aspect, the disclosure provides a gene modifying polypeptide comprising:

a DNA binding domain (DBD) that binds to a target nucleic acid sequence,

the RT domain of an GALV RT, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto, and

a linker disposed between the DBD and the RT domain (e.g., a linker comprising an amino acid sequence as listed in Table 10, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto);

wherein the DBD is heterologous to the RT domain (e.g., a Cas domain, e.g., a Cas nickase domain, e.g., a Cas9 nickase domain); optionally wherein the RT domain is C-terminal of the Cas domain.

In an aspect, the disclosure provides a gene modifying polypeptide comprising:

a DNA binding domain (DBD) that binds to a target nucleic acid sequence,

the RT domain of an KORV RT, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto, and

a linker disposed between the DBD and the RT domain (e.g., a linker comprising an amino acid sequence as listed in Table 10, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto);

wherein the DBD is heterologous to the RT domain (e.g., a Cas domain, e.g., a Cas nickase domain, e.g., a Cas9 nickase domain); optionally wherein the RT domain is C-terminal of the Cas domain.

In an aspect, the disclosure provides a gene modifying polypeptide comprising:

a DNA binding domain (DBD) that binds to a target nucleic acid sequence,

the RT domain of an MLVAV RT, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto, and

a linker disposed between the DBD and the RT domain (e.g., a linker comprising an amino acid sequence as listed in Table 10, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto);

wherein the DBD is heterologous to the RT domain (e.g., a Cas domain, e.g., a Cas nickase domain, e.g., a Cas9 nickase domain); optionally wherein the RT domain is C-terminal of the Cas domain.

In an aspect, the disclosure provides a gene modifying polypeptide comprising:

a DNA binding domain (DBD) that binds to a target nucleic acid sequence,

the RT domain of an MLVBM RT, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto, and

a linker disposed between the DBD and the RT domain (e.g., a linker comprising an amino acid sequence as listed in Table 10, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto);

wherein the DBD is heterologous to the RT domain (e.g., a Cas domain, e.g., a Cas nickase domain, e.g., a Cas9 nickase domain); optionally wherein the RT domain is C-terminal of the Cas domain.

In an aspect, the disclosure provides a gene modifying polypeptide comprising:

a DNA binding domain (DBD) that binds to a target nucleic acid sequence,

the RT domain of an MLVCB RT, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto, and

a linker disposed between the DBD and the RT domain (e.g., a linker comprising an amino acid sequence as listed in Table 10, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto);

wherein the DBD is heterologous to the RT domain (e.g., a Cas domain, e.g., a Cas nickase domain, e.g., a Cas9 nickase domain); optionally wherein the RT domain is C-terminal of the Cas domain.

In an aspect, the disclosure provides a gene modifying polypeptide comprising:

a DNA binding domain (DBD) that binds to a target nucleic acid sequence,

the RT domain of an MLVFF RT, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto, and

a linker disposed between the DBD and the RT domain (e.g., a linker comprising an amino acid sequence as listed in Table 10, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto);

wherein the DBD is heterologous to the RT domain (e.g., a Cas domain, e.g., a Cas nickase domain, e.g., a Cas9 nickase domain); optionally wherein the RT domain is C-terminal of the Cas domain.

In an aspect, the disclosure provides a gene modifying polypeptide comprising:

a DNA binding domain (DBD) that binds to a target nucleic acid sequence,

the RT domain of an MLVMS RT, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto, and

a linker disposed between the DBD and the RT domain (e.g., a linker comprising an amino acid sequence as listed in Table 10, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto);

wherein the DBD is heterologous to the RT domain (e.g., a Cas domain, e.g., a Cas nickase domain, e.g., a Cas9 nickase domain); optionally wherein the RT domain is C-terminal of the Cas domain.

In an aspect, the disclosure provides a gene modifying polypeptide comprising:

a DNA binding domain (DBD) that binds to a target nucleic acid sequence,

the RT domain of an PERV RT, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto, and

a linker disposed between the DBD and the RT domain (e.g., a linker comprising an amino acid sequence as listed in Table 10, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto);

wherein the DBD is heterologous to the RT domain (e.g., a Cas domain, e.g., a Cas nickase domain, e.g., a Cas9 nickase domain); optionally wherein the RT domain is C-terminal of the Cas domain.

In an aspect, the disclosure provides a gene modifying polypeptide comprising:

a DNA binding domain (DBD) that binds to a target nucleic acid sequence,

the RT domain of an SFV1 RT, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto, and

a linker disposed between the DBD and the RT domain (e.g., a linker comprising an amino acid sequence as listed in Table 10, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto);

wherein the DBD is heterologous to the RT domain (e.g., a Cas domain, e.g., a Cas nickase domain, e.g., a Cas9 nickase domain); optionally wherein the RT domain is C-terminal of the Cas domain.

In an aspect, the disclosure provides a gene modifying polypeptide comprising:

a DNA binding domain (DBD) that binds to a target nucleic acid sequence,

the RT domain of an SFV3L RT, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto, and

a linker disposed between the DBD and the RT domain (e.g., a linker comprising an amino acid sequence as listed in Table 10, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto);

wherein the DBD is heterologous to the RT domain (e.g., a Cas domain, e.g., a Cas nickase domain, e.g., a Cas9 nickase domain); optionally wherein the RT domain is C-terminal of the Cas domain.

In an aspect, the disclosure provides a gene modifying polypeptide comprising:

a DNA binding domain (DBD) that binds to a target nucleic acid sequence,

the RT domain of an WMSV RT, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto, and

a linker disposed between the DBD and the RT domain (e.g., a linker comprising an amino acid sequence as listed in Table 10, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto);

wherein the DBD is heterologous to the RT domain (e.g., a Cas domain, e.g., a Cas nickase domain, e.g., a Cas9 nickase domain); optionally wherein the RT domain is C-terminal of the Cas domain.

In an aspect, the disclosure provides a gene modifying polypeptide comprising:

a DNA binding domain (DBD) that binds to a target nucleic acid sequence,

the RT domain of an XMRV6 RT, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto, and

a linker disposed between the DBD and the RT domain (e.g., a linker comprising an amino acid sequence as listed in Table 10, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto);

wherein the DBD is heterologous to the RT domain (e.g., a Cas domain, e.g., a Cas nickase domain, e.g., a Cas9 nickase domain); optionally wherein the RT domain is C-terminal of the Cas domain.

In an aspect, the disclosure provides a gene modifying polypeptide comprising:

a DNA binding domain (DBD) that binds to a target nucleic acid sequence,

the RT domain of an BLVAU RT, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto, and

a linker disposed between the DBD and the RT domain (e.g., a linker comprising an amino acid sequence as listed in Table 10, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto);

wherein the DBD is heterologous to the RT domain (e.g., a Cas domain, e.g., a Cas nickase domain, e.g., a Cas9 nickase domain); optionally wherein the RT domain is C-terminal of the Cas domain.

In an aspect, the disclosure provides a gene modifying polypeptide comprising:

a DNA binding domain (DBD) that binds to a target nucleic acid sequence,

the RT domain of an BLVJ RT, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto, and

a linker disposed between the DBD and the RT domain (e.g., a linker comprising an amino acid sequence as listed in Table 10, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto);

wherein the DBD is heterologous to the RT domain (e.g., a Cas domain, e.g., a Cas nickase domain, e.g., a Cas9 nickase domain); optionally wherein the RT domain is C-terminal of the Cas domain.

In an aspect, the disclosure provides a gene modifying polypeptide comprising:

a DNA binding domain (DBD) that binds to a target nucleic acid sequence,

the RT domain of an HTL1A RT, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto, and

a linker disposed between the DBD and the RT domain (e.g., a linker comprising an amino acid sequence as listed in Table 10, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto);

wherein the DBD is heterologous to the RT domain (e.g., a Cas domain, e.g., a Cas nickase domain, e.g., a Cas9 nickase domain); optionally wherein the RT domain is C-terminal of the Cas domain.

In an aspect, the disclosure provides a gene modifying polypeptide comprising:

a DNA binding domain (DBD) that binds to a target nucleic acid sequence,

the RT domain of an HTL1C RT, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto, and

a linker disposed between the DBD and the RT domain (e.g., a linker comprising an amino acid sequence as listed in Table 10, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto);

wherein the DBD is heterologous to the RT domain (e.g., a Cas domain, e.g., a Cas nickase domain, e.g., a Cas9 nickase domain); optionally wherein the RT domain is C-terminal of the Cas domain.

In an aspect, the disclosure provides a gene modifying polypeptide comprising:

a DNA binding domain (DBD) that binds to a target nucleic acid sequence,

the RT domain of an HTL1L RT, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto, and

a linker disposed between the DBD and the RT domain (e.g., a linker comprising an amino acid sequence as listed in Table 10, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto);

wherein the DBD is heterologous to the RT domain (e.g., a Cas domain, e.g., a Cas nickase domain, e.g., a Cas9 nickase domain); optionally wherein the RT domain is C-terminal of the Cas domain.

In an aspect, the disclosure provides a gene modifying polypeptide comprising:

a DNA binding domain (DBD) that binds to a target nucleic acid sequence,

the RT domain of an HTL32 RT, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto, and

a linker disposed between the DBD and the RT domain (e.g., a linker comprising an amino acid sequence as listed in Table 10, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto);

wherein the DBD is heterologous to the RT domain (e.g., a Cas domain, e.g., a Cas nickase domain, e.g., a Cas9 nickase domain); optionally wherein the RT domain is C-terminal of the Cas domain.

In an aspect, the disclosure provides a gene modifying polypeptide comprising:

a DNA binding domain (DBD) that binds to a target nucleic acid sequence,

the RT domain of an HTL3P RT, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto, and

a linker disposed between the DBD and the RT domain (e.g., a linker comprising an amino acid sequence as listed in Table 10, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto);

wherein the DBD is heterologous to the RT domain (e.g., a Cas domain, e.g., a Cas nickase domain, e.g., a Cas9 nickase domain); optionally wherein the RT domain is C-terminal of the Cas domain.

In an aspect, the disclosure provides a gene modifying polypeptide comprising:

a DNA binding domain (DBD) that binds to a target nucleic acid sequence,

the RT domain of an HTLV2 RT, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto, and

a linker disposed between the DBD and the RT domain (e.g., a linker comprising an amino acid sequence as listed in Table 10, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto);

wherein the DBD is heterologous to the RT domain (e.g., a Cas domain, e.g., a Cas nickase domain, e.g., a Cas9 nickase domain); optionally wherein the RT domain is C-terminal of the Cas domain.

In an aspect, the disclosure provides a gene modifying polypeptide comprising:

a DNA binding domain (DBD) that binds to a target nucleic acid sequence,

the RT domain of an JSRV RT, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto, and

a linker disposed between the DBD and the RT domain (e.g., a linker comprising an amino acid sequence as listed in Table 10, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto);

wherein the DBD is heterologous to the RT domain (e.g., a Cas domain, e.g., a Cas nickase domain, e.g., a Cas9 nickase domain); optionally wherein the RT domain is C-terminal of the Cas domain.

In an aspect, the disclosure provides a gene modifying polypeptide comprising:

a DNA binding domain (DBD) that binds to a target nucleic acid sequence,

the RT domain of an MLVF5 RT, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto, and

a linker disposed between the DBD and the RT domain (e.g., a linker comprising an amino acid sequence as listed in Table 10, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto);

wherein the DBD is heterologous to the RT domain (e.g., a Cas domain, e.g., a Cas nickase domain, e.g., a Cas9 nickase domain); optionally wherein the RT domain is C-terminal of the Cas domain.

In an aspect, the disclosure provides a gene modifying polypeptide comprising:

a DNA binding domain (DBD) that binds to a target nucleic acid sequence,

the RT domain of an MLVRD RT, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto, and

a linker disposed between the DBD and the RT domain (e.g., a linker comprising an amino acid sequence as listed in Table 10, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto);

wherein the DBD is heterologous to the RT domain (e.g., a Cas domain, e.g., a Cas nickase domain, e.g., a Cas9 nickase domain); optionally wherein the RT domain is C-terminal of the Cas domain.

In an aspect, the disclosure provides a gene modifying polypeptide comprising:

a DNA binding domain (DBD) that binds to a target nucleic acid sequence,

the RT domain of an MMTVB RT, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto, and

a linker disposed between the DBD and the RT domain (e.g., a linker comprising an amino acid sequence as listed in Table 10, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto);

wherein the DBD is heterologous to the RT domain (e.g., a Cas domain, e.g., a Cas nickase domain, e.g., a Cas9 nickase domain); optionally wherein the RT domain is C-terminal of the Cas domain.

In an aspect, the disclosure provides a gene modifying polypeptide comprising:

a DNA binding domain (DBD) that binds to a target nucleic acid sequence,

the RT domain of an MPMV RT, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto, and

a linker disposed between the DBD and the RT domain (e.g., a linker comprising an amino acid sequence as listed in Table 10, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto);

wherein the DBD is heterologous to the RT domain (e.g., a Cas domain, e.g., a Cas nickase domain, e.g., a Cas9 nickase domain); optionally wherein the RT domain is C-terminal of the Cas domain.

In an aspect, the disclosure provides a gene modifying polypeptide comprising:

a DNA binding domain (DBD) that binds to a target nucleic acid sequence,

the RT domain of an SFVCP RT, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto, and

a linker disposed between the DBD and the RT domain (e.g., a linker comprising an amino acid sequence as listed in Table 10, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto);

wherein the DBD is heterologous to the RT domain (e.g., a Cas domain, e.g., a Cas nickase domain, e.g., a Cas9 nickase domain); optionally wherein the RT domain is C-terminal of the Cas domain.

In an aspect, the disclosure provides a gene modifying polypeptide comprising:

a DNA binding domain (DBD) that binds to a target nucleic acid sequence,

the RT domain of an SMRVH RT, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto, and

a linker disposed between the DBD and the RT domain (e.g., a linker comprising an amino acid sequence as listed in Table 10, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto);

wherein the DBD is heterologous to the RT domain (e.g., a Cas domain, e.g., a Cas nickase domain, e.g., a Cas9 nickase domain); optionally wherein the RT domain is C-terminal of the Cas domain.

In an aspect, the disclosure provides a gene modifying polypeptide comprising:

a DNA binding domain (DBD) that binds to a target nucleic acid sequence,

the RT domain of an SRV1 RT, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto, and

a linker disposed between the DBD and the RT domain (e.g., a linker comprising an amino acid sequence as listed in Table 10, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto);

wherein the DBD is heterologous to the RT domain (e.g., a Cas domain, e.g., a Cas nickase domain, e.g., a Cas9 nickase domain); optionally wherein the RT domain is C-terminal of the Cas domain.

In an aspect, the disclosure provides a gene modifying polypeptide comprising:

a DNA binding domain (DBD) that binds to a target nucleic acid sequence,

the RT domain of an SRV2 RT, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto, and

a linker disposed between the DBD and the RT domain (e.g., a linker comprising an amino acid sequence as listed in Table 10, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto);

wherein the DBD is heterologous to the RT domain (e.g., a Cas domain, e.g., a Cas nickase domain, e.g., a Cas9 nickase domain); optionally wherein the RT domain is C-terminal of the Cas domain.

In an aspect, the disclosure provides a gene modifying polypeptide comprising:

a DNA binding domain (DBD) that binds to a target nucleic acid sequence,

the RT domain of an WDSV RT, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto, and

a linker disposed between the DBD and the RT domain (e.g., a linker comprising an amino acid sequence as listed in Table 10, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto);

wherein the DBD is heterologous to the RT domain (e.g., a Cas domain, e.g., a Cas nickase domain, e.g., a Cas9 nickase domain); optionally wherein the RT domain is C-terminal of the Cas domain.

Gene modifying domain (RT Domain)

In certain aspects of the present invention, the gene modifying domain of the gene modifying system possesses reverse transcriptase activity and is also referred to as a reverse transcriptase domain (an 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), 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., UniProt P23074), 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: 15461) or YMDD motif (SEQ ID NO: 15462) in an RT domain (e.g., in a reverse transcriptase) is replaced with YVDD (SEQ ID NO: 15463). In embodiments, replacement of the YADD (SEQ ID NO: 15461) or YMDD (SEQ ID NO: 15462) or YVDD (SEQ ID NO: 15463) 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	TAPLEEEYRLFLEAPIQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYPITLEAKRSLRETIRKFRAAGILRPVH SPWNTPLLPVRKSGTSEYRMVQDLREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEEGE SGQLTWTRLPQGFKNSPTLFDEALNRDLQGFRLDHPSVSLLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEV TYLGFKIHKGSRSLSNSRTQAILQIPVPKTKRQVREFLGTIGYCRLWIPGFAELAQPLYAATRGGNDPLVWGEKEEEAFQSLKLALTQ

RT Name	SEQ ID NO:	RT amino acid sequence
		PPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSKRLDPVAAGWPRCLRAIAAAALLTREASKLTFGQDIEITSSHNLE SLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTSTRPDLTDQPLAQAEATLFTDGSSYI RDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGLLTAGGKAIKNAPEILA LLTAVWLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATIS
AVIRE_P03360_3mut	8,002	TAPLEEEYRLFLEAPIQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYPITLEAKRSLRETIRKFRAAGILRPVH SPWNTPLLPVRKSGTSEYRMVQDLREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEEGE SGQLTWTRLPQGFKNSPTLFNEALNRDLQGFRLDHPSVSLLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEV TYLGFKIHKGSRSLSNSRTQAILQIPVPKTKRQVREFLGTIGYCRLWIPGFAELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQP PALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSKRLDPVAAGWPRCLRAIAAAALLTREASKLTFGQDIEITSSHNLESL LRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTSTRPDLTDQPLAQAEATLFTDGSSYIRD GKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWLTAGGKAIKNAPEILALL TAVWLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATIS
AVIRE_P03360_3mutA	8,003	TAPLEEEYRLFLEAPIQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYPITLEAKRSLRETIRKFRAAGILRPVH SPWNTPLLPVRKSGTSEYRMVQDLREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEEGE SGQLTWTRLPQGFKNSPTLFNEALNRDLQGFRLDHPSVSLLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEV TYLGFKIHKGSRSLSNSRTQAILQIPVPKTKRQVREFLGKIGYCRLFIPGFAELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQP PALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSKRLDPVAAGWPRCLRAIAAAALLTREASKLTFGQDIEITSSHNLESL LRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTSTRPDLTDQPLAQAEATLFTDGSSYIRD GKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWLTAGGKAIKNAPEILALL TAVWLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATIS
BAEVM_P10272	8,004	TVSLQDEHRLFDIPVTTSLPDVWLQDFPQAWAETGGLGRAKCQAPIIIDLKPTAVPVSIKQYPMSLEAHMGIRQHIIKFLELGVLRPCRS PWNTPLLPVKKPGTQDYRPVQDLREINKRTVDIHPTVPNPYNLLSTLKPDYSWYTVLDLKDAFFCLPLAPQSQELFAFEWKDPERGIS GQLTWTRLPQGFKNSPTLFDEALHRDLTDFRTQHPEVTLLQYVDDLLLAAPTKKACTQGTRHLLQELGEKGYRASAKKAQICQTKVT YLGYILSEGKRWLTPGRIETVARIPPPRNPREVREFLGTAGFCRLWIPGFAELAAPLYALTKESTPFTWQTEHQLAFEALKKALLSAPA LGLPDTSKPFTLFLDERQGIAKGVLTQKLGPWKRPVAYLSKKLDPVAAGWPPCLRIMAATAMLVKDSAKLTLGQPLTVITPHTLEAIVR QPPDRWITNARLTHYQALLLDTDRVQFGPPVTLNPATLLPVPENQPSPHDCRQVLAETHGTREDLKDQELPDADHTWYTDGSSYLD SGTRRAGAAVVDGHNTIWAQSLPPGTSAQKAELIALTKALELSKGKKANIYTDSRYAFATAHTHGSIYERRGLLTSEGKEIKNKAEIIAL LKALFLPQEVAIIHCPGHQKGQDPVAVGNRQADRVARQAAMAEVLTLATEPDNTSHIT
BAEVM_P10272_3mut	8,005	TVSLQDEHRLFDIPVTTSLPDVWLQDFPQAWAETGGLGRAKCQAPIIIDLKPTAVPVSIKQYPMSLEAHMGIRQHIIKFLELGVLRPCRS PWNTPLLPVKKPGTQDYRPVQDLREINKRTVDIHPTVPNPYNLLSTLKPDYSWYTVLDLKDAFFCLPLAPQSQELFAFEWKDPERGIS GQLTWTRLPQGFKNSPTLFNEALHRDLTDFRTQHPEVTLLQYVDDLLLAAPTKKACTQGTRHLLQELGEKGYRASAKKAQICQTKVT YLGYILSEGKRWLTPGRIETVARIPPPRNPREVREFLGTAGFCRLWIPGFAELAAPLYALTKPSTPFTWQTEHQLAFEALKKALLSAPA LGLPDTSKPFTLFLDERQGIAKGVLTQKLGPWKRPVAYLSKKLDPVAAGWPPCLRIMAATAMLVKDSAKLTLGQPLTVITPHTLEAIVR QPPDRWITNARLTHYQALLLDTDRVQFGPPVTLNPATLLPVPENQPSPHDCRQVLAETHGTREDLKDQELPDADHTWYTDGSSYLD SGTRRAGAAVVDGHNTIWAQSLPPGTSAQKAELIALTKALELSKGKKANIYTDSRYAFATAHTHGSIYERRGWLTSEGKEIKNKAEIIA LLKALFLPQEVAIIHCPGHQKGQDPVAVGNRQADRVARQAAMAEVLTLATEPDNTSHIT
BAEVM_P10272_3mutA	8,006	TVSLQDEHRLFDIPVTTSLPDVWLQDFPQAWAETGGLGRAKCQAPIIIDLKPTAVPVSIKQYPMSLEAHMGIRQHIIKFLELGVLRPCRS PWNTPLLPVKKPGTQDYRPVQDLREINKRTVDIHPTVPNPYNLLSTLKPDYSWYTVLDLKDAFFCLPLAPQSQELFAFEWKDPERGIS GQLTWTRLPQGFKNSPTLFNEALHRDLTDFRTQHPEVTLLQYVDDLLLAAPTKKACTQGTRHLLQELGEKGYRASAKKAQICQTKVT YLGYILSEGKRWLTPGRIETVARIPPPRNPREVREFLGKAGFCRLFIPGFAELAAPLYALTKPSTPFTWQTEHQLAFEALKKALLSAPA LGLPDTSKPFTLFLDERQGIAKGVLTQKLGPWKRPVAYLSKKLDPVAAGWPPCLRIMAATAMLVKDSAKLTLGQPLTVITPHTLEAIVR QPPDRWITNARLTHYQALLLDTDRVQFGPPVTLNPATLLPVPENQPSPHDCRQVLAETHGTREDLKDQELPDADHTWYTDGSSYLD SGTRRAGAAVVDGHNTIWAQSLPPGTSAQKAELIALTKALELSKGKKANIYTDSRYAFATAHTHGSIYERRGWLTSEGKEIKNKAEIIA LLKALFLPQEVAIIHCPGHQKGQDPVAVGNRQADRVARQAAMAEVLTLATEPDNTSHIT
BLVAU_P25059	8,007	GVLDAPPSHIGLEHLPPPPEVPQFPLNLERLQALQDLVHRSLEAGYISPWDGPGNNPVFPVRKPNGAWRFVHDLRVTNALTKPIPAL SPGPPDLTAIPTHLPHIICLDLKDAFFQIPVEDRFRSYFAFTLPTPGGLQPHRRFAWRVLPQGFINSPALFERALQEPLRQVSAAFSQS LLVSYMDDILYVSPTEEQRLQCYQTMAAHLRDLGFQVASEKTRQTPSPVPFLGQMVHERMVTYQSLPTLQISSPISLHQLQTVLGDL QWVSRGTPTTRRPLQLLYSSLKGIDDPRAIIHLSPEQQQGIAELRQALSHNARSRYNEQEPLLAYVHLTRAGSTLVLFQKGAQFPLAY FQTPLTDNQASPWGLLLLLGCQYLQAQALSSYAKTILKYYHNLPKTSLDNWIQSSEDPRVQELLQLWPQISSQGIQPPGPWKTLVTR AEVFLTPQFSPEPIPAALCLFSDGAARRGAYCLWKDHLLDFQAVPAPESAQKGELAGLLAGLAAAPPEPLNIWVDSKYLYSLLRTLVL GAWLQPDPVPSYALLYKSLLRHPAIFVGHVRSHSSASHPIASLNNYVDQL
BLVAU_P25059_2mut	8,008	GVLDAPPSHIGLEHLPPPPEVPQFPLNLERLQALQDLVHRSLEAGYISPWDGPGNNPVFPVRKPNGAWRFVHDLRVTNALTKPIPAL SPGPPDLTAIPTHLPHIICLDLKDAFFQIPVEDRFRSYFAFTLPTPGGLQPHRRFAWRVLPQGFINSPALFQRALQEPLRQVSAAFSQS LLVSYMDDILYVSPTEEQRLQCYQTMAAHLRDLGFQVASEKTRQTPSPVPFLGQMVHERMVTYQSLPTLQISSPISLHQLQTVLGDL QWVSRGTPTTRRPLQLLYSSLKPIDDPRAIIHLSPEQQQGIAELRQALSHNARSRYNEQEPLLAYVHLTRAGSTLVLFQKGAQFPLAY FQTPLTDNQASPWGLLLLLGCQYLQAQALSSYAKTILKYYHNLPKTSLDNWIQSSEDPRVQELLQLWPQISSQGIQPPGPWKTLVTR AEVFLTPQFSPEPIPAALCLFSDGAARRGAYCLWKDHLLDFQAVPAPESAQKGELAGLLAGLAAAPPEPLNIWVDSKYLYSLLRTLVL GAWLQPDPVPSYALLYKSLLRHPAIFVGHVRSHSSASHPIASLNNYVDQL

RT Name	SEQ ID NO:	RT amino acid sequence
BLVJ_P03361	8,009	GVLDTPPSHIGLEHLPPPPEVPQFPLNLERLQALQDLVHRSLEAGYISPWDGPGNNPVFPVRKPNGAWRFVHDLRATNALTKPIPAL SPGPPDLTAIPTHPPHIICLDLKDAFFQIPVEDRFRFYLSFTLPSPGGLQPHRRFAWRVLPQGFINSPALFERALQEPLRQVSAAFSQS LLVSYMDDILYASPTEEQRSQCYQALAARLRDLGFQVASEKTSQTPSPVPFLGQMVHEQIVTYQSLPTLQISSPISLHQLQAVLGDLQ WVSRGTPTTRRPLQLLYSSLKRHHDPRAIIQLSPEQLQGIAELRQALSHNARSRYNEQEPLLAYVHLTRAGSTLVLFQKGAQFPLAYF QTPLTDNQASPWGLLLLLGCQYLQTQALSSYAKPILKYYHNLPKTSLDNWIQSSEDPRVQELLQLWPQISSQGIQPPGPWKTLITRAE VFLTPQFSPDPIPAALCLFSDGATGRGAYCLWKDHLLDFQAVPAPESAQKGELAGLLAGLAAAPPEPVNIWVDSKYLYSLLRTLVLGA WLQPDPVPSYALLYKSLLRHPAIVVGHVRSHSSASHPIASLNNYVDQL
BLVJ_P03361_2mut	8,010	GVLDTPPSHIGLEHLPPPPEVPQFPLNLERLQALQDLVHRSLEAGYISPWDGPGNNPVFPVRKPNGAWRFVHDLRATNALTKPIPAL SPGPPDLTAIPTHPPHIICLDLKDAFFQIPVEDRFRFYLSFTLPSPGGLQPHRRFAWRVLPQGFINSPALFNRALQEPLRQVSAAFSQS LLVSYMDDILYASPTEEQRSQCYQALAARLRDLGFQVASEKTSQTPSPVPFLGQMVHEQIVTYQSLPTLQISSPISLHQLQAVLGDLQ WVSRGTPTTRRPLQLLYSSLKRHHDPRAIIQLSPEQLQGIAELRQALSHNARSRYNEQEPLLAYVHLTRAGSTLVLFQKGAQFPLAYF QTPLTDNQASPWGLLLLLGCQYLQTQALSSYAKPILKYYHNLPKTSLDNWIQSSEDPRVQELLQLWPQISSQGIQPPGPWKTLITRAE VFLTPQFSPDPIPAALCLFSDGATGRGAYCLWKDHLLDFQAVPAPESAQKGELAGLLAGLAAAPPEPVNIWVDSKYLYSLLRTWVLG AWLQPDPVPSYALLYKSLLRHPAIVVGHVRSHSSASHPIASLNNYVDQL
BLVJ_P03361_2mutB	8,011	GVLDTPPSHIGLEHLPPPPEVPQFPLNLERLQALQDLVHRSLEAGYISPWDGPGNNPVFPVRKPNGAWRFVHDLRATNALTKPIPAL SPGPPDLTAPPTHPPHIICLDLKDAFFQIPVEDRFRFYLSFTLPSPGGLQPHRRFAWRVLPQGFINSPALFQRALQEPLRQVSAAFSQ SLLVSYMDDILYASPTEEQRSQCYQALAARLRDLGFQVASEKTSQTPSPVPFLGQMVHEQIVTYQSLPTLQISSPISLHQLQAVLGDL QWVSRGTPTTRRPLQLLYSSLKRHHDPRAIIQLSPEQLQGIAELRQALSHNARSRYNEQEPLLAYVHLTRAGSTLVLFQKGAQFPLAY FQTPLTDNQASPWGLLLLLGCQYLQTQALSSYAKPILKYYHNLPKTSLDNWIQSSEDPRVQELLQLWPQISSQGIQPPGPWKTLITRA EVFLTPQFSPDPIPAALCLFSDGATGRGAYCLWKDHLLDFQAVPAPESAQKGELAGLLAGLAAAPPEPVNIWVDSKYLYSLLRTWVL GAWLQPDPVPSYALLYKSLLRHPAIVVGHVRSHSSASHPIASLNNYVDQL
FFV_O93209	8,012	MDLLKPLTVERKGVKIKGYWNSQADITCVPKDLLQGEEPVRQQNVTTIHGTQEGDVYYVNLKIDGRRINTEVIGTTLDYAIITPGDVPW ILKKPLELTIKLDLEEQQGTLLNNSILSKKGKEELKQLFEKYSALWQSWENQVGHRRIRPHKIATGTVKPTPQKQYHINPKAKPDIQIVIN DLLKQGVLIQKESTMNTPVYPVPKPNGRWRMVLDYRAVNKVTPLIAVQNQHSYGILGSLFKGRYKTTIDLSNGFWAHPIVPEDYWITA FTWQGKQYCWTVLPQGFLNSPGLFTGDVVDLLQGIPNVEVYVDDVYISHDSEKEHLEYLDILFNRLKEAGYIISLKKSNIANSIVDFLGF QITNEGRGLTDTFKEKLENITAPTTLKQLQSILGLLNFARNFIPDFTELIAPLYALIPKSTKNYVPWQIEHSTTLETLITKLNGAEYLQGRK GDKTLIMKVNASYTTGYIRYYNEGEKKPISYVSIVFSKTELKFTELEKLLTTVHKGLLKALDLSMGQNIHVYSPIVSMQNIQKTPQTAKK ALASRWLSWLSYLEDPRIRFFYDPQMPALKDLPAVDTGKDNKKHPSNFQHIFYTDGSAITSPTKEGHLNAGMGIVYFINKDGNLQKQ QEWSISLGNHTAQFAEIAAFEFALKKCLPLGGNILVVTDSNYVAKAYNEELDVWASNGFVNNRKKPLKHISKWKSVADLKRLRPDVVV THEPGHQKLDSSPHAYGNNLADQLATQASFKVH
FFV_O93209_2mut	8,013	MDLLKPLTVERKGVKIKGYWNSQADITCVPKDLLQGEEPVRQQNVTTIHGTQEGDVYYVNLKIDGRRINTEVIGTTLDYAIITPGDVPW ILKKPLELTIKLDLEEQQGTLLNNSILSKKGKEELKQLFEKYSALWQSWENQVGHRRIRPHKIATGTVKPTPQKQYHINPKAKPDIQIVIN DLLKQGVLIQKESTMNTPVYPVPKPNGRWRMVLDYRAVNKVTPLIAVQNQHSYGILGSLFKGRYKTTIDLSNGFWAHPIVPEDYWITA FTWQGKQYCWTVLPQGFLNSPGLFNGDVVDLLQGIPNVEVYVDDVYISHDSEKEHLEYLDILFNRLKEAGYIISLKKSNIANSIVDFLG FQITNEGRGLTDTFKEKLENITAPTTLKQLQSILGLLNFARNFIPDFTELIAPLYALIPKSPKNYVPWQIEHSTTLETLITKLNGAEYLQGR KGDKTLIMKVNASYTTGYIRYYNEGEKKPISYVSIVFSKTELKFTELEKLLTTVHKGLLKALDLSMGQNIHVYSPIVSMQNIQKTPQTAK KALASRWLSWLSYLEDPRIRFFYDPQMPALKDLPAVDTGKDNKKHPSNFQHIFYTDGSAITSPTKEGHLNAGMGIVYFINKDGNLQK QQEWSISLGNHTAQFAEIAAFEFALKKCLPLGGNILVVTDSNYVAKAYNEELDVWASNGFVNNRKKPLKHISKWKSVADLKRLRPDV VVTHEPGHQKLDSSPHAYGNNLADQLATQASFKVH
FFV_O93209_2mutA	8,014	MDLLKPLTVERKGVKIKGYWNSQADITCVPKDLLQGEEPVRQQNVTTIHGTQEGDVYYVNLKIDGRRINTEVIGTTLDYAIITPGDVPW ILKKPLELTIKLDLEEQQGTLLNNSILSKKGKEELKQLFEKYSALWQSWENQVGHRRIRPHKIATGTVKPTPQKQYHINPKAKPDIQIVIN DLLKQGVLIQKESTMNTPVYPVPKPNGRWRMVLDYRAVNKVTPLIAVQNQHSYGILGSLFKGRYKTTIDLSNGFWAHPIVPEDYWITA FTWQGKQYCWTVLPQGFLNSPGLFNGDVVDLLQGIPNVEVYVDDVYISHDSEKEHLEYLDILFNRLKEAGYIISLKKSNIANSIVDFLG FQITNEGRGLTDTFKEKLENITAPTTLKQLQSILGKLNFARNFIPDFTELIAPLYALIPKSPKNYVPWQIEHSTTLETLITKLNGAEYLQGR KGDKTLIMKVNASYTTGYIRYYNEGEKKPISYVSIVFSKTELKFTELEKLLTTVHKGLLKALDLSMGQNIHVYSPIVSMQNIQKTPQTAK KALASRWLSWLSYLEDPRIRFFYDPQMPALKDLPAVDTGKDNKKHPSNFQHIFYTDGSAITSPTKEGHLNAGMGIVYFINKDGNLQK QQEWSISLGNHTAQFAEIAAFEFALKKCLPLGGNILVVTDSNYVAKAYNEELDVWASNGFVNNRKKPLKHISKWKSVADLKRLRPDV VVTHEPGHQKLDSSPHAYGNNLADQLATQASFKVH
FFV_O93209-Pro	8,015	VPWILKKPLELTIKLDLEEQQGTLLNNSILSKKGKEELKQLFEKYSALWQSWENQVGHRRIRPHKIATGTVKPTPQKQYHINPKAKPDI QIVINDLLKQGVLIQKESTMNTPVYPVPKPNGRWRMVLDYRAVNKVTPLIAVQNQHSYGILGSLFKGRYKTTIDLSNGFWAHPIVPED YWITAFTWQGKQYCWTVLPQGFLNSPGLFTGDVVDLLQGIPNVEVYVDDVYISHDSEKEHLEYLDILFNRLKEAGYIISLKKSNIANSIV DFLGFQITNEGRGLTDTFKEKLENITAPTTLKQLQSILGLLNFARNFIPDFTELIAPLYALIPKSTKNYVPWQIEHSTTLETLITKLNGAEYL QGRKGDKTLIMKVNASYTTGYIRYYNEGEKKPISYVSIVFSKTELKFTELEKLLTTVHKGLLKALDLSMGQNIHVYSPIVSMQNIQKTPQ TAKKALASRWLSWLSYLEDPRIRFFYDPQMPALKDLPAVDTGKDNKKHPSNFQHIFYTDGSAITSPTKEGHLNAGMGIVYFINKDGNL QKQQEWSISLGNHTAQFAEIAAFEFALKKCLPLGGNILVVTDSNYVAKAYNEELDVWASNGFVNNRKKPLKHISKWKSVADLKRLRP DVVVTHEPGHQKLDSSPHAYGNNLADQLATQASFKVH
FFV_O93209-	8,016	VPWILKKPLELTIKLDLEEQQGTLLNNSILSKKGKEELKQLFEKYSALWQSWENQVGHRRIRPHKIATGTVKPTPQKQYHINPKAKPDI QIVINDLLKQGVLIQKESTMNTPVYPVPKPNGRWRMVLDYRAVNKVTPLIAVQNQHSYGILGSLFKGRYKTTIDLSNGFWAHPIVPED YWITAFTWQGKQYCWTVLPQGFLNSPGLFNGDVVDLLQGIPNVEVYVDDVYISHDSEKEHLEYLDILFNRLKEAGYIISLKKSNIANSIV DFLGFQITNEGRGLTDTFKEKLENITAPTTLKQLQSILGLLNFARNFIPDFTELIAPLYALIPKSPKNYVPWQIEHSTTLETLITKLNGAEYL

RT Name	SEQ ID NO:	RT amino acid sequence
Pro_2 mut		QGRKGDKTLIMKVNASYTTGYIRYYNEGEKKPISYVSIVFSKTELKFTELEKLLTTVHKGLLKALDLSMGQNIHVYSPIVSMQNIQKTPQ TAKKALASRWLSWLSYLEDPRIRFFYDPQMPALKDLPAVDTGKDNKKHPSNFQHIFYTDGSAITSPTKEGHLNAGMGIVYFINKDGNL QKQQEWSISLGNHTAQFAEIAAFEFALKKCLPLGGNILVVTDSNYVAKAYNEELDVWASNGFVNNRKKPLKHISKWKSVADLKRLRP DVVVTHEPGHQKLDSSPHAYGNNLADQLATQASFKVH
FFV_ O93209- Pro_2 mutA	8,017	VPWILKKPLELTIKLDLEEQQGTLLNNSILSKKGKEELKQLFEKYSALWQSWENQVGHRRIRPHKIATGTVKPTPQKQYHINPKAKPDI QIVINDLLKQGVLIQKESTMNTPVYPVPKPNGRWRMVLDYRAVNKVTPLIAVQNQHSYGILGSLFKGRYKTTIDLSNGFWAHPIVPED YWITAFTWQGKQYCWTVLPQGFLNSPGLFNGDVVDLLQGIPNVEVYVDDVYISHDSEKEHLEYLDILFNRLKEAGYIISLKKSNIANSIV DFLGFQITNEGRGLTDTFKEKLENITAPTTLKQLQSILGKLNFARNFIPDFTELIAPLYALIPKSPKNYVPWQIEHSTTLETLITKLNGAEY LQGRKGDKTLIMKVNASYTTGYIRYYNEGEKKPISYVSIVFSKTELKFTELEKLLTTVHKGLLKALDLSMGQNIHVYSPIVSMQNIQKTP QTAKKALASRWLSWLSYLEDPRIRFFYDPQMPALKDLPAVDTGKDNKKHPSNFQHIFYTDGSAITSPTKEGHLNAGMGIVYFINKDGN LQKQQEWSISLGNHTAQFAEIAAFEFALKKCLPLGGNILVVTDSNYVAKAYNEELDVWASNGFVNNRKKPLKHISKWKSVADLKRLRP DVVVTHEPGHQKLDSSPHAYGNNLADQLATQASFKVH
FLV_P 10273	8,018	TLQLEEEYRLFEPESTQKQEMDIWLKNFPQAWAETGGMGTAHCQAPVLIQLKATATPISIRQYPMPHEAYQGIKPHIRRMLDQGILKP CQSPWNTPLLPVKKPGTEDYRPVQDLREVNKRVEDIHPTVPNPYNLLSTLPPSHPWYTVLDLKDAFFCLRLHSESQLLFAFEWRDPE IGLSGQLTWTRLPQGFKNSPTLFDEALHSDLADFRVRYPALVLLQYVDDLLLAAATRTECLEGTKALLETLGNKGYRASAKKAQICLQ EVTYLGYSLKDGQRWLTKARKEAILSIPVPKNSRQVREFLGTAGYCRLWIPGFAELAAPLYPLTRPGTLFQWGTEQQLAFEDIKKALL SSPALGLPDITKPFELFIDENSGFAKGVLVQKLGPWKRPVAYLSKKLDTVASGWPPCLRMVAAIAILVKDAGKLTLGQPLTILTSHPVE ALVRQPPNKWLSNARMTHYQAMLLDAERVHFGPTVSLNPATLLPLPSGGNHHDCLQILAETHGTRPDLTDQPLPDADLTWYTDGSS FIRNGEREAGAAVTTESEVIWAAPLPPGTSAQRAELIALTQALKMAEGKKLTVYTDSRYAFATTHVHGEIYRRRGLLTSEGKEIKNKNE ILALLEALFLPKRLSIIHCPGHQKGDSPQAKGNRLADDTAKKAATETHSSLTVLP
FLV_P 10273 _3mut	8,019	TLQLEEEYRLFEPESTQKQEMDIWLKNFPQAWAETGGMGTAHCQAPVLIQLKATATPISIRQYPMPHEAYQGIKPHIRRMLDQGILKP CQSPWNTPLLPVKKPGTEDYRPVQDLREVNKRVEDIHPTVPNPYNLLSTLPPSHPWYTVLDLKDAFFCLRLHSESQLLFAFEWRDPE IGLSGQLTWTRLPQGFKNSPTLFNEALHSDLADFRVRYPALVLLQYVDDLLLAAATRTECLEGTKALLETLGNKGYRASAKKAQICLQ EVTYLGYSLKDGQRWLTKARKEAILSIPVPKNSRQVREFLGTAGYCRLWIPGFAELAAPLYPLTRPGTLFQWGTEQQLAFEDIKKALL SSPALGLPDITKPFELFIDENSGFAKGVLVQKLGPWKRPVAYLSKKLDTVASGWPPCLRMVAAIAILVKDAGKLTLGQPLTILTSHPVE ALVRQPPNKWLSNARMTHYQAMLLDAERVHFGPTVSLNPATLLPLPSGGNHHDCLQILAETHGTRPDLTDQPLPDADLTWYTDGSS FIRNGEREAGAAVTTESEVIWAAPLPPGTSAQRAELIALTQALKMAEGKKLTVYTDSRYAFATTHVHGEIYRRRGWLTSEGKEIKNKN EILALLEALFLPKRLSIIHCPGHQKGDSPQAKGNRLADDTAKKAATETHSSLTVLP
FLV_P 10273 _3mut A	8,020	TLQLEEEYRLFEPESTQKQEMDIWLKNFPQAWAETGGMGTAHCQAPVLIQLKATATPISIRQYPMPHEAYQGIKPHIRRMLDQGILKP CQSPWNTPLLPVKKPGTEDYRPVQDLREVNKRVEDIHPTVPNPYNLLSTLPPSHPWYTVLDLKDAFFCLRLHSESQLLFAFEWRDPE IGLSGQLTWTRLPQGFKNSPTLFNEALHSDLADFRVRYPALVLLQYVDDLLLAAATRTECLEGTKALLETLGNKGYRASAKKAQICLQ EVTYLGYSLKDGQRWLTKARKEAILSIPVPKNSRQVREFLGKAGYCRLFIPGFAELAAPLYPLTRPGTLFQWGTEQQLAFEDIKKALLS SPALGLPDITKPFELFIDENSGFAKGVLVQKLGPWKRPVAYLSKKLDTVASGWPPCLRMVAAIAILVKDAGKLTLGQPLTILTSHPVEA LVRQPPNKWLSNARMTHYQAMLLDAERVHFGPTVSLNPATLLPLPSGGNHHDCLQILAETHGTRPDLTDQPLPDADLTWYTDGSSFI RNGEREAGAAVTTESEVIWAAPLPPGTSAQRAELIALTQALKMAEGKKLTVYTDSRYAFATTHVHGEIYRRRGWLTSEGKEIKNKNEI LALLEALFLPKRLSIIHCPGHQKGDSPQAKGNRLADDTAKKAATETHSSLTVLP
FOAM V_P14 350	8,021	MNPLQLLQPLPAEIKGTKLLAHWNSGATITCIPESFLEDEQPIKKTLIKTIHGEKQQNVYYVTFKVKGRKVEAEVIASPYEYILLSPTDVP WLTQQPLQLTILVPLQEYQEKILSKTALPEDQKQQLKTLFVKYDNLWQHWENQVGHRKIRPHNIATGDYPPRPQKQYPINPKAKPSIQ IVIDDLLKQGVLTPQNSTMNTPVYPVPKPDGRWRMVLDYREVNKTIPLTAAQNQHSAGILATIVRQKYKTTLDLANGFWAHPITPESY WLTAFTWQGKQYCWTRLPQGFLNSPALFTADVVDLLKEIPNVQVYVDDIYLSHDDPKEHVQQLEKVFQILLQAGYVVSLKKSEIGQK TVEFLGFNITKEGRGLTDTFKTKLLNITPPKDLKQLQSILGLLNFARNFIPNFAELVQPLYNLIASAKGKYIEWSEENTKQLNMVIEALNT ASNLEERLPEQRLVIKVNTSPSAGYVRYYNETGKKPIMYLNYVFSKAELKFSMLEKLLTTMHKALIKAMDLAMGQEILVYSPIVSMTKIQ KTPLPERKALPIRWITWMTYLEDPRIQFHYDKTLPELKHIPDVYTSSQSPVKHPSQYEGVFYTDGSAIKSPDPTKSNNAGMGIVHATY KPEYQVLNQWSIPLGNHTAQMAEIAAVEFACKKALKIPGPVLVITDSFYVAESANKELPYWKSNGFVNNKKKPLKHISKWKSIAECLS MKPDITIQHEKGISLQIPVFILKGNALADKLATQGSYVVN
FOAM V_P14 350_2 mut	8,022	MNPLQLLQPLPAEIKGTKLLAHWNSGATITCIPESFLEDEQPIKKTLIKTIHGEKQQNVYYVTFKVKGRKVEAEVIASPYEYILLSPTDVP WLTQQPLQLTILVPLQEYQEKILSKTALPEDQKQQLKTLFVKYDNLWQHWENQVGHRKIRPHNIATGDYPPRPQKQYPINPKAKPSIQ IVIDDLLKQGVLTPQNSTMNTPVYPVPKPDGRWRMVLDYREVNKTIPLTAAQNQHSAGILATIVRQKYKTTLDLANGFWAHPITPESY WLTAFTWQGKQYCWTRLPQGFLNSPALFNADVVDLLKEIPNVQVYVDDIYLSHDDPKEHVQQLEKVFQILLQAGYVVSLKKSEIGQK TVEFLGFNITKEGRGLTDTFKTKLLNITPPKDLKQLQSILGLLNFARNFIPNFAELVQPLYNLIAPAKGKYIEWSEENTKQLNMVIEALNT ASNLEERLPEQRLVIKVNTSPSAGYVRYYNETGKKPIMYLNYVFSKAELKFSMLEKLLTTMHKALIKAMDLAMGQEILVYSPIVSMTKIQ KTPLPERKALPIRWITWMTYLEDPRIQFHYDKTLPELKHIPDVYTSSQSPVKHPSQYEGVFYTDGSAIKSPDPTKSNNAGMGIVHATY KPEYQVLNQWSIPLGNHTAQMAEIAAVEFACKKALKIPGPVLVITDSFYVAESANKELPYWKSNGFVNNKKKPLKHISKWKSIAECLS MKPDITIQHEKGISLQIPVFILKGNALADKLATQGSYVVN
FOAM V_P14 350_2 mutA	8,023	MNPLQLLQPLPAEIKGTKLLAHWNSGATITCIPESFLEDEQPIKKTLIKTIHGEKQQNVYYVTFKVKGRKVEAEVIASPYEYILLSPTDVP WLTQQPLQLTILVPLQEYQEKILSKTALPEDQKQQLKTLFVKYDNLWQHWENQVGHRKIRPHNIATGDYPPRPQKQYPINPKAKPSIQ IVIDDLLKQGVLTPQNSTMNTPVYPVPKPDGRWRMVLDYREVNKTIPLTAAQNQHSAGILATIVRQKYKTTLDLANGFWAHPITPESY WLTAFTWQGKQYCWTRLPQGFLNSPALFNADVVDLLKEIPNVQVYVDDIYLSHDDPKEHVQQLEKVFQILLQAGYVVSLKKSEIGQK TVEFLGFNITKEGRGLTDTFKTKLLNITPPKDLKQLQSILGKLNFARNFIPNFAELVQPLYNLIAPAKGKYIEWSEENTKQLNMVIEALNT ASNLEERLPEQRLVIKVNTSPSAGYVRYYNETGKKPIMYLNYVFSKAELKFSMLEKLLTTMHKALIKAMDLAMGQEILVYSPIVSMTKIQ

RT Name	SEQ ID NO:	RT amino acid sequence
		KTPLPERKALPIRWITWMTYLEDPRIQFHYDKTLPELKHIPDVYTSSQSPVKHPSQYEGVFYTDGSAIKSPDPTKSNNAGMGIVHATY KPEYQVLNQWSIPLGNHTAQMAEIAAVEFACKKALKIPGPVLVITDSFYVAESANKELPYWKSNGFVNNKKKPLKHISKWKSIAECLS MKPDITIQHEKGISLQIPVFILKGNALADKLATQGSYVVN
FOAMV_P1450-Pro	8,024	VPWLTQQPLQLTILVPLQEYQEKILSKTALPEDQKQQLKTLFVKYDNLWQHWENQVGHRKIRPHNIATGDYPPRPQKQYPINPKAKP SIQIVIDDLLKQGVLTPQNSTMNTPVYPVPKPDGRWRMVLDYREVNKTIPLTAAQNQHSAGILATIVRQKYKTTLDLANGFWAHPITPE SYWLTAFTWQGKQYCWTRLPQGFLNSPALFTADVVDLLKEIPNVQVYVDDIYLSHDDPKEHVQQLEKVFQILLQAGYVVSLKKSEIG QKTVEFLGFNITKEGRGLTDTFKTKLLNITPPKDLKQLQSILGLLNFARNFIPNFAELVQPLYNLIASAKGKYIEWSEENTKQLNMVIEAL NTASNLEERLPEQRLVIKVNTSPSAGYVRYYNETGKKPIMYLNYVFSKAELKFSMLEKLLTTMHKALIKAMDLAMGQEILVYSPIVSMT KIQKTPLPERKALPIRWITWMTYLEDPRIQFHYDKTLPELKHIPDVYTSSQSPVKHPSQYEGVFYTDGSAIKSPDPTKSNNAGMGIVHA TYKPEYQVLNQWSIPLGNHTAQMAEIAAVEFACKKALKIPGPVLVITDSFYVAESANKELPYWKSNGFVNNKKKPLKHISKWKSIAECL SMKPDITIQHEKGISLQIPVFILKGNALADKLATQGSYVVN
FOAMV_P1450-Pro_2mut	8,025	VPWLTQQPLQLTILVPLQEYQEKILSKTALPEDQKQQLKTLFVKYDNLWQHWENQVGHRKIRPHNIATGDYPPRPQKQYPINPKAKP SIQIVIDDLLKQGVLTPQNSTMNTPVYPVPKPDGRWRMVLDYREVNKTIPLTAAQNQHSAGILATIVRQKYKTTLDLANGFWAHPITPE SYWLTAFTWQGKQYCWTRLPQGFLNSPALFNADVVDLLKEIPNVQVYVDDIYLSHDDPKEHVQQLEKVFQILLQAGYVVSLKKSEIG QKTVEFLGFNITKEGRGLTDTFKTKLLNITPPKDLKQLQSILGLLNFARNFIPNFAELVQPLYNLIAPAKGKYIEWSEENTKQLNMVIEAL NTASNLEERLPEQRLVIKVNTSPSAGYVRYYNETGKKPIMYLNYVFSKAELKFSMLEKLLTTMHKALIKAMDLAMGQEILVYSPIVSMT KIQKTPLPERKALPIRWITWMTYLEDPRIQFHYDKTLPELKHIPDVYTSSQSPVKHPSQYEGVFYTDGSAIKSPDPTKSNNAGMGIVHA TYKPEYQVLNQWSIPLGNHTAQMAEIAAVEFACKKALKIPGPVLVITDSFYVAESANKELPYWKSNGFVNNKKKPLKHISKWKSIAECL SMKPDITIQHEKGISLQIPVFILKGNALADKLATQGSYVVN
FOAMV_P1450-Pro_2mutA	8,026	VPWLTQQPLQLTILVPLQEYQEKILSKTALPEDQKQQLKTLFVKYDNLWQHWENQVGHRKIRPHNIATGDYPPRPQKQYPINPKAKP SIQIVIDDLLKQGVLTPQNSTMNTPVYPVPKPDGRWRMVLDYREVNKTIPLTAAQNQHSAGILATIVRQKYKTTLDLANGFWAHPITPE SYWLTAFTWQGKQYCWTRLPQGFLNSPALFNADVVDLLKEIPNVQVYVDDIYLSHDDPKEHVQQLEKVFQILLQAGYVVSLKKSEIG QKTVEFLGFNITKEGRGLTDTFKTKLLNITPPKDLKQLQSILGKLNFARNFIPNFAELVQPLYNLIAPAKGKYIEWSEENTKQLNMVIEAL NTASNLEERLPEQRLVIKVNTSPSAGYVRYYNETGKKPIMYLNYVFSKAELKFSMLEKLLTTMHKALIKAMDLAMGQEILVYSPIVSMT KIQKTPLPERKALPIRWITWMTYLEDPRIQFHYDKTLPELKHIPDVYTSSQSPVKHPSQYEGVFYTDGSAIKSPDPTKSNNAGMGIVHA TYKPEYQVLNQWSIPLGNHTAQMAEIAAVEFACKKALKIPGPVLVITDSFYVAESANKELPYWKSNGFVNNKKKPLKHISKWKSIAECL SMKPDITIQHEKGISLQIPVFILKGNALADKLATQGSYVVN
GALV_P21414	8,027	VLNLEEEYRLHEKPVPSSIDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMSKEAREGIRPHIQKFLDLGVLVP CRSPWNTPLLPVKKPGTNDYRPVQDLREINKRVQDIHPTVPNPYNLLSSLPPSYTWYSVLDLKDAFFCLRLHPNSQPLFAFEWKDPE KGNTGQLTWTRLPQGFKNSPTLFDEALHRDLAPFRALNPQVVLLQYVDDLLVAAPTYEDCKKGTQKLLQELSKLGYRVSAKKAQLC QREVTYLGYLLKEGKRWLTPARKATVMKIPVPTTPRQVREFLGTAGFCRLWIPGFASLAAPLYPLTKPESIPFIWTEEHQQAFDHIKKAL LSAPALALPDLTKPFTLYIDERAGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAVAAVALLLKDADKLTLGQNVTVIASHS LESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVHRCSEILAEETGTRRDLEDQPLPGVPTWYTDGSS FITEGKRRAGAPIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKNINIYTDSRYAFATAHIHGAIYKQRGLLTSAGKDIKNKEEI LALLEAIHLPRRVAIIHCPGHQRGSNPVATGNRRADEAAKQAALSTRVLAGTTKP
GALV_P21414_3mut	8,028	VLNLEEEYRLHEKPVPSSIDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMSKEAREGIRPHIQKFLDLGVLVP CRSPWNTPLLPVKKPGTNDYRPVQDLREINKRVQDIHPTVPNPYNLLSSLPPSYTWYSVLDLKDAFFCLRLHPNSQPLFAFEWKDPE KGNTGQLTWTRLPQGFKNSPTLFNEALHRDLAPFRALNPQVVLLQYVDDLLVAAPTYEDCKKGTQKLLQELSKLGYRVSAKKAQLC QREVTYLGYLLKEGKRWLTPARKATVMKIPVPTTPRQVREFLGTAGFCRLWIPGFASLAAPLYPLTKPSIPFIWTEEHQQAFDHIKKAL LSAPALALPDLTKPFTLYIDERAGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAVAAVALLLKDADKLTLGQNVTVIASHS LESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVHRCSEILAEETGTRRDLEDQPLPGVPTWYTDGSS FITEGKRRAGAPIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKNINIYTDSRYAFATAHIHGAIYKQRGWLTSAGKDIKNKEEI LALLEAIHLPRRVAIIHCPGHQRGSNPVATGNRRADEAAKQAALSTRVLAGTTKP
GALV_P21414_3mutA	8,029	VLNLEEEYRLHEKPVPSSIDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMSKEAREGIRPHIQKFLDLGVLVP CRSPWNTPLLPVKKPGTNDYRPVQDLREINKRVQDIHPTVPNPYNLLSSLPPSYTWYSVLDLKDAFFCLRLHPNSQPLFAFEWKDPE KGNTGQLTWTRLPQGFKNSPTLFNEALHRDLAPFRALNPQVVLLQYVDDLLVAAPTYEDCKKGTQKLLQELSKLGYRVSAKKAQLC QREVTYLGYLLKEGKRWLTPARKATVMKIPVPTTPRQVREFLGKAGFCRLFIPGFASLAAPLYPLTKPSIPFIWTEEHQQAFDHIKKAL LSAPALALPDLTKPFTLYIDERAGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAVAAVALLLKDADKLTLGQNVTVIASHS LESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVHRCSEILAEETGTRRDLEDQPLPGVPTWYTDGSS FITEGKRRAGAPIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKNINIYTDSRYAFATAHIHGAIYKQRGWLTSAGKDIKNKEEI LALLEAIHLPRRVAIIHCPGHQRGSNPVATGNRRADEAAKQAALSTRVLAGTTKP
HTL1A_P03362	8,030	AVLGLEHLPRPPQISQFPLNPERLQALQHLVRKALEAGHIEPYTGPGNNPVFPVKKANGTWRFIHDLRATNSLTIDLSSSSPGPPDLS SLPTTLAHLQTIDLRDAFFQIPLPKQFQPYFAFTVPQQCNYGPGTRYAWKVLPQGFKNSPTLFEMQLAHILQPIRQAFPQCTILQYMD DILLASPSHEDLLLLSEATMASLISHGLPVSENKTQQTPGTIKFLGQIISPNHLTYDAVPTVPIRSRWALPELQALLGEIQWVSKGTPTLR QPLHSLYCALQRHTDPRDQIYLNPSQVQSLVQLRQALSQNCRSRLVQTLPLLGAIMLTLTGTTTVVFQSKEQWPLVWLHAPLPHTSQ CPWGQLLASAVLLLDKYTLQSYGLLCQTIHHNISTQTFNQFIQTSDHPSVPILLHHSHRFKNLGAQTGELWNTFLKTAAPLAPVKALMP VFTLSPVIINTAPCLFSDGSTSRAAYILWDKQILSQRSFPLPPPHKSAQRAELLGLLHGLSSARSWRCLNIFLDSKYLYHYLRTLALGTF QGRSSQAPFQALLPRLLSRKVVYLHHVRSHTNLPDPISRLNALTDALLITPVLQL
HTL1A_P033	8,031	AVLGLEHLPRPPQISQFPLNPERLQALQHLVRKALEAGHIEPYTGPGNNPVFPVKKANGTWRFIHDLRATNSLTIDLSSSSPGPPDLS SLPTTLAHLQTIDLRDAFFQIPLPKQFQPYFAFTVPQQCNYGPGTRYAWKVLPQGFKNSPTLFQMQLAHILQPIRQAFPQCTILQYMD

RT Name	SEQ ID NO:	RT amino acid sequence
62_2mut		DILLASPSHEDLLLLSEATMASLISHGLPVSENKTQQTPGTIKFLGQIISPNHLTYDAVPTVPIRSRWALPELQALLGEIQWVSKGTPTLR QPLHSLYCALQPHTDPRDQIYLNPSQVQSLVQLRQALSQNCRSRLVQTLPLLGAIMLTLTGTTTVVFQSKEQWPLVWLHAPLPHTSQ CPWGQLLASAVLLLDKYTLQSYGLLCQTIHHNISTQTFNQFIQTSDHPSVPILLHHSHRFKNLGAQTGELWNTFLKTAAPLAPVKALMP VFTLSPVIINTAPCLFSDGSTSRAAYILWDKQILSQRSFPLPPPHKSAQRAELLGLLHGLSSARSWRCLNIFLDSKYLYHYLRTLALGTF QGRSSQAPFQALLPRLLSRKVVYLHHVRSHTNLPDPISRLNALTDALLITPVLQL
HTL1A_P03362_2mutB 8,032		AVLGLEHLPRPPQISQFPLNPERLQALQHLVRKALEAGHIEPYTGPGNNPVFPVKKANGTWRFIHDLRATNSLTIDLSSSSPGPPDLS SPPTTLAHLQTIDLRDAFFQIPLPKQFQPYFAFTVPQQCNYGPGTRYAWKVLPQGFKNSPTLFQMQLAHILQPIRQAFPQCTILQYMD DILLASPSHEDLLLLSEATMASLISHGLPVSENKTQQTPGTIKFLGQIISPNHLTYDAVPTVPIRSRWALPELQALLGEIQWVSKGTPTLR QPLHSLYCALQPHTDPRDQIYLNPSQVQSLVQLRQALSQNCRSRLVQTLPLLGAIMLTLTGTTTVVFQSKEQWPLVWLHAPLPHTSQ CPWGQLLASAVLLLDKYTLQSYGLLCQTIHHNISTQTFNQFIQTSDHPSVPILLHHSHRFKNLGAQTGELWNTFLKTAAPLAPVKALMP VFTLSPVIINTAPCLFSDGSTSRAAYILWDKQILSQRSFPLPPPHKSAQRAELLGLLHGLSSARSWRCLNIFLDSKYLYHYLRTLALGTF QGRSSQAPFQALLPRLLSRKVVYLHHVRSHTNLPDPISRLNALTDALLITPVLQL
HTL1C_P14078 8,033		AVLGLEHLPRPPEISQFPLNPERLQALQHLVRKALEAGHIEPYTGPGNNPVFPVKKANGTWRFIHDLRATNSLTIDLSSSSPGPPDLSS LPTTLAHLQTIDLKDAFFQIPLPKQFQPYFAFTVPQQCNYGPGTRYAWRVLPQGFKNSPTLFEMQLAHILQPIRQAFPQCTILQYMDDI LLASPSHADLQLLSEATMASLISHGLPVSENKTQQTPGTIKFLGQIISPNHLTYDAVPKVPIRSRWALPELQALLGEIQWVSKGTPTLR QPLHSLYCALQRHTDPRDQIYLNPSQVQSLVQLRQALSQNCRSRLVQTLPLLGAIMLTLTGTTTVVFQSKQQWPLVWLHAPLPHTSQ CPWGQLLASAVLLLDKYTLQSYGLLCQTIHHNISTQTFNQFIQTSDHPSVPILLHHSHRFKNLGAQTGELWNTFLKTTAPLAPVKALMP VFTLSPVIINTAPCLFSDGSTSQAAYILWDKHILSQRSFPLPPPHKSAQRAELLGLLHGLSSARSWRCLNIFLDSKYLYHYLRTLALGTF QGRSSQAPFQALLPRLLSRKVVYLHHVRSHTNLPDPISRLNALTDALLITPVLQL
HTL1C_P14078_2mut 8,034		AVLGLEHLPRPPEISQFPLNPERLQALQHLVRKALEAGHIEPYTGPGNNPVFPVKKANGTWRFIHDLRATNSLTIDLSSSSPGPPDLSS LPTTLAHLQTIDLKDAFFQIPLPKQFQPYFAFTVPQQCNYGPGTRYAWRVLPQGFKNSPTLFQMQLAHILQPIRQAFPQCTILQYMDDI LLASPSHADLQLLSEATMASLISHGLPVSENKTQQTPGTIKFLGQIISPNHLTYDAVPKVPIRSRWALPELQALLGEIQWVSKGTPTLR QPLHSLYCALQPHTDPRDQIYLNPSQVQSLVQLRQALSQNCRSRLVQTLPLLGAIMLTLTGTTTVVFQSKQQWPLVWLHAPLPHTSQ CPWGQLLASAVLLLDKYTLQSYGLLCQTIHHNISTQTFNQFIQTSDHPSVPILLHHSHRFKNLGAQTGELWNTFLKTTAPLAPVKALMP VFTLSPVIINTAPCLFSDGSTSQAAYILWDKHILSQRSFPLPPPHKSAQRAELLGLLHGLSSARSWRCLNIFLDSKYLYHYLRTLALGTF QGRSSQAPFQALLPRLLSRKVVYLHHVRSHTNLPDPISRLNALTDALLITPVLQL
HTL1L_P0C211 8,035		GLEHLPRPPEISQFPLNPERLQALQHLVRKALEAGHIEPYTGPGNNPVFPVKKANGTWRFIHDLRATNSLTVDLSSSSPGPPDLSSLP TTLAHLQTIDLKDAFFQIPLPKQFQPYFAFTVPQQCNYGPGTRYAWKVLPQGFKNSPTLFEMQLASILQPIRQAFPQCVILQYMDDILL ASPSPEDLQQLSEATMASLISHGLPVSQDKTQQTPGTIKFLGQIISPNHITYDAVPTVPIRSRWALPELQALLGEIQWVSKGTPTLRQP LHSLYCALQGHTDPRDQIYLNPSQVQSLMQLQQALSQNCRSRLAQTLPLLGAIMLTLTGTTTVVFQSKQQWPLVWLHAPLPHTSQC PWGQLLASAVLLLDKYTLQSYGLLCQTIHHNISIQTFNQFIQTSDHPSVPILLHHSHRFKNLGAQTGELWNTFLKTAAPLAPVKALTPVF TLSPIIINTAPCLFSDGSTSQAAYILWDKHILSQRSFPLPPPHKSAQQAELLGLLHGLSSARSWHCLNIFLDSKYLYHYLRTLALGTFQG KSSQAPFQALLPRLLAHKVIYLHHVRSHTNLPDPISKLNALTDALLITPIL
HTL1L_P0C211_2mut 8,036		GLEHLPRPPEISQFPLNPERLQALQHLVRKALEAGHIEPYTGPGNNPVFPVKKANGTWRFIHDLRATNSLTVDLSSSSPGPPDLSSLP TTLAHLQTIDLKDAFFQIPLPKQFQPYFAFTVPQQCNYGPGTRYAWKVLPQGFKNSPTLFQMQLASILQPIRQAFPQCVILQYMDDILL ASPSPEDLQQLSEATMASLISHGLPVSQDKTQQTPGTIKFLGQIISPNHITYDAVPTVPIRSRWALPELQALLGEIQWVSKGTPTLRQP LHSLYCALQGHTDPRDQIYLNPSQVQSLMQLQQALSQNCRSRLAQTLPLLGAIMLTLTGTTTVVFQSKQQWPLVWLHAPLPHTSQC PWGQLLASAVLLLDKYTLQSYGLLCQTIHHNISIQTFNQFIQTSDHPSVPILLHHSHRFKNLGAQTGELWNTFLKTAAPLAPVKALTPVF TLSPIIINTAPCLFSDGSTSQAAYILWDKHILSQRSFPLPPPHKSAQQAELLGLLHGLSSARSWHCLNIFLDSKYLYHYLRTLAWGTFQG KSSQAPFQALLPRLLAHKVIYLHHVRSHTNLPDPISKLNALTDALLITPIL
HTL1L_P0C211_2mutB 8,037		GLEHLPRPPEISQFPLNPERLQALQHLVRKALEAGHIEPYTGPGNNPVFPVKKANGTWRFIHDLRATNSLTVDLSSSSPGPPDLSSPP TTLAHLQTIDLKDAFFQIPLPKQFQPYFAFTVPQQCNYGPGTRYAWKVLPQGFKNSPTLFQMQLASILQPIRQAFPQCVILQYMDDILL ASPSPEDLQQLSEATMASLISHGLPVSQDKTQQTPGTIKFLGQIISPNHITYDAVPTVPIRSRWALPELQALLGEIQWVSKGTPTLRQP LHSLYCALQGHTDPRDQIYLNPSQVQSLMQLQQALSQNCRSRLAQTLPLLGAIMLTLTGTTTVVFQSKQQWPLVWLHAPLPHTSQC PWGQLLASAVLLLDKYTLQSYGLLCQTIHHNISIQTFNQFIQTSDHPSVPILLHHSHRFKNLGAQTGELWNTFLKTAAPLAPVKALTPVF TLSPIIINTAPCLFSDGSTSQAAYILWDKHILSQRSFPLPPPHKSAQQAELLGLLHGLSSARSWHCLNIFLDSKYLYHYLRTLAWGTFQG KSSQAPFQALLPRLLAHKVIYLHHVRSHTNLPDPISKLNALTDALLITPIL
HTL32_Q0R5R2 8,038		GLEHLPPPPEVSQFPLNPERLQALTDLVSRALEAKHIEPYQGPGNNPIFPVKKPNGKWRFIHDLRATNSVTRDLASPSPGPPDLTSLP QGLPHLRTIDLTDAFFQIPLPTIFQPYFAFTLPQPNNYGPGTRYSWRVLPQGFKNSPTLFEQQLSHILTPVRKTFPNSLIIQYMDDILLAS PAPGELAALTDKVTNALTKEGLPLSPEKTQATPGPIHFLGQVISQDCITYETLPSINVKSTWSLAELQSMLGELQWVSKGTPVLRSSLH QLYLALRGHRDPRDTIKLTSIQVQALRTIQKALTLNCRSRLVNQLPILALIMLRPTGTTAVLFQTKQKWPLVWLHTPHPATSLRPWGQL LANAVIILDKYSLQHYGQVCKSFHHNISNQALTYYLHTSDQSSVAILLQHSHRFHNLGAQPSGPWRSLLQMPQIFQNIDVLRPPFTISP VVINHAPCLFSDGSASKAAFIIWDRQVIHQQVLSLPSTCSAQAGELFGLLAGLQKSQPWVALNIFLDSKFLIGHLRRMALGAFPGPSTQ CELHTQLLPLLQGKTVYVHHVRSHTLLQDPISRLNEATDALMLAPLLPL
HTL32_Q0R5R2_2mut 8,039		GLEHLPPPPEVSQFPLNPERLQALTDLVSRALEAKHIEPYQGPGNNPIFPVKKPNGKWRFIHDLRATNSVTRDLASPSPGPPDLTSLP QGLPHLRTIDLTDAFFQIPLPTIFQPYFAFTLPQPNNYGPGTRYSWRVLPQGFKNSPTLFQQQLSHILTPVRKTFPNSLIIQYMDDILLA SPAPGELAALTDKVTNALTKEGLPLSPEKTQATPGPIHFLGQVISQDCITYETLPSINVKSTWSLAELQSMLGELQWVSKGTPVLRSSL HQLYLALRGHRDPRDTIKLTSIQVQALRTIQKALTLNCRSRLVNQLPILALIMLRPTGTTAVLFQTKQKWPLVWLHTPHPATSLRPWGQ LLANAVIILDKYSLQHYGQVCKSFHHNISNQALTYYLHTSDQSSVAILLQHSHRFHNLGAQPSGPWRSLLQMPQIFQNIDVLRPPFTIS

RT Name	SEQ ID NO:	RT amino acid sequence
		PVVINHAPCLFSDGSASKAAFIIWDRQVIHQQVLSLPSTCSAQAGELFGLLAGLQKSQPWVALNIFLDSKFLIGHLRRMAWGAFPGPS TQCELHTQLLPLLQGKTVYVHHVRSHTLLQDPISRLNEATDALMLAPLLPL
HTL32_Q0R5R2_2mutB	8,040	GLEHLPPPPEVSQFPLNPERLQALTDLVSRALEAKHIEPYQGPGNNPIFPVKKPNGKWRFIHDLRATNSVTRDLASPSPGPPDLTSPP QGLPHLRTIDLTDAFFQIPLPTIFQPYFAFTLPQPNNYGPGTRYSWRVLPQGFKNSPTLFQQQLSHILTPVRKTFPNSLIIQYMDDILLA SPAPGELAALTDKVTNALTKEGLPLSPEKTQATPGPIHFLGQVISQDCITYETLPSINVKSTWSLAELQSMLGELQWVSKGTPVLRSSL HQLYLALRGHRDPRDTIKLTSIQVQALRTIQKALTLNCRSRLVNQLPILALIMLRPTGTTAVLFQTKQKWPLVWLHTPHPATSLRPWGQ LLANAVIILDKYSLQHYGQVCKSFHHNISNQALTYYLHTSDQSSVAILLQHSHRFHNLGAQPSGPWRSLLQMPQIFQNIDVLRPPFTIS PVVINHAPCLFSDGSASKAAFIIWDRQVIHQQVLSLPSTCSAQAGELFGLLAGLQKSQPWVALNIFLDSKFLIGHLRRMAWGAFPGPS TQCELHTQLLPLLQGKTVYVHHVRSHTLLQDPISRLNEATDALMLAPLLPL
HTL3P_Q4U0X6	8,041	GLEHLPPPPEVSQFPLNPERLQALTDLVSRALEAKHIEPYQGPGNNPIFPVKKPNGKWRFIHDLRATNSLTRDLASPSPGPPDLTSLP QDLPHLRTIDLTDAFFQIPLPAVFQPYFAFTLPQPNNHGPGTRYSWRVLPQGFKNSPTLFEQQLSHILAPVRKAFPNSLIIQYMDDILLA SPALRELTALTDKVTNALTKEGLPMSLEKTQATPGSIHFLGQVISPDCITYETLPSIHVKSIWSLAELQSMLGELQWVSKGTPVLRSSL HQLYLALRGHRDPRDTIELTSTQVQALKTIQKALALNCRSRLVSQLPILALIILRPTGTTAVLFQTKQKWPLVWLHTPHPATSLRPWGQ LLANAIITLDKYSLQHYGQICKSFHHNISNQALTYYLHTSDQSSVAILLQHSHRFHNLGAQPSGPWRSLLQVPQIFQNIDVLRPPFIISPV VIDHAPCLFSDGATSKAAFILWDKQVIHQQVLPLPSTCSAQAGELFGLLAGLQKSKPWPALNIFLDSKFLIGHLRRMALGAFLGPSTQC DLHARLFPLLQGKTVYVHHVRSHTLLQDPISRLNEATDALMLAPLLPL
HTL3P_Q4U0X6_2mut	8,042	GLEHLPPPPEVSQFPLNPERLQALTDLVSRALEAKHIEPYQGPGNNPIFPVKKPNGKWRFIHDLRATNSLTRDLASPSPGPPDLTSLP QDLPHLRTIDLTDAFFQIPLPAVFQPYFAFTLPQPNNHGPGTRYSWRVLPQGFKNSPTLFQQQLSHILAPVRKAFPNSLIIQYMDDILLA SPALRELTALTDKVTNALTKEGLPMSLEKTQATPGSIHFLGQVISPDCITYETLPSIHVKSIWSLAELQSMLGELQWVSKGTPVLRSSL HQLYLALRGHRDPRDTIELTSTQVQALKTIQKALALNCRSRLVSQLPILALIILRPTGTTAVLFQTKQKWPLVWLHTPHPATSLRPWGQ LLANAIITLDKYSLQHYGQICKSFHHNISNQALTYYLHTSDQSSVAILLQHSHRFHNLGAQPSGPWRSLLQVPQIFQNIDVLRPPFIISPV VIDHAPCLFSDGATSKAAFILWDKQVIHQQVLPLPSTCSAQAGELFGLLAGLQKSKPWPALNIFLDSKFLIGHLRRMAWGAFLGPSTQ CDLHARLFPLLQGKTVYVHHVRSHTLLQDPISRLNEATDALMLAPLLPL
HTL3P_Q4U0X6_2mutB	8,043	GLEHLPPPPEVSQFPLNPERLQALTDLVSRALEAKHIEPYQGPGNNPIFPVKKPNGKWRFIHDLRATNSLTRDLASPSPGPPDLTSPP QDLPHLRTIDLTDAFFQIPLPAVFQPYFAFTLPQPNNHGPGTRYSWRVLPQGFKNSPTLFQQQLSHILAPVRKAFPNSLIIQYMDDILLA SPALRELTALTDKVTNALTKEGLPMSLEKTQATPGSIHFLGQVISPDCITYETLPSIHVKSIWSLAELQSMLGELQWVSKGTPVLRSSL HQLYLALRGHRDPRDTIELTSTQVQALKTIQKALALNCRSRLVSQLPILALIILRPTGTTAVLFQTKQKWPLVWLHTPHPATSLRPWGQ LLANAIITLDKYSLQHYGQICKSFHHNISNQALTYYLHTSDQSSVAILLQHSHRFHNLGAQPSGPWRSLLQVPQIFQNIDVLRPPFIISPV VIDHAPCLFSDGATSKAAFILWDKQVIHQQVLPLPSTCSAQAGELFGLLAGLQKSKPWPALNIFLDSKFLIGHLRRMAWGAFLGPSTQ CDLHARLFPLLQGKTVYVHHVRSHTLLQDPISRLNEATDALMLAPLLPL
HTLV2_P03363_2mut	8,044	HLPPPPQVDQFPLNLPERLQALNDLVSKALEAGHIEPYSGPGNNPVFPVKKPNGKWRFIHDLRATNAITTTLTSPSPGPPDLTSLPTA LPHLQTIDLTDAFFQIPLPKQYQPYFAFTIPQPCNYGPGTRYAWTVLPQGFKNSPTLFQQQLAAVLNPMRKMFPTSTIVQYMDDILLAS PTNEELQQLSQLTLQALTTHGLPISQEKTQQTPGQIRFLGQVISPNHITYESTPTIPIKSQWTLTELQVILGEIQWVSKGTPILRKHLQSL YSALHPYRDPRACITLTPQQLHALHAIQQALQHNCRGRLNPALPLLGLISLSTSGTTSVIFQPKQNWPLAWLHTPHPPTSLCPWGHLL ACTILTLDKYTLQHYGQLCQSFHHNMSKQALCDFLRNSPHPSVGILIHHMGRFHNLGSQPSGPWKTLLHLPTLLQEPRLLRPIFTLSP VVLDTAPCLFSDGSPQKAAYVLWDQTILQQDITPLPSHETHSAQKGELLALICGLRAAKPWPSLNIFLDSKYLIKYLHSLAIGAFLGTSA HQTLQAALPPLLQGKTIYLHHVRSHTNLPDPISTFNEYTDSLILAPLVPL
JSRV_P31623	8,045	PLGTSDSPVTHADPIDWKSEEPVWVDQWPLTQEKLSAAQQLVQEQLRLGHIEPSTSAWNSPIFVIKKKSGKWRLLQDLRKVNETMM HMGALQPGLPTPSAIPDKSYIIVIDLKDCFYTIPLAPQDCKRFAFSLPSVNFKEPMQRYQWRVLPQGMTNSPTLCQKFVATAIAPVRQ RFPQLYLVHYMDDILLAHTDEHLLYQAFSILKQHLSLNGLVIADEKIQTHFPYNYLGFSLYPRVYNTQLVKLQTDHLKTLNDFQKLLGDI NWIRPYLKLPTYTLQPLFDILKGDSDPASPRTLSLEGRTALQSIEEAIRQQQITYCDYQRSWGLYILPTPRAPTGVLYQDKPLRWIYLSA TPTKHLLPYYELVAKIIAKGRHEAIQYFGMEPPFICVPYALEQQDWLFQFSDNWSIAFANYPGQITHHYPSDKLLQFASSHAFIFPKIVR RQPIPEATLIFTDGSSNGTAALIINHQTYYAQTSFSSAQVVELFAVHQALLTVPTSFNLFTDSSYVVGALQMIETVPIIGTTSPEVLNLFTL IQQVLHCRQHPCFFGHIRAHSTLPGALVQGNHTADVLTKQVFFQS
JSRV_P31623_2mutB	8,046	PLGTSDSPVTHADPIDWKSEEPVWVDQWPLTQEKLSAAQQLVQEQLRLGHIEPSTSAWNSPIFVIKKKSGKWRLLQDLRKVNETMM HMGALQPGLPTPSPIPDKSYIIVIDLKDCFYTIPLAPQDCKRFAFSLPSVNFKEPMQRYQWRVLPQGMTNSPTLCQKFVATAIAPVRQ RFPQLYLVHYMDDILLAHTDEHLLYQAFSILKQHLSLNGLVIADEKIQTHFPYNYLGFSLYPRVYNTQLVKLQTDHLKTLNDFQKLLGDI NWIRPYLKLPTYTLQPLFDILKGDSDPASPRTLSLEGRTALQSIEEAIRQQQITYCDYQRSWGLYILPTPRAPTGVLYQDKPLRWIYLSA TPTKHLLPYYELVAKIIAKGRHEAIQYFGMEPPFICVPYALEQQDWLFQFSDNWSIAFANYPGQITHHYPSDKLLQFASSHAFIFPKIVR RQPIPEATLIFTDGSSNGTAALIINHQTYYAQTSFSSAQVVELFAVHQALLTVPTSFNLFTDSSYVVGALQMIETVPIIGTTSPEVLNLFTL IQQVLHCRQHPCFFGHIRAHSTLPGALVQGNHTADVLTKQVFFQS
KORV_Q9TTC1	8,047	TLGDQGSRGSDPLPEPRVTLTVEGIPTEFLVNTGAEHSVLTKPMGKMGSKRTVVAGATGSKVYPWTTKRLLKIGQKQVTHSFLVIPE CPAPLLGRDLLTKLKAQIQFSTEGPQVTWEDRPAMCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPMVWAEKAGMGLANQVPPVVVE LKSDASPVAVRQYPMSKEAREGIRPHIQRFLDLGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSL PPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFDEALHRDLASFRALNPQVVMLQYVDD LLVAAPTYRDCKEGTRRLLQELSKLGYRVSAKKAQLCREEVTYLGYLLKGGKRWLTPARKATVMKIPTPTTPRQVREFLGTAGFCRL WIPGFASLAAPLYPLTREKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFALYVDEKEGVARGVLTQTLGPWRRPVAYLSKKLD PVASGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAILNPATLLPVESDD TPIHICSEILAEETGTRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALTQALRLAEGKSIN

RT Name	SEQ ID NO:	RT amino acid sequence
		IYTDSRYAFATAHVHGAIYKQRGLLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTET TKN
KORV_Q9TTC1_3mut	8,048	TLGDQGSRGSDPLPEPRVTLTVEGIPTEFLVNTGAEHSVLTKPMGKMGSKRTVVAGATGSKVYPWTTKRLLKIGQKQVTHSFLVIPE CPAPLLGRDLLTKLKAQIQFSTEGPQVTWEDRPAMCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPMVWAEKAGMGLANQVPPVVVE LKSDASPVAVRQYPMSKEAREGIRPHIQRFLDLGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSL PPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLASFRALNPQVVMLQYVDD LLVAAPTYRDCKEGTRRLLQELSKLGYRVSAKKAQLCREEVTYLGYLLKGGKRWLTPARKATVMKIPTPTTPRQVREFLGTAGFCRL WIPGFASLAAPLYPLTRPKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFALYVDEKEGVARGVLTQTLGPWRRPVAYLSKKLD PVASGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAILNPATLLPVESDD TPIHICSEILAEETGTRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALTQALRLAEGKSIN IYTDSRYAFATAHVHGAIYKQRGWLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTET TKN
KORV_Q9TTC1_3mutA	8,049	TLGDQGSRGSDPLPEPRVTLTVEGIPTEFLVNTGAEHSVLTKPMGKMGSKRTVVAGATGSKVYPWTTKRLLKIGQKQVTHSFLVIPE CPAPLLGRDLLTKLKAQIQFSTEGPQVTWEDRPAMCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPMVWAEKAGMGLANQVPPVVVE LKSDASPVAVRQYPMSKEAREGIRPHIQRFLDLGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSL PPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLASFRALNPQVVMLQYVDD LLVAAPTYRDCKEGTRRLLQELSKLGYRVSAKKAQLCREEVTYLGYLLKGGKRWLTPARKATVMKIPTPTTPRQVREFLGKAGFCRL FIPGFASLAAPLYPLTRPKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFALYVDEKEGVARGVLTQTLGPWRRPVAYLSKKLD PVASGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAILNPATLLPVESDD TPIHICSEILAEETGTRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALTQALRLAEGKSIN IYTDSRYAFATAHVHGAIYKQRGWLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTET TKN
KORV_Q9TTC1-Pro	8,050	LLGRDLLTKLKAQIQFSTEGPQVTWEDRPAMCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPMVWAEKAGMGLANQVPPVVVELKSD ASPVAVRQYPMSKEAREGIRPHIQRFLDLGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPS HTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFDEALHRDLASFRALNPQVVMLQYVDDLLV AAPTYRDCKEGTRRLLQELSKLGYRVSAKKAQLCREEVTYLGYLLKGGKRWLTPARKATVMKIPTPTTPRQVREFLGTAGFCRLWIP GFASLAAPLYPLTREKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFALYVDEKEGVARGVLTQTLGPWRRPVAYLSKKLDPVA SGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAILNPATLLPVESDDTPI HICSEILAEETGTRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALTQALRLAEGKSINIYT DSRYAFATAHVHGAIYKQRGLLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTETTKN
KORV_Q9TTC1-Pro_3mut	8,051	LLGRDLLTKLKAQIQFSTEGPQVTWEDRPAMCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPMVWAEKAGMGLANQVPPVVVELKSD ASPVAVRQYPMSKEAREGIRPHIQRFLDLGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPS HTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLASFRALNPQVVMLQYVDDLLV AAPTYRDCKEGTRRLLQELSKLGYRVSAKKAQLCREEVTYLGYLLKGGKRWLTPARKATVMKIPTPTTPRQVREFLGTAGFCRLWIP GFASLAAPLYPLTRPKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFALYVDEKEGVARGVLTQTLGPWRRPVAYLSKKLDPVA SGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAILNPATLLPVESDDTPI HICSEILAEETGTRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALTQALRLAEGKSINIYT DSRYAFATAHVHGAIYKQRGWLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTETTK N
KORV_Q9TTC1-Pro_3mutA	8,052	LLGRDLLTKLKAQIQFSTEGPQVTWEDRPAMCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPMVWAEKAGMGLANQVPPVVVELKSD ASPVAVRQYPMSKEAREGIRPHIQRFLDLGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPS HTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLASFRALNPQVVMLQYVDDLLV AAPTYRDCKEGTRRLLQELSKLGYRVSAKKAQLCREEVTYLGYLLKGGKRWLTPARKATVMKIPTPTTPRQVREFLGKAGFCRLFIP GFASLAAPLYPLTRPKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFALYVDEKEGVARGVLTQTLGPWRRPVAYLSKKLDPVA SGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAILNPATLLPVESDDTPI HICSEILAEETGTRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALTQALRLAEGKSINIYT DSRYAFATAHVHGAIYKQRGWLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTETTK N
MLVAV_P03356	8,053	TLNLEDEYRLYETSAEPEVSPGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEAKLGIKPHIQRLLDQGILVP CQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHRWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDP GMGISGQLTWTRLPQGFKNSPTLFDEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLLTLGNLGYRASAKKAQLCQ KQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKTGTLFNWGPDQQKAYQEIKQ ALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLRKDAGKLTMGQPLVILA PHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQPIPDADHTWYT DGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGLLTSEGREI KNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLL
MLVAV_P03356_3mut	8,054	TLNLEDEYRLYETSAEPEVSPGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEAKLGIKPHIQRLLDQGILVP CQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHRWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDP GMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLLTLGNLGYRASAKKAQLCQ KQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQ

RT Name	SEQ ID NO:	RT amino acid sequence
		ALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLRKDAGKLTMGQPLVILA PHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQPIPDADHTWYT DGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREI KNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLL
MLVAV_P03356_3mutA	8,055	TLNLEDEYRLYETSAEPEVSPGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEAKLGIKPHIQ RLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHRWYTVLDLKDAFFC LRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDC QQGTRALLLTLGNLGYRASAKKAQLCQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFI PGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPV AYLSKKLDPVAAGWPPCLRMVAAIAVLRKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDR VQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIW ARALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALFLPKR LSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLL
MLVBM_Q7SVK7	8,056	TLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQR LLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCL RLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFDEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQ QGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGTAGFCRLWI PGFAEMAAPLYPLTKTGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPV AYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRV QFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWA GALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGLLTSEGREIKNKSEILALLKALFLPKRL SIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLL
MLVBM_Q7SVK7	8,057	TLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQR LLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCL RLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFDEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQ QGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGTAGFCRLWI PGFAEMAAPLYPLTKTGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPV AYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRV QFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWA GALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGLLTSEGREIKNKSEILALLKALFLPKRL SIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLL
MLVBM_Q7SVK7_3mut	8,058	TLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQR LLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCL RLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQ QGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGTAGFCRLWI PGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPV AYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRV QFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWA GALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALFLPKRL SIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLL
MLVBM_Q7SVK7_3mut	8,059	TLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQR LLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCL RLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQ QGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGTAGFCRLWI PGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPV AYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRV QFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWA GALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALFLPKRL SIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLL
MLVBM_Q7SVK7_3mut	8,060	LGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRL LDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLR LHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQ GTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKAGFCRLFIPG FAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAY

RT Name	SEQ ID NO:	RT amino acid sequence
A_W S		LSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQF GPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGA LPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALFLPKRLSII HCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLI
MLVB M_Q7 SVK7 _3mut A_W S	8,061	LGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRL LDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLR LHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQ GTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKAGFCRLFIPG FAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAY LSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQF GPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGA LPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALFLPKRLSII HCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLI
MLVC B_P0 8361	8,062	TLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQR LLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCL RLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFDEALHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQ QGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGTAGFCRLWIP GFAEMAAPLYPLTKTGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVA YLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQ FGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWA RALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGLLTSEGKEIKNKDEILALLKALFLPKRL SIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLL
MLVC B_P0 8361_ 3mut	8,063	TLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQR LLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCL RLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQ QGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGTAGFCRLWIP GFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVA YLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQ FGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWA RALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRL SIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLL
MLVC B_P0 8361_ 3mut A	8,064	TLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQR LLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCL RLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQ QGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGKAGFCRLFIP GFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVA YLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQ FGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWA RALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRL SIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLL
MLVF 5_P2 6810	8,065	TLNIEDEYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAFRQAPLIISLKATSTPVSIKQYPMSQEARLGIKPHIQR LLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCL RLHPTSQSLFAFEWKDPEMGISGQLTWTRLPQGFKNSPTLFDEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQ QGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGLCRLWI PGFAEMAAPLYPLTKTGTLFKWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPV AYLSKKLDPVAAGWPPCLRMVAAIAVLTKDVGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRV QFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSFLQEGQRRAGAAVTTETEVIWA KALPAGTSAQRAELIALTQALKMAAGKKLNVYTDSRYAFATAHIHGEIYRRRGLLTSEGKEIKNKDEILALLKALFLPKRL SIIHCPGHQKGNHAEARGNRMADQAAREVATRETPETSTLL
MLVF 5_P2 6810_ 3mut	8,066	TLNIEDEYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAFRQAPLIISLKATSTPVSIKQYPMSQEARLGIKPHIQR LLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCL RLHPTSQSLFAFEWKDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQ QGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGLCRLWI PGFAEMAAPLYPLTKPGTLFKWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPV

RT Name	SEQ ID NO:	RT amino acid sequence
		AYLSKKLDPVAAGWPPCLRMVAAIAVLTKDVGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRV QFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSFLQEGQRRAGAAVTTETEVIWA KALPAGTSAQRAELIALTQALKMAAGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRL SIIHCPGHQKGNHAEARGNRMADQAARE VATRETPETSTLL
MLVF5_P26810_3mutA	8,067	TLNIEDEYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAFRQAPLIISLKATSTPVSIKQYPMSQEARLGIKPHIQR LLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCL RLHPTSQSLFAFEWKDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQ QGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGLCRLFIP GFAEMAAPLYPLTKPGTLFKWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVA YLSKKLDPVAAGWPPCLRMVAAIAVLTKDVGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQ FGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSFLQEGQRRAGAAVTTETEVIWAK ALPAGTSAQRAELIALTQALKMAAGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLS IIHCPGHQKGNHAEARGNRMADQAAREVATRETPETSTLL
MLVFF_P26809_3mut	8,068	TLNIEDEYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQR LLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCL RLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQ QGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWI PGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPV AYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRV QFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVW AKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKR LSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLL
MLVFF_P26809_3mutA	8,069	TLNIEDEYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQR LLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCL RLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQ QGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIP GFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVA YLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQ FGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWA KALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRL SIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLL
MLVMS_P03355	8,070	TLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQR LLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCL RLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFDEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQ QGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWI PGFAEMAAPLYPLTKTGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPV AYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRV QFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIW AKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGLLTSEGKEIKNKDEILALLKALFLPKR LSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLL
MLVMS_reference	8,137	TLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQR LLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCL RLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQ QGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIP GFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVA YLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQ FGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWA KALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRL SIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSP
MLVMS_P03355	8,071	TLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQR LLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCL RLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFDEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQ QGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWI PGFAEMAAPLYPLTKTGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPV

RT Name	SEQ ID NO:	RT amino acid sequence
		AYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRV QFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIW AKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGLLTSEGKEIKNKDEILALLKALFLPKR LSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLL
MLV MS_P 03355 _3mut	8,072	TLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQR LLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCL RLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQ QGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWI PGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPV AYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRV QFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIW AKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKR LSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLL
MLV MS_P 03355 _3mut	8,073	TLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQR LLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCL RLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQ QGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWI PGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPV AYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRV QFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIW AKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKR LSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLL
MLV MS_P 03355 _3mut A_W S	8,074	TLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQR LLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCL RLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQ QGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIP GFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVA YLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQ FGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWA KALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRL SIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLL
MLV MS_P 03355 _3mut A_W S	8,075	TLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQR LLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCL RLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQ QGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIP GFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVA YLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQ FGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWA KALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRL SIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLL
MLV MS_P 03355 _PLV 919	8,076	TLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQR LLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCL RLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQ QGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIP GFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVA YLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQ FGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWA KALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRL SIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFE
MLV MS_P 03355 _PLV 919	8,077	TLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQR LLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCL RLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQ QGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIP GFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVA

RT Name	SEQ ID NO:	RT amino acid sequence
		YLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQ FGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWA KALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRL SIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFE
MLVRD_P11227	8,078	TLNIEDEYRLHEISTEPDVSPGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEAKLGIKPHIQR LLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQGLREVNKRVEDIHPTVPNPYNLLSGLPTSHRWYTVLDLKDAFFCL RLHPTSQPLFASEWRDPGMGISGQLTWTRLPQGFKNSPTLFDEALHRGLADFRIQHPDLILLQYVDDLLLAATSELDCQ QGTRALLKTLGNLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWI PRFAEMAAPLYPLTKTGTLFNWGPDQQKAYHEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPV AYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRV QFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTEPDLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWA RALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYKRRGLLTSEGREIKNKSEILALLKALFLPKRL SIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLL
MLVRD_P11227_3mut	8,079	TLNIEDEYRLHEISTEPDVSPGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEAKLGIKPHIQR LLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQGLREVNKRVEDIHPTVPNPYNLLSGLPTSHRWYTVLDLKDAFFCL RLHPTSQPLFASEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRGLADFRIQHPDLILLQYVDDLLLAATSELDCQ QGTRALLKTLGNLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWI PRFAEMAAPLYPLTKPGTLFNWGPDQQKAYHEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPV AYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRV QFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTEPDLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWA RALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYKRRGWLTSEGREIKNKSEILALLKALFLPKRL SIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLL
MMTVB_P03365	8,080	WVQEISDSRPMLHIYLNGRRFLGLLNTGADKTCIAGRDWPANWPIHQTESSLQGLGMACGVARSSQPLRWQHEDKS GIIHPFVIPTLPFTLWGRDIMKDIKVRLMTDSPDDSQDLMIGAIESNLFADQISWKSDQPVWLNQWPLKQEKLQALQQLV TEQLQLGHLEESNSPWNTPVFVIKKKSGKWRLLQDLRAVNATMHDMGALQPGLPSPVAVPKGWEIIIIDLQDCFFNIKL HPEDCKRFAFSVPSPNFKRPYQRFQWKVLPQGMKNSPTLCQKFVDKAILTVRDKYQDSYIVHYMDDILLAHPSRSIVD EILTSMIQALNKHGLVVSTEKIQKYDNLKYLGTHIQGDSVSYQKLQIRTDKLRTLNDFQKLLGNINWIRPFLKLTTGELKPL FEILNGDSNPISTRKLTPEACKALQLMNERLSTARVKRLDLSQPWSLCILKTEYTPTACLWQDGVVEWIHLPHISPKVITP YDIFCTQLIIKGRHRSKELFSKDPDYIVVPYTKVQFDLLLQEKEDWPISLLGFLGEVHFHLPKDPLLTFTLQTAIIFPHMTST TPLEKGIVIFTDGSANGRSVTYIQGREPIIKENTQNTAQQAEIVAVITAFEEVSQPFNLYTDSKYVTGLFPEIETATLSPRT KIYTELKHLQRLIHKRQEKFYIGHIRGHTGLPGPLAQGNAYADSLTRILT
MMTVB_P03365	8,081	WVQEISDSRPMLHIYLNGRRFLGLLNTGADKTCIAGRDWPANWPIHQTESSLQGLGMACGVARSSQPLRWQHEDKS GIIHPFVIPTLPFTLWGRDIMKDIKVRLMTDSPDDSQDLMIGAIESNLFADQISWKSDQPVWLNQWPLKQEKLQALQQLV TEQLQLGHLEESNSPWNTPVFVIKKKSGKWRLLQDLRAVNATMHDMGALQPGLPSPVAVPKGWEIIIIDLQDCFFNIKL HPEDCKRFAFSVPSPNFKRPYQRFQWKVLPQGMKNSPTLCQKFVDKAILTVRDKYQDSYIVHYMDDILLAHPSRSIVD EILTSMIQALNKHGLVVSTEKIQKYDNLKYLGTHIQGDSVSYQKLQIRTDKLRTLNDFQKLLGNINWIRPFLKLTTGELKPL FEILNGDSNPISTRKLTPEACKALQLMNERLSTARVKRLDLSQPWSLCILKTEYTPTACLWQDGVVEWIHLPHISPKVITP YDIFCTQLIIKGRHRSKELFSKDPDYIVVPYTKVQFDLLLQEKEDWPISLLGFLGEVHFHLPKDPLLTFTLQTAIIFPHMTST TPLEKGIVIFTDGSANGRSVTYIQGREPIIKENTQNTAQQAEIVAVITAFEEVSQPFNLYTDSKYVTGLFPEIETATLSPRT KIYTELKHLQRLIHKRQEKFYIGHIRGHTGLPGPLAQGNAYADSLTRILT
MMTVB_P03365_2mut	8,082	WVQEISDSRPMLHIYLNGRRFLGLLNTGADKTCIAGRDWPANWPIHQTESSLQGLGMACGVARSSQPLRWQHEDKS GIIHPFVIPTLPFTLWGRDIMKDIKVRLMTDSPDDSQDLMIGAIESNLFADQISWKSDQPVWLNQWPLKQEKLQALQQLV TEQLQLGHLEESNSPWNTPVFVIKKKSGKWRLLQDLRAVNATMHDMGALQPGLPSPVAVPKGWEIIIIDLQDCFFNIKL HPEDCKRFAFSVPSPNFKRPYQRFQWKVLPQGMKNSPTLCQKFVDKAILTVRDKYQDSYIVHYMDDILLAHPSRSIVD EILTSMIQALNKHGLVVSTEKIQKYDNLKYLGTHIQGDSVSYQKLQIRTDKLRTLNDFQKLLGNINWIRPFLKLTTGELKPL FEILNPDSNPISTRKLTPEACKALQLMNERLSTARVKRLDLSQPWSLCILKTEYTPTACLWQDGVVEWIHLPHISPKVITP YDIFCTQLIIKGRHRSKELFSKDPDYIVVPYTKVQFDLLLQEKEDWPISLLGFLGEVHFHLPKDPLLTFTLQTAIIFPHMTST TPLEKGIVIFTDGSANGRSVTYIQGREPIIKENTQNTAQQAEIVAVITAFEEVSQPFNLYTDSKYVTGLFPEIETATLSPRT KIYTELKHLQRLIHKRQEKFYIGHIRGHTGLPGPLAQGNAYADSLTRILT
MMTVB_P03365_2mut_WS	8,083	VQEISDSRPMLHIYLNGRRFLGLLDTGADKTCIAGRDWPANWPIHQTESSLQGLGMACGVARSSQPLRWQHEDKSGII HPFVIPTLPFTLWGRDIMKDIKVRLMTDSPDDSQDLMIGAIESNLFADQISWKSDQPVWLNQWPLKQEKLQALQQLVTE QLQLGHLEESNSPWNTPVFVIKKKSGKWRLLQDLRAVNATMHDMGALQPGLPSPVAVPKGWEIIIIDLQDCFFNIKLHP EDCKRFAFSVPSPNFKRPYQRFQWKVLPQGMKNSPTLCQKFVDKAILTVRDKYQDSYIVHYMDDILLAHPSRSIVDEIL TSMIQALNKHGLVVSTEKIQKYDNLKYLGTHIQGDSVSYQKLQIRTDKLRTLNDFQKLLGNINWIRPFLKLTTGELKPLFEI

RT Name	SEQ ID NO:	RT amino acid sequence
		LNPDSNPISTRKLTPEACKALQLMNERLSTARVKRLDLSQPWSLCILKTEYTPTACLWQDGVVEWIHLPHISPKVITPYDI FCTQLIIKGRHRSKELFSKDPDYIVVPYTKVQFDLLLQEKEDWPISLLGFLGEVHFHLPKDPLLTFTLQTAIIFPHMTSTTP LEKGIVIFTDGSANGRSVTYIQGREPIIKENTQNTAQQAEIVAVITAFEEVSQPFNLYTDSKYVTGLFPEIETATLSPRTKIY TELKHLQRLIHKRQEKFYIGHIRGHTGLPGPLAQGNAYADSLTRILTA
MMT VB_P 03365 _2mut _WS	8,084	VQEISDSRPMLHIYLNGRRFLGLLDTGADKTCIAGRDWPANWPIHQTESSLQGLGMACGVARSSQPLRWQHEDKSGII HPFVIPTLPFTLWGRDIMKDIKVRLMTDSPDDSQDLMIGAIESNLFADQISWKSDQPVWLNQWPLKQEKLQALQQLVTE QLQLGHLEESNSPWNTPVFVIKKKSGKWRLLQDLRAVNATMHDMGALQPGLPSPVAVPKGWEIIIIDLQDCFFNIKLHP EDCKRFAFSVPSPNFKRPYQRFQWKVLPQGMKNSPTLCQKFVDKAILTVRDKYQDSYIVHYMDDILLAHPSRSIVDEIL TSMIQALNKHGLVVSTEKIQKYDNLKYLGTHIQGDSVSYQKLQIRTDKLRTLNDFQKLLGNINWIRPFLKLTTGELKPLFEI LNPDSNPISTRKLTPEACKALQLMNERLSTARVKRLDLSQPWSLCILKTEYTPTACLWQDGVVEWIHLPHISPKVITPYDI FCTQLIIKGRHRSKELFSKDPDYIVVPYTKVQFDLLLQEKEDWPISLLGFLGEVHFHLPKDPLLTFTLQTAIIFPHMTSTTP LEKGIVIFTDGSANGRSVTYIQGREPIIKENTQNTAQQAEIVAVITAFEEVSQPFNLYTDSKYVTGLFPEIETATLSPRTKIY TELKHLQRLIHKRQEKFYIGHIRGHTGLPGPLAQGNAYADSLTRILTA
MMT VB_P 03365 _2mut B	8,085	WVQEISDSRPMLHIYLNGRRFLGLLNTGADKTCIAGRDWPANWPIHQTESSLQGLGMACGVARSSQPLRWQHEDKS GIIHPFVIPTLPFTLWGRDIMKDIKVRLMTDSPDDSQDLMIGAIESNLFADQISWKSDQPVWLNQWPLKQEKLQALQQLV TEQLQLGHLEESNSPWNTPVFVIKKKSGKWRLLQDLRAVNATMHDMGALQPGLPSPVAPPKGWEIIIIDLQDCFFNIKL HPEDCKRFAFSVPSPNFKRPYQRFQWKVLPQGMKNSPTLCQKFVDKAILTVRDKYQDSYIVHYMDDILLAHPSRSIVD EILTSMIQALNKHGLVVSTEKIQKYDNLKYLGTHIQGDSVSYQKLQIRTDKLRTLNDFQKLLGNINWIRPFLKLTTGELKPL FEILNPDSNPISTRKLTPEACKALQLMNERLSTARVKRLDLSQPWSLCILKTEYTPTACLWQDGVVEWIHLPHISPKVITP YDIFCTQLIIKGRHRSKELFSKDPDYIVVPYTKVQFDLLLQEKEDWPISLLGFLGEVHFHLPKDPLLTFTLQTAIIFPHMTST TPLEKGIVIFTDGSANGRSVTYIQGREPIIKENTQNTAQQAEIVAVITAFEEVSQPFNLYTDSKYVTGLFPEIETATLSPRT KIYTELKHLQRLIHKRQEKFYIGHIRGHTGLPGPLAQGNAYADSLTRILT
MMT VB_P 03365 _2mut B	8,086	WVQEISDSRPMLHIYLNGRRFLGLLNTGADKTCIAGRDWPANWPIHQTESSLQGLGMACGVARSSQPLRWQHEDKS GIIHPFVIPTLPFTLWGRDIMKDIKVRLMTDSPDDSQDLMIGAIESNLFADQISWKSDQPVWLNQWPLKQEKLQALQQLV TEQLQLGHLEESNSPWNTPVFVIKKKSGKWRLLQDLRAVNATMHDMGALQPGLPSPVAPPKGWEIIIIDLQDCFFNIKL HPEDCKRFAFSVPSPNFKRPYQRFQWKVLPQGMKNSPTLCQKFVDKAILTVRDKYQDSYIVHYMDDILLAHPSRSIVD EILTSMIQALNKHGLVVSTEKIQKYDNLKYLGTHIQGDSVSYQKLQIRTDKLRTLNDFQKLLGNINWIRPFLKLTTGELKPL FEILNPDSNPISTRKLTPEACKALQLMNERLSTARVKRLDLSQPWSLCILKTEYTPTACLWQDGVVEWIHLPHISPKVITP YDIFCTQLIIKGRHRSKELFSKDPDYIVVPYTKVQFDLLLQEKEDWPISLLGFLGEVHFHLPKDPLLTFTLQTAIIFPHMTST TPLEKGIVIFTDGSANGRSVTYIQGREPIIKENTQNTAQQAEIVAVITAFEEVSQPFNLYTDSKYVTGLFPEIETATLSPRT KIYTELKHLQRLIHKRQEKFYIGHIRGHTGLPGPLAQGNAYADSLTRILT
MMT VB_P 03365 _2mut B_W S	8,087	VQEISDSRPMLHIYLNGRRFLGLLDTGADKTCIAGRDWPANWPIHQTESSLQGLGMACGVARSSQPLRWQHEDKSGII HPFVIPTLPFTLWGRDIMKDIKVRLMTDSPDDSQDLMIGAIESNLFADQISWKSDQPVWLNQWPLKQEKLQALQQLVTE QLQLGHLEESNSPWNTPVFVIKKKSGKWRLLQDLRAVNATMHDMGALQPGLPSPPAVPKGWEIIIIDLQDCFFNIKLHP EDCKRFAFSVPSPNFKRPYQRFQWKVLPQGMKNSPTLCQKFVDKAILTVRDKYQDSYIVHYMDDILLAHPSRSIVDEIL TSMIQALNKHGLVVSTEKIQKYDNLKYLGTHIQGDSVSYQKLQIRTDKLRTLNDFQKLLGNINWIRPFLKLTTGELKPLFEI LNPDSNPISTRKLTPEACKALQLMNERLSTARVKRLDLSQPWSLCILKTEYTPTACLWQDGVVEWIHLPHISPKVITPYDI FCTQLIIKGRHRSKELFSKDPDYIVVPYTKVQFDLLLQEKEDWPISLLGFLGEVHFHLPKDPLLTFTLQTAIIFPHMTSTTP LEKGIVIFTDGSANGRSVTYIQGREPIIKENTQNTAQQAEIVAVITAFEEVSQPFNLYTDSKYVTGLFPEIETATLSPRTKIY TELKHLQRLIHKRQEKFYIGHIRGHTGLPGPLAQGNAYADSLTRILTA
MMT VB_P 03365 _2mut B_W S	8,088	VQEISDSRPMLHIYLNGRRFLGLLDTGADKTCIAGRDWPANWPIHQTESSLQGLGMACGVARSSQPLRWQHEDKSGII HPFVIPTLPFTLWGRDIMKDIKVRLMTDSPDDSQDLMIGAIESNLFADQISWKSDQPVWLNQWPLKQEKLQALQQLVTE QLQLGHLEESNSPWNTPVFVIKKKSGKWRLLQDLRAVNATMHDMGALQPGLPSPPAVPKGWEIIIIDLQDCFFNIKLHP EDCKRFAFSVPSPNFKRPYQRFQWKVLPQGMKNSPTLCQKFVDKAILTVRDKYQDSYIVHYMDDILLAHPSRSIVDEIL TSMIQALNKHGLVVSTEKIQKYDNLKYLGTHIQGDSVSYQKLQIRTDKLRTLNDFQKLLGNINWIRPFLKLTTGELKPLFEI LNPDSNPISTRKLTPEACKALQLMNERLSTARVKRLDLSQPWSLCILKTEYTPTACLWQDGVVEWIHLPHISPKVITPYDI FCTQLIIKGRHRSKELFSKDPDYIVVPYTKVQFDLLLQEKEDWPISLLGFLGEVHFHLPKDPLLTFTLQTAIIFPHMTSTTP LEKGIVIFTDGSANGRSVTYIQGREPIIKENTQNTAQQAEIVAVITAFEEVSQPFNLYTDSKYVTGLFPEIETATLSPRTKIY TELKHLQRLIHKRQEKFYIGHIRGHTGLPGPLAQGNAYADSLTRILTA
MMT VB_P 03365 _WS	8,089	VQEISDSRPMLHIYLNGRRFLGLLDTGADKTCIAGRDWPANWPIHQTESSLQGLGMACGVARSSQPLRWQHEDKSGII HPFVIPTLPFTLWGRDIMKDIKVRLMTDSPDDSQDLMIGAIESNLFADQISWKSDQPVWLNQWPLKQEKLQALQQLVTE QLQLGHLEESNSPWNTPVFVIKKKSGKWRLLQDLRAVNATMHDMGALQPGLPSPVAVPKGWEIIIIDLQDCFFNIKLHP EDCKRFAFSVPSPNFKRPYQRFQWKVLPQGMKNSPTLCQKFVDKAILTVRDKYQDSYIVHYMDDILLAHPSRSIVDEIL TSMIQALNKHGLVVSTEKIQKYDNLKYLGTHIQGDSVSYQKLQIRTDKLRTLNDFQKLLGNINWIRPFLKLTTGELKPLFEI

RT Name	SEQ ID NO:	RT amino acid sequence
		LNGDSNPISTRKLTPEACKALQLMNERLSTARVKRLDLSQPWSLCILKTEYTPTACLWQDGVVEWIHLPHISPKVITPYD IFCTQLIIKGRHRSKELFSKDPDYIVVPYTKVQFDLLLQEKEDWPISLLGFLGEVHFHLPKDPLLTFTLQTAIIFPHMTSTTP LEKGIVIFTDGSANGRSVTYIQGREPIIKENTQNTAQQAEIVAVITAFEEVSQPFNLYTDSKYVTGLFPEIETATLSPRTKIY TELKHLQRLIHKRQEKFYIGHIRGHTGLPGPLAQGNAYADSLTRILTA
MMT VB_P 03365 _WS	8,090	VQEISDSRPMLHIYLNGRRFLGLLDTGADKTCIAGRDWPANWPIHQTESSLQGLGMACGVARSSQPLRWQHEDKSGII HPFVIPTLPFTLWGRDIMKDIKVRLMTDSPDDSQDLMIGAIESNLFADQISWKSDQPVWLNQWPLKQEKLQALQQLVTE QLQLGHLEESNSPWNTPVFVIKKKSGKWRLLQDLRAVNATMHDMGALQPGLPSPVAVPKGWEIIIIDLQDCFFNIKLHP EDCKRFAFSVPSPNFKRPYQRFQWKVLPQGMKNSPTLCQKFVDKAILTVRDKYQDSYIVHYMDDILLAHPSRSIVDEIL TSMIQALNKHGLVVSTEKIQKYDNLKYLGTHIQGDSVSYQKLQIRTDKLRTLNDFQKLLGNINWIRPFLKLTTGELKPLFEI LNGDSNPISTRKLTPEACKALQLMNERLSTARVKRLDLSQPWSLCILKTEYTPTACLWQDGVVEWIHLPHISPKVITPYD IFCTQLIIKGRHRSKELFSKDPDYIVVPYTKVQFDLLLQEKEDWPISLLGFLGEVHFHLPKDPLLTFTLQTAIIFPHMTSTTP LEKGIVIFTDGSANGRSVTYIQGREPIIKENTQNTAQQAEIVAVITAFEEVSQPFNLYTDSKYVTGLFPEIETATLSPRTKIY TELKHLQRLIHKRQEKFYIGHIRGHTGLPGPLAQGNAYADSLTRILTA
MMT VB_P 03365 -Pro	8,091	GRDIMKDIKVRLMTDSPDDSQDLMIGAIESNLFADQISWKSDQPVWLNQWPLKQEKLQALQQLVTEQLQLGHLEESNS PWNTPVFVIKKKSGKWRLLQDLRAVNATMHDMGALQPGLPSPVAVPKGWEIIIIDLQDCFFNIKLHPEDCKRFAFSVPS PNFKRPYQRFQWKVLPQGMKNSPTLCQKFVDKAILTVRDKYQDSYIVHYMDDILLAHPSRSIVDEILTSMIQALNKHGLV VSTEKIQKYDNLKYLGTHIQGDSVSYQKLQIRTDKLRTLNDFQKLLGNINWIRPFLKLTTGELKPLFEILNGDSNPISTRKL TPEACKALQLMNERLSTARVKRLDLSQPWSLCILKTEYTPTACLWQDGVVEWIHLPHISPKVITPYDIFCTQLIIKGRHRS KELFSKDPDYIVVPYTKVQFDLLLQEKEDWPISLLGFLGEVHFHLPKDPLLTFTLQTAIIFPHMTSTTPLEKGIVIFTDGSA NGRSVTYIQGREPIIKENTQNTAQQAEIVAVITAFEEVSQPFNLYTDSKYVTGLFPEIETATLSPRTKIYTELKHLQRLIHK RQEKFYIGHIRGHTGLPGPLAQGNAYADSLTRILT
MMT VB_P 03365 -Pro	8,092	GRDIMKDIKVRLMTDSPDDSQDLMIGAIESNLFADQISWKSDQPVWLNQWPLKQEKLQALQQLVTEQLQLGHLEESNS PWNTPVFVIKKKSGKWRLLQDLRAVNATMHDMGALQPGLPSPVAVPKGWEIIIIDLQDCFFNIKLHPEDCKRFAFSVPS PNFKRPYQRFQWKVLPQGMKNSPTLCQKFVDKAILTVRDKYQDSYIVHYMDDILLAHPSRSIVDEILTSMIQALNKHGLV VSTEKIQKYDNLKYLGTHIQGDSVSYQKLQIRTDKLRTLNDFQKLLGNINWIRPFLKLTTGELKPLFEILNGDSNPISTRKL TPEACKALQLMNERLSTARVKRLDLSQPWSLCILKTEYTPTACLWQDGVVEWIHLPHISPKVITPYDIFCTQLIIKGRHRS KELFSKDPDYIVVPYTKVQFDLLLQEKEDWPISLLGFLGEVHFHLPKDPLLTFTLQTAIIFPHMTSTTPLEKGIVIFTDGSA NGRSVTYIQGREPIIKENTQNTAQQAEIVAVITAFEEVSQPFNLYTDSKYVTGLFPEIETATLSPRTKIYTELKHLQRLIHK RQEKFYIGHIRGHTGLPGPLAQGNAYADSLTRILT
MMT VB_P 03365 - Pro_2 mut	8,093	GRDIMKDIKVRLMTDSPDDSQDLMIGAIESNLFADQISWKSDQPVWLNQWPLKQEKLQALQQLVTEQLQLGHLEESNS PWNTPVFVIKKKSGKWRLLQDLRAVNATMHDMGALQPGLPSPVAVPKGWEIIIIDLQDCFFNIKLHPEDCKRFAFSVPS PNFKRPYQRFQWKVLPQGMKNSPTLCQKFVDKAILTVRDKYQDSYIVHYMDDILLAHPSRSIVDEILTSMIQALNKHGLV VSTEKIQKYDNLKYLGTHIQGDSVSYQKLQIRTDKLRTLNDFQKLLGNINWIRPFLKLTTGELKPLFEILNPDSNPISTRKL TPEACKALQLMNERLSTARVKRLDLSQPWSLCILKTEYTPTACLWQDGVVEWIHLPHISPKVITPYDIFCTQLIIKGRHRS KELFSKDPDYIVVPYTKVQFDLLLQEKEDWPISLLGFLGEVHFHLPKDPLLTFTLQTAIIFPHMTSTTPLEKGIVIFTDGSA NGRSVTYIQGREPIIKENTQNTAQQAEIVAVITAFEEVSQPFNLYTDSKYVTGLFPEIETATLSPRTKIYTELKHLQRLIHK RQEKFYIGHIRGHTGLPGPLAQGNAYADSLTRILT
MMT VB_P 03365 - Pro_2 mut	8,094	GRDIMKDIKVRLMTDSPDDSQDLMIGAIESNLFADQISWKSDQPVWLNQWPLKQEKLQALQQLVTEQLQLGHLEESNS PWNTPVFVIKKKSGKWRLLQDLRAVNATMHDMGALQPGLPSPVAVPKGWEIIIIDLQDCFFNIKLHPEDCKRFAFSVPS PNFKRPYQRFQWKVLPQGMKNSPTLCQKFVDKAILTVRDKYQDSYIVHYMDDILLAHPSRSIVDEILTSMIQALNKHGLV VSTEKIQKYDNLKYLGTHIQGDSVSYQKLQIRTDKLRTLNDFQKLLGNINWIRPFLKLTTGELKPLFEILNPDSNPISTRKL TPEACKALQLMNERLSTARVKRLDLSQPWSLCILKTEYTPTACLWQDGVVEWIHLPHISPKVITPYDIFCTQLIIKGRHRS KELFSKDPDYIVVPYTKVQFDLLLQEKEDWPISLLGFLGEVHFHLPKDPLLTFTLQTAIIFPHMTSTTPLEKGIVIFTDGSA NGRSVTYIQGREPIIKENTQNTAQQAEIVAVITAFEEVSQPFNLYTDSKYVTGLFPEIETATLSPRTKIYTELKHLQRLIHK RQEKFYIGHIRGHTGLPGPLAQGNAYADSLTRILT
MMT VB_P 03365 - Pro_2 mutB	8,095	GRDIMKDIKVRLMTDSPDDSQDLMIGAIESNLFADQISWKSDQPVWLNQWPLKQEKLQALQQLVTEQLQLGHLEESNS PWNTPVFVIKKKSGKWRLLQDLRAVNATMHDMGALQPGLPSPVAPPKGWEIIIIDLQDCFFNIKLHPEDCKRFAFSVPS PNFKRPYQRFQWKVLPQGMKNSPTLCQKFVDKAILTVRDKYQDSYIVHYMDDILLAHPSRSIVDEILTSMIQALNKHGLV VSTEKIQKYDNLKYLGTHIQGDSVSYQKLQIRTDKLRTLNDFQKLLGNINWIRPFLKLTTGELKPLFEILNPDSNPISTRKL TPEACKALQLMNERLSTARVKRLDLSQPWSLCILKTEYTPTACLWQDGVVEWIHLPHISPKVITPYDIFCTQLIIKGRHRS KELFSKDPDYIVVPYTKVQFDLLLQEKEDWPISLLGFLGEVHFHLPKDPLLTFTLQTAIIFPHMTSTTPLEKGIVIFTDGSA NGRSVTYIQGREPIIKENTQNTAQQAEIVAVITAFEEVSQPFNLYTDSKYVTGLFPEIETATLSPRTKIYTELKHLQRLIHK RQEKFYIGHIRGHTGLPGPLAQGNAYADSLTRILT

RT Name	SEQ ID NO:	RT amino acid sequence
MMTVB_P03365-Pro_2mutB	8,096	GRDIMKDIKVRLMTDSPDDSQDLMIGAIESNLFADQISWKSDQPVWLNQWPLKQEKLQALQQLVTEQLQLGHLEESNS PWNTPVFVIKKKSGKWRLLQDLRAVNATMHDMGALQPGLPSPVAPPKGWEIIIIDLQDCFFNIKLHPEDCKRFAFSVPS PNFKRPYQRFQWKVLPQGMKNSPTLCQKFVDKAILTVRDKYQDSYIVHYMDDILLAHPSRSIVDEILTSMIQALNKHGLV VSTEKIQKYDNLKYLGTHIQGDSVSYQKLQIRTDKLRTLNDFQKLLGNINWIRPFLKLTTGELKPLFEILNPDSNPISTRKL TPEACKALQLMNERLSTARVKRLDLSQPWSLCILKTEYTPTACLWQDGVVEWIHLPHISPKVITPYDIFCTQLIIKGRHRS KELFSKDPDYIVVPYTKVQFDLLLQEKEDWPISLLGFLGEVHFHLPKDPLLTFTLQTAIIFPHMTSTTPLEKGIVIFTDGSA NGRSVTYIQGREPIIKENTQNTAQQAEIVAVITAFEEVSQPFNLYTDSKYVTGLFPEIETATLSPRTKIYTELKHLQRLIHK RQEKFYIGHIRGHTGLPGPLAQGNAYADSLTRILT
MPMV_P07572	8,097	LTAAIDILAPQQCAEPITWKSDEPVWVDQWPLTNDKLAAAQQLVQEQLEAGHITESSSPWNTPIFVIKKKSGKWRLLQD LRAVNATMVLMGALQPGLPSPVAIPQGYLKIIIDLKDCFFSIPLHPSDQKRFAFSLPSTNFKEPMQRFQWKVLPQGMAN SPTLCQKYVATAIHKVRHAWKQMYIIHYMDDILIAGKDGQQVLQCFDQLKQELTAAGLHIAPEKVQLQDPYTYLGFELN GPKITNQKAVIRKDKLQTLNDFQKLLGDINWLRPYLKLTTGDLKPLFDTLKGDSDPNSHRSLSKEALASLEKVETAIAEQ FVTHINYSLPLIFLIFNTALTPTGLFWQDNPIMWIHLPASPKKVLLPYYDAIADLIILGRDHSKKYFGIEPSTIIQPYSKSQID WLMQNTEMWPIACASFVGILDNHYPPNKLIQFCKLHTFVFPQIISKTPLNNALLVFTDGSSTGMAAYTLTDTTIKFQTNLN SAQLVELQALIAVLSAFPNQPLNIYTDSAYLAHSIPLLETVAQIKHISETAKLFLQCQQLIYNRSIPFYIGHVRAHSGLPGPI AQGNQRADLATKIVASNINT
MPMV_P07572_2mutB	8,098	LTAAIDILAPQQCAEPITWKSDEPVWVDQWPLTNDKLAAAQQLVQEQLEAGHITESSSPWNTPIFVIKKKSGKWRLLQD LRAVNATMVLMGALQPGLPSPVAPPQGYLKIIIDLKDCFFSIPLHPSDQKRFAFSLPSTNFKEPMQRFQWKVLPQGMAN SPTLCQKYVATAIHKVRHAWKQMYIIHYMDDILIAGKDGQQVLQCFDQLKQELTAAGLHIAPEKVQLQDPYTYLGFELN GPKITNQKAVIRKDKLQTLNDFQKLLGDINWLRPYLKLTTGDLKPLFDTLKPDSDPNSHRSLSKEALASLEKVETAIAEQF VTHINYSLPLIFLIFNTALTPTGLFWQDNPIMWIHLPASPKKVLLPYYDAIADLIILGRDHSKKYFGIEPSTIIQPYSKSQIDW LMQNTEMWPIACASFVGILDNHYPPNKLIQFCKLHTFVFPQIISKTPLNNALLVFTDGSSTGMAAYTLTDTTIKFQTNLNS AQLVELQALIAVLSAFPNQPLNIYTDSAYLAHSIPLLETVAQIKHISETAKLFLQCQQLIYNRSIPFYIGHVRAHSGLPGPIA QGNQRADLATKIVASNINT
PERV_Q4VFZ2	8,099	TLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQ RLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCL RLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFDEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDC LEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIP GFATLAAPLYPLTKEKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAY LSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPP AALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLP EGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGLLTSAGREIKNKEEILSLLEALHLPKRLAIIHC PGHQKAKDPISRGNQMADRVAKQAAQGVNLL
PERV_Q4VFZ2	8,100	TLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQ RLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCL RLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFDEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDC LEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIP GFATLAAPLYPLTKEKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAY LSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPP AALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLP EGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGLLTSAGREIKNKEEILSLLEALHLPKRLAIIHC PGHQKAKDPISRGNQMADRVAKQAAQGVNLL
PERV_Q4VFZ2_3mut	8,101	TLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQ RLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCL RLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDC LEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIP GFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAY LSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPP AALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLP EGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRLAIIHC PGHQKAKDPISRGNQMADRVAKQAAQGVNLL
PERV_Q4V	8,102	TLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQ RLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCL RLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDC

RT Name	SEQ ID NO:	RT amino acid sequence
FZ2_3mut		LEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIP GFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAY LSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPP AALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLP EGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRLAIIHC PGHQKAKDPISRGNQMADRVAKQAAQGVNLL
PERV_Q4V FZ2_3mut A_W S	8,103	LDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLI QQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRL HPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLE GTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFCRLFIPGF ATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLS KKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAA LNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEG TSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRLAIIHCPG HQKAKDPISRGNQMADRVAKQAAQGVNLLP
PERV_Q4V FZ2_3mut A_W S	8,104	LDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLI QQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRL HPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLE GTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFCRLFIPGF ATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLS KKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAA LNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEG TSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRLAIIHCPG HQKAKDPISRGNQMADRVAKQAAQGVNLLP
SFV1_P23074	8,105	MDPLQLLQPLEAEIKGTKLKAHWNSGATITCVPEAFLEDERPIQTMLIKTIHGEKQQDVYYLTFKVQGRKVEAEVLASPY DYILLNPSDVPWLMKKPLQLTVLVPLHEYQERLLQQTALPKEQKELLQKLFLKYDALWQHWENQVGHRRIKPHNIATGT LAPRPQKQYPINPKAKPSIQIVIDDLLKQGVLIQQNSTMNTPVYPVPKPDGKWRMVLDYREVNKTIPLIAAQNQHSAGIL SSIYRGKYKTTLDLTNGFWAHPITPESYWLTAFTWQGKQYCWTRLPQGFLNSPALFTADVVDLLKEIPNVQAYVDDIYI SHDDPQEHLEQLEKIFSILLNAGYVVSLKKSEIAQREVEFLGFNITKEGRGLTDTFKQKLLNITPPKDLKQLQSILGLLNFA RNFIPNYSELVKPLYTIVANANGKFISWTEDNSNQLQHIISVLNQADNLEERNPETRLIIKVNSSPSAGYIRYYNEGSKRPI MYVNYIFSKAEAKFTQTEKLLTTMHKGLIKAMDLAMGQEILVYSPIVSMTKIQRTPLPERKALPVRWITWMTYLEDPRIQF HYDKSLPELQQIPNVTEDVIAKTKHPSEFAMVFYTDGSAIKHPDVNKSHSAGMGIAQVQFIPEYKIVHQWSIPLGDHTAQ LAEIAAVEFACKKALKISGPVLIVTDSFYVAESANKELPYWKSNGFLNNKKKPLRHVSKWKSIAECLQLKPDIIIMHEKGH QQPMTTLHTEGNNLADKLATQGSYVVH
SFV1_P23074_2mut	8,106	MDPLQLLQPLEAEIKGTKLKAHWNSGATITCVPEAFLEDERPIQTMLIKTIHGEKQQDVYYLTFKVQGRKVEAEVLASPY DYILLNPSDVPWLMKKPLQLTVLVPLHEYQERLLQQTALPKEQKELLQKLFLKYDALWQHWENQVGHRRIKPHNIATGT LAPRPQKQYPINPKAKPSIQIVIDDLLKQGVLIQQNSTMNTPVYPVPKPDGKWRMVLDYREVNKTIPLIAAQNQHSAGIL SSIYRGKYKTTLDLTNGFWAHPITPESYWLTAFTWQGKQYCWTRLPQGFLNSPALFNADVVDLLKEIPNVQAYVDDIYI SHDDPQEHLEQLEKIFSILLNAGYVVSLKKSEIAQREVEFLGFNITKEGRGLTDTFKQKLLNITPPKDLKQLQSILGLLNFA RNFIPNYSELVKPLYTIVAPANGKFISWTEDNSNQLQHIISVLNQADNLEERNPETRLIIKVNSSPSAGYIRYYNEGSKRPI MYVNYIFSKAEAKFTQTEKLLTTMHKGLIKAMDLAMGQEILVYSPIVSMTKIQRTPLPERKALPVRWITWMTYLEDPRIQF HYDKSLPELQQIPNVTEDVIAKTKHPSEFAMVFYTDGSAIKHPDVNKSHSAGMGIAQVQFIPEYKIVHQWSIPLGDHTAQ LAEIAAVEFACKKALKISGPVLIVTDSFYVAESANKELPYWKSNGFLNNKKKPLRHVSKWKSIAECLQLKPDIIIMHEKGH QQPMTTLHTEGNNLADKLATQGSYVVH
SFV1_P23074_2mutA	8,107	MDPLQLLQPLEAEIKGTKLKAHWNSGATITCVPEAFLEDERPIQTMLIKTIHGEKQQDVYYLTFKVQGRKVEAEVLASPY DYILLNPSDVPWLMKKPLQLTVLVPLHEYQERLLQQTALPKEQKELLQKLFLKYDALWQHWENQVGHRRIKPHNIATGT LAPRPQKQYPINPKAKPSIQIVIDDLLKQGVLIQQNSTMNTPVYPVPKPDGKWRMVLDYREVNKTIPLIAAQNQHSAGIL SSIYRGKYKTTLDLTNGFWAHPITPESYWLTAFTWQGKQYCWTRLPQGFLNSPALFNADVVDLLKEIPNVQAYVDDIYI SHDDPQEHLEQLEKIFSILLNAGYVVSLKKSEIAQREVEFLGFNITKEGRGLTDTFKQKLLNITPPKDLKQLQSILGKLNFA RNFIPNYSELVKPLYTIVAPANGKFISWTEDNSNQLQHIISVLNQADNLEERNPETRLIIKVNSSPSAGYIRYYNEGSKRPI MYVNYIFSKAEAKFTQTEKLLTTMHKGLIKAMDLAMGQEILVYSPIVSMTKIQRTPLPERKALPVRWITWMTYLEDPRIQF HYDKSLPELQQIPNVTEDVIAKTKHPSEFAMVFYTDGSAIKHPDVNKSHSAGMGIAQVQFIPEYKIVHQWSIPLGDHTAQ LAEIAAVEFACKKALKISGPVLIVTDSFYVAESANKELPYWKSNGFLNNKKKPLRHVSKWKSIAECLQLKPDIIIMHEKGH QQPMTTLHTEGNNLADKLATQGSYVVH

RT Name	SEQ ID NO:	RT amino acid sequence
SFV1_P2374-Pro	8,108	VPWLMKKPLQLTVLVPLHEYQERLLQQTALPKEQKELLQKLFLKYDALWQHWENQVGHRRIKPHNIATGTLAPRPQKQ YPINPKAKPSIQIVIDDLLKQGVLIQQNSTMNTPVYPVPKPDGKWRMVLDYREVNKTIPLIAAQNQHSAGILSSIYRGKYK TTLDLTNGFWAHPITPESYWLTAFTWQGKQYCWTRLPQGFLNSPALFTADVVDLLKEIPNVQAYVDDIYISHDDPQEHL EQLEKIFSILLNAGYVVSLKKSEIAQREVEFLGFNITKEGRGLTDTFKQKLLNITPPKDLKQLQSILGLLNFARNFIPNYSEL VKPLYTIVANANGKFISWTEDNSNQLQHIISVLNQADNLEERNPETRLIIKVNSSPSAGYIRYYNEGSKRPIMYVNYIFSKA EAKFTQTEKLLTTMHKGLIKAMDLAMGQEILVYSPIVSMTKIQRTPLPERKALPVRWITWMTYLEDPRIQFHYDKSLPEL QQIPNVTEDVIAKTKHPSEFAMVFYTDGSAIKHPDVNKSHSAGMGIAQVQFIPEYKIVHQWSIPLGDHTAQLAEIAAVEF ACKKALKISGPVLIVTDSFYVAESANKELPYWKSNGFLNNKKKPLRHVSKWKSIAECLQLKPDIIIMHEKGHQQPMTTLH TEGNNLADKLATQGSYVVH
SFV1_P2374-Pro_2mut	8,109	VPWLMKKPLQLTVLVPLHEYQERLLQQTALPKEQKELLQKLFLKYDALWQHWENQVGHRRIKPHNIATGTLAPRPQKQ YPINPKAKPSIQIVIDDLLKQGVLIQQNSTMNTPVYPVPKPDGKWRMVLDYREVNKTIPLIAAQNQHSAGILSSIYRGKYK TTLDLTNGFWAHPITPESYWLTAFTWQGKQYCWTRLPQGFLNSPALFNADVVDLLKEIPNVQAYVDDIYISHDDPQEHL EQLEKIFSILLNAGYVVSLKKSEIAQREVEFLGFNITKEGRGLTDTFKQKLLNITPPKDLKQLQSILGLLNFARNFIPNYSEL VKPLYTIVAPANGKFISWTEDNSNQLQHIISVLNQADNLEERNPETRLIIKVNSSPSAGYIRYYNEGSKRPIMYVNYIFSKA EAKFTQTEKLLTTMHKGLIKAMDLAMGQEILVYSPIVSMTKIQRTPLPERKALPVRWITWMTYLEDPRIQFHYDKSLPEL QQIPNVTEDVIAKTKHPSEFAMVFYTDGSAIKHPDVNKSHSAGMGIAQVQFIPEYKIVHQWSIPLGDHTAQLAEIAAVEF ACKKALKISGPVLIVTDSFYVAESANKELPYWKSNGFLNNKKKPLRHVSKWKSIAECLQLKPDIIIMHEKGHQQPMTTLH TEGNNLADKLATQGSYVVH
SFV1_P2374-Pro_2mutA	8,110	VPWLMKKPLQLTVLVPLHEYQERLLQQTALPKEQKELLQKLFLKYDALWQHWENQVGHRRIKPHNIATGTLAPRPQKQ YPINPKAKPSIQIVIDDLLKQGVLIQQNSTMNTPVYPVPKPDGKWRMVLDYREVNKTIPLIAAQNQHSAGILSSIYRGKYK TTLDLTNGFWAHPITPESYWLTAFTWQGKQYCWTRLPQGFLNSPALFNADVVDLLKEIPNVQAYVDDIYISHDDPQEHL EQLEKIFSILLNAGYVVSLKKSEIAQREVEFLGFNITKEGRGLTDTFKQKLLNITPPKDLKQLQSILGKLNFARNFIPNYSEL VKPLYTIVAPANGKFISWTEDNSNQLQHIISVLNQADNLEERNPETRLIIKVNSSPSAGYIRYYNEGSKRPIMYVNYIFSKA EAKFTQTEKLLTTMHKGLIKAMDLAMGQEILVYSPIVSMTKIQRTPLPERKALPVRWITWMTYLEDPRIQFHYDKSLPEL QQIPNVTEDVIAKTKHPSEFAMVFYTDGSAIKHPDVNKSHSAGMGIAQVQFIPEYKIVHQWSIPLGDHTAQLAEIAAVEF ACKKALKISGPVLIVTDSFYVAESANKELPYWKSNGFLNNKKKPLRHVSKWKSIAECLQLKPDIIIMHEKGHQQPMTTLH TEGNNLADKLATQGSYVVH
SFV3L_P27401	8,111	MDPLQLLQPLEAEIKGTKLKAHWNSGATITCVPQAFLEEEVPIKNIWIKTIHGEKEQPVYYLTFKIQGRKVEAEVISSPYD YILVSPSDIPWLMKKPLQLTTLVPLQEYEERLLKQTMLTGSYKEKLQSLFLKYDALWQHWENQVGHRRIKPHHIATGTV NPRPQKQYPINPKAKASIQTVINDLLKQGVLIQQNSIMNTPVYPVPKPDGKWRMVLDYREVNKTIPLIAAQNQHSAGILS SIFRGKYKTTLDLSNGFWAHSITPESYWLTAFTWLGQQYCWTRLPQGFLNSPALFTADVVDLLKEVPNVQVYVDDIYIS HDDPREHLEQLEKVFSLLLNAGYVVSLKKSEIAQHEVEFLGFNITKEGRGLTETFKQKLLNITPPRDLKQLQSILGLLNFA RNFIPNFSELVKPLYNIIATANGKYITWTTDNSQQLQNIISMLNSAENLEERNPEVRLIMKVNTSPSAGYIRFYNEFAKRPI MYLNYVVYTKAEVKFTNTEKLLTTIHKGLIKALDLGMGQEILVYSPIVSMTKIQKTPLPERKALPIRWITWMSYLEDPRIQFH YDKTLPELQQVPTVTDDIIAKIKHPSEFSMVFYTDGSAIKHPNVNKSHNAGMGIAQVQFKPEFTVINTWSIPLGDHTAQL AEVAAVEFACKKALKIDGPVLIVTDSFYVAESVNKELPYWQSNGFFNNKKKPLKHVSKWKSIADCIQLKPDIIIIHEKGHQ PTASTFHTEGNNLADKLATQGSYVVN
SFV3L_P27401_2mut	8,112	MDPLQLLQPLEAEIKGTKLKAHWNSGATITCVPQAFLEEEVPIKNIWIKTIHGEKEQPVYYLTFKIQGRKVEAEVISSPYD YILVSPSDIPWLMKKPLQLTTLVPLQEYEERLLKQTMLTGSYKEKLQSLFLKYDALWQHWENQVGHRRIKPHHIATGTV NPRPQKQYPINPKAKASIQTVINDLLKQGVLIQQNSIMNTPVYPVPKPDGKWRMVLDYREVNKTIPLIAAQNQHSAGILS SIFRGKYKTTLDLSNGFWAHSITPESYWLTAFTWLGQQYCWTRLPQGFLNSPALFNADVVDLLKEVPNVQVYVDDIYIS HDDPREHLEQLEKVFSLLLNAGYVVSLKKSEIAQHEVEFLGFNITKEGRGLTETFKQKLLNITPPRDLKQLQSILGLLNFA RNFIPNFSELVKPLYNIIATAPGKYITWTTDNSQQLQNIISMLNSAENLEERNPEVRLIMKVNTSPSAGYIRFYNEFAKRPI MYLNYVVYTKAEVKFTNTEKLLTTIHKGLIKALDLGMGQEILVYSPIVSMTKIQKTPLPERKALPIRWITWMSYLEDPRIQFH YDKTLPELQQVPTVTDDIIAKIKHPSEFSMVFYTDGSAIKHPNVNKSHNAGMGIAQVQFKPEFTVINTWSIPLGDHTAQL AEVAAVEFACKKALKIDGPVLIVTDSFYVAESVNKELPYWQSNGFFNNKKKPLKHVSKWKSIADCIQLKPDIIIIHEKGHQ PTASTFHTEGNNLADKLATQGSYVVN
SFV3L_P27401_2mutA	8,113	MDPLQLLQPLEAEIKGTKLKAHWNSGATITCVPQAFLEEEVPIKNIWIKTIHGEKEQPVYYLTFKIQGRKVEAEVISSPYD YILVSPSDIPWLMKKPLQLTTLVPLQEYEERLLKQTMLTGSYKEKLQSLFLKYDALWQHWENQVGHRRIKPHHIATGTV NPRPQKQYPINPKAKASIQTVINDLLKQGVLIQQNSIMNTPVYPVPKPDGKWRMVLDYREVNKTIPLIAAQNQHSAGILS SIFRGKYKTTLDLSNGFWAHSITPESYWLTAFTWLGQQYCWTRLPQGFLNSPALFNADVVDLLKEVPNVQVYVDDIYIS HDDPREHLEQLEKVFSLLLNAGYVVSLKKSEIAQHEVEFLGFNITKEGRGLTETFKQKLLNITPPRDLKQLQSILGKLNFA RNFIPNFSELVKPLYNIIATAPGKYITWTTDNSQQLQNIISMLNSAENLEERNPEVRLIMKVNTSPSAGYIRFYNEFAKRPI MYLNYVVYTKAEVKFTNTEKLLTTIHKGLIKALDLGMGQEILVYSPIVSMTKIQKTPLPERKALPIRWITWMSYLEDPRIQFH

RT Name	SEQ ID NO:	RT amino acid sequence
		YDKTLPELQQVPTVTDDIIAKIKHPSEFSMVFYTDGSAIKHPNVNKSHNAGMGIAQVQFKPEFTVINTWSIPLGDHTAQL AEVAAVEFACKKALKIDGPVLIVTDSFYVAESVNKELPYWQSNGFFNNKKKPLKHVSKWKSIADCIQLKPDIIIIHEKGHQ PTASTFHTEGNNLADKLATQGSYVVN
SFV3 L_P2 7401-Pro	8,114	IPWLMKKPLQLTTLVPLQEYEERLLKQTMLTGSYKEKLQSLFLKYDALWQHWENQVGHRRIKPHHIATGTVNPRPQKQ YPINPKAKASIQTVINDLLKQGVLIQQNSIMNTPVYPVPKPDGKWRMVLDYREVNKTIPLIAAQNQHSAGILSSIFRGKYK TTLDLSNGFWAHSITPESYWLTAFTWLGQQYCWTRLPQGFLNSPALFTADVVDLLKEVPNVQVYVDDIYISHDDPREH LEQLEKVFSLLLNAGYVVSLKKSEIAQHEVEFLGFNITKEGRGLTETFKQKLLNITPPRDLKQLQSILGLLNFARNFIPNFS ELVKPLYNIIATANGKYITWTTDNSQQLQNIISMLNSAENLEERNPEVRLIMKVNTSPSAGYIRFYNEFAKRPIMYLNYVY TKAEVKFTNTEKLLTTIHKGLIKALDLGMGQEILVYSPIVSMTKIQKTPLPERKALPIRWITWMSYLEDPRIQFHYDKTLPE LQQVPTVTDDIIAKIKHPSEFSMVFYTDGSAIKHPNVNKSHNAGMGIAQVQFKPEFTVINTWSIPLGDHTAQLAEVAAVE FACKKALKIDGPVLIVTDSFYVAESVNKELPYWQSNGFFNNKKKPLKHVSKWKSIADCIQLKPDIIIIHEKGHQPTASTFH TEGNNLADKLATQGSYVVN
SFV3 L_P2 7401-Pro_2 mut	8,115	IPWLMKKPLQLTTLVPLQEYEERLLKQTMLTGSYKEKLQSLFLKYDALWQHWENQVGHRRIKPHHIATGTVNPRPQKQ YPINPKAKASIQTVINDLLKQGVLIQQNSIMNTPVYPVPKPDGKWRMVLDYREVNKTIPLIAAQNQHSAGILSSIFRGKYK TTLDLSNGFWAHSITPESYWLTAFTWLGQQYCWTRLPQGFLNSPALFNADVVDLLKEVPNVQVYVDDIYISHDDPREH LEQLEKVFSLLLNAGYVVSLKKSEIAQHEVEFLGFNITKEGRGLTETFKQKLLNITPPRDLKQLQSILGLLNFARNFIPNFS ELVKPLYNIIATAPGKYITWTTDNSQQLQNIISMLNSAENLEERNPEVRLIMKVNTSPSAGYIRFYNEFAKRPIMYLNYVYT KAEVKFTNTEKLLTTIHKGLIKALDLGMGQEILVYSPIVSMTKIQKTPLPERKALPIRWITWMSYLEDPRIQFHYDKTLPEL QQVPTVTDDIIAKIKHPSEFSMVFYTDGSAIKHPNVNKSHNAGMGIAQVQFKPEFTVINTWSIPLGDHTAQLAEVAAVEF ACKKALKIDGPVLIVTDSFYVAESVNKELPYWQSNGFFNNKKKPLKHVSKWKSIADCIQLKPDIIIIHEKGHQPTASTFHT EGNNLADKLATQGSYVVN
SFV3 L_P2 7401-Pro_2 mutA	8,116	IPWLMKKPLQLTTLVPLQEYEERLLKQTMLTGSYKEKLQSLFLKYDALWQHWENQVGHRRIKPHHIATGTVNPRPQKQ YPINPKAKASIQTVINDLLKQGVLIQQNSIMNTPVYPVPKPDGKWRMVLDYREVNKTIPLIAAQNQHSAGILSSIFRGKYK TTLDLSNGFWAHSITPESYWLTAFTWLGQQYCWTRLPQGFLNSPALFNADVVDLLKEVPNVQVYVDDIYISHDDPREH LEQLEKVFSLLLNAGYVVSLKKSEIAQHEVEFLGFNITKEGRGLTETFKQKLLNITPPRDLKQLQSILGKLNFARNFIPNFS ELVKPLYNIIATAPGKYITWTTDNSQQLQNIISMLNSAENLEERNPEVRLIMKVNTSPSAGYIRFYNEFAKRPIMYLNYVYT KAEVKFTNTEKLLTTIHKGLIKALDLGMGQEILVYSPIVSMTKIQKTPLPERKALPIRWITWMSYLEDPRIQFHYDKTLPEL QQVPTVTDDIIAKIKHPSEFSMVFYTDGSAIKHPNVNKSHNAGMGIAQVQFKPEFTVINTWSIPLGDHTAQLAEVAAVEF ACKKALKIDGPVLIVTDSFYVAESVNKELPYWQSNGFFNNKKKPLKHVSKWKSIADCIQLKPDIIIIHEKGHQPTASTFHT EGNNLADKLATQGSYVVN
SFVC P_Q8 7040	8,117	MNPLQLLQPLPAEVKGTKLLAHWNSGATITCIPESFLEDEQPIKQTLIKTIHGEKQQNVYYLTFKVKGRKVEAEVIASPYE YILLSPTDVPWLTQQPLQLTILVPLQEYQDRILNKTALPEEQKQQLKALFTKYDNLWQHWENQVGHRKIRPHNIATGDY PPRPQKQYPINPKAKPSIQIVIDDLLKQGVLTPQNSTMNTPVYPVPKPDGRWRMVLDYREVNKTIPLTAAQNQHSAGIL ATIVRQKYKTTLDLANGFWAHPITPDSYWLTAFTWQGKQYCWTRLPQGFLNSPALFTADAVDLLKEVPNVQVYVDDIY LSHDNPHEHIQQLEKVFQILLQAGYVVSLKKSEIGQRTVEFLGFNITKEGRGLTDTFKTKLLNVTPPKDLKQLQSILGLLN FARNFIPNFAELVQTLYNLIASSKGKYIEWTEDNTKQLNKVIEALNTASNLEERLPDQRLVIKVNTSPSAGYVRYYNESG KKPIMYLNYVFSKAELKFSMLEKLLTTMHKALIKAMDLAMGQEILVYSPIVSMTKIQKTPLPERKALPIRWITWMTYLEDP RIQFHYDKTLPELKHIPDVYTSSIPPLKHPSQYEGVFCTDGSAIKSPDPTKSNNAGMGIVHAIYNPEYKILNQWSIPLGHH TAQMAEIAAVEFACKKALKVPGPVLVITDSFYVAESANKELPYWKSNGFVNNKKEPLKHISKWKSIAECLSIKPDITIQHE KGHQPINTSIHTEGNALADKLATQGSYVVN
SFVC P_Q8 7040_ 2mut	8,118	MNPLQLLQPLPAEVKGTKLLAHWNSGATITCIPESFLEDEQPIKQTLIKTIHGEKQQNVYYLTFKVKGRKVEAEVIASPYE YILLSPTDVPWLTQQPLQLTILVPLQEYQDRILNKTALPEEQKQQLKALFTKYDNLWQHWENQVGHRKIRPHNIATGDY PPRPQKQYPINPKAKPSIQIVIDDLLKQGVLTPQNSTMNTPVYPVPKPDGRWRMVLDYREVNKTIPLTAAQNQHSAGIL ATIVRQKYKTTLDLANGFWAHPITPDSYWLTAFTWQGKQYCWTRLPQGFLNSPALFNADAVDLLKEVPNVQVYVDDIY LSHDNPHEHIQQLEKVFQILLQAGYVVSLKKSEIGQRTVEFLGFNITKEGRGLTDTFKTKLLNVTPPKDLKQLQSILGLLN FARNFIPNFAELVQTLYNLIASSPGKYIEWTEDNTKQLNKVIEALNTASNLEERLPDQRLVIKVNTSPSAGYVRYYNESG KKPIMYLNYVFSKAELKFSMLEKLLTTMHKALIKAMDLAMGQEILVYSPIVSMTKIQKTPLPERKALPIRWITWMTYLEDP RIQFHYDKTLPELKHIPDVYTSSIPPLKHPSQYEGVFCTDGSAIKSPDPTKSNNAGMGIVHAIYNPEYKILNQWSIPLGHH TAQMAEIAAVEFACKKALKVPGPVLVITDSFYVAESANKELPYWKSNGFVNNKKEPLKHISKWKSIAECLSIKPDITIQHE KGHQPINTSIHTEGNALADKLATQGSYVVN
SFVC P_Q87 040_2 mutA	8,119	MNPLQLLQPLPAEVKGTKLLAHWNSGATITCIPESFLEDEQPIKQTLIKTIHGEKQQNVYYLTFKVKGRKVEAEVIASPYEYILLSPTDV PWLTQQPLQLTILVPLQEYQDRILNKTALPEEQKQQLKALFTKYDNLWQHWENQVGHRKIRPHNIATGDYPPRPQKQYPINPKAKPSI QIVIDDLLKQGVLTPQNSTMNTPVYPVPKPDGRWRMVLDYREVNKTIPLTAAQNQHSAGILATIVRQKYKTTLDLANGFWAHPITPDS YWLTAFTWQGKQYCWTRLPQGFLNSPALFNADAVDLLKEVPNVQVYVDDIYLSHDNPHEHIQQLEKVFQILLQAGYVVSLKKSEIGQ

RT Name	SEQ ID NO:	RT amino acid sequence
		RTVEFLGFNITKEGRGLTDTFKTKLLNVTPPKDLKQLQSILGKLNFARNFIPNFAELVQTLYNLIASSPGKYIEWTEDNTKQLNKVIEALN TASNLEERLPDQRLVIKVNTSPSAGYVRYYNESGKKPIMYLNYVFSKAELKFSMLEKLLTTMHKALIKAMDLAMGQEILVYSPIVSMTKI QKTPLPERKALPIRWITWMTYLEDPRIQFHYDKTLPELKHIPDVYTSSIPPLKHPSQYEGVFCTDGSAIKSPDPTKSNNAGMGIVHAIYN PEYKILNQWSIPLGHHTAQMAEIAAVEFACKKALKVPGPVLVITDSFYVAESANKELPYWKSNGFVNNKKEPLKHISKWKSIAECLSIK PDITIQHEKGHQPINTSIHTEGNALADKLATQGSYVVN
SFVCP_Q87040-Pro	8,120	VPWLTQQPLQLTILVPLQEYQDRILNKTALPEEQKQQLKALFTKYDNLWQHWENQVGHRKIRPHNIATGDYPPRPQKQYPINPKAKP SIQIVIDDLLKQGVLTPQNSTMNTPVYPVPKPDGRWRMVLDYREVNKTIPLTAAQNQHSAGILATIVRQKYKTTLDLANGFWAHPITPD SYWLTAFTWQGKQYCWTRLPQGFLNSPALFTADAVDLLKEVPNVQVYVDDIYLSHDNPHEHIQQLEKVFQILLQAGYVVSLKKSEIG QRTVEFLGFNITKEGRGLTDTFKTKLLNVTPPKDLKQLQSILGLLNFARNFIPNFAELVQTLYNLIASSKGKYIEWTEDNTKQLNKVIEAL NTASNLEERLPDQRLVIKVNTSPSAGYVRYYNESGKKPIMYLNYVFSKAELKFSMLEKLLTTMHKALIKAMDLAMGQEILVYSPIVSMT KIQKTPLPERKALPIRWITWMTYLEDPRIQFHYDKTLPELKHIPDVYTSSIPPLKHPSQYEGVFCTDGSAIKSPDPTKSNNAGMGIVHAI YNPEYKILNQWSIPLGHHTAQMAEIAAVEFACKKALKVPGPVLVITDSFYVAESANKELPYWKSNGFVNNKKEPLKHISKWKSIAECLS IKPDITIQHEKGHQPINTSIHTEGNALADKLATQGSYVVN
SFVCP_Q87040-Pro_2mut	8,121	VPWLTQQPLQLTILVPLQEYQDRILNKTALPEEQKQQLKALFTKYDNLWQHWENQVGHRKIRPHNIATGDYPPRPQKQYPINPKAKP SIQIVIDDLLKQGVLTPQNSTMNTPVYPVPKPDGRWRMVLDYREVNKTIPLTAAQNQHSAGILATIVRQKYKTTLDLANGFWAHPITPD SYWLTAFTWQGKQYCWTRLPQGFLNSPALFNADAVDLLKEVPNVQVYVDDIYLSHDNPHEHIQQLEKVFQILLQAGYVVSLKKSEIG QRTVEFLGFNITKEGRGLTDTFKTKLLNVTPPKDLKQLQSILGLLNFARNFIPNFAELVQTLYNLIASSPGKYIEWTEDNTKQLNKVIEAL NTASNLEERLPDQRLVIKVNTSPSAGYVRYYNESGKKPIMYLNYVFSKAELKFSMLEKLLTTMHKALIKAMDLAMGQEILVYSPIVSMT KIQKTPLPERKALPIRWITWMTYLEDPRIQFHYDKTLPELKHIPDVYTSSIPPLKHPSQYEGVFCTDGSAIKSPDPTKSNNAGMGIVHAI YNPEYKILNQWSIPLGHHTAQMAEIAAVEFACKKALKVPGPVLVITDSFYVAESANKELPYWKSNGFVNNKKEPLKHISKWKSIAECLS IKPDITIQHEKGHQPINTSIHTEGNALADKLATQGSYVVN
SFVCP_Q87040-Pro_2mutA	8,122	VPWLTQQPLQLTILVPLQEYQDRILNKTALPEEQKQQLKALFTKYDNLWQHWENQVGHRKIRPHNIATGDYPPRPQKQYPINPKAKP SIQIVIDDLLKQGVLTPQNSTMNTPVYPVPKPDGRWRMVLDYREVNKTIPLTAAQNQHSAGILATIVRQKYKTTLDLANGFWAHPITPD SYWLTAFTWQGKQYCWTRLPQGFLNSPALFNADAVDLLKEVPNVQVYVDDIYLSHDNPHEHIQQLEKVFQILLQAGYVVSLKKSEIG QRTVEFLGFNITKEGRGLTDTFKTKLLNVTPPKDLKQLQSILGKLNFARNFIPNFAELVQTLYNLIASSPGKYIEWTEDNTKQLNKVIEAL NTASNLEERLPDQRLVIKVNTSPSAGYVRYYNESGKKPIMYLNYVFSKAELKFSMLEKLLTTMHKALIKAMDLAMGQEILVYSPIVSMT KIQKTPLPERKALPIRWITWMTYLEDPRIQFHYDKTLPELKHIPDVYTSSIPPLKHPSQYEGVFCTDGSAIKSPDPTKSNNAGMGIVHAI YNPEYKILNQWSIPLGHHTAQMAEIAAVEFACKKALKVPGPVLVITDSFYVAESANKELPYWKSNGFVNNKKEPLKHISKWKSIAECLS IKPDITIQHEKGHQPINTSIHTEGNALADKLATQGSYVVN
SMRVH_P03364	8,123	PRSRAIDIPVPHADKISWKITDPVWVDQWPLTYEKTLAAIALVQEQLAAGHIEPTNSPWNTPIFIIKKKSGSWRLLQDLRAVNKVMVPM GALQPGLPSPVAIPLNYHKIVIDLKDCFFTIPLHPEDRPYFAFSVPQINFQSPMPRYQWKVLPQGMANSPTLCQKFVAAAIAPVRSQW PEAYILHYMDDILLACDSAEAAKACYAHIISCLTSYGLKIAPDKVQVSEPFSYLGFELHHQQVFTPRVCLKTDHLKTLNDFQKLLGDIQW LRPYLKLPTSALVPLNNILKGDPNPLSVRALTPEAKQSLALINKAIQNQSVQQISYNLPLVLLLLPTPHTPTAVFWQPNGTDPTKNGSPL LWLHLPASPSKVLLTYPSLLAMLIIKGRYTGRQLFGRDPHSIIIPYTQDQLTWLLQTSDEWAIALSSFTGDIDNHYPSDPVIQFAKLHQFI FPKITKCAPIPQATLVFTDGSSNGIAAYVIDNQPISIKSPYLSAQLVELYAILQVFTVLAHQPFNLYTDSAYIAQSVPLLETVPFIKSSTNAT PLFSKLQQLILNRQHPFFIGHLRAHLNLPGPLAEGNALADAATQIFPIISD
SMRVH_P03364_2mut	8,124	PRSRAIDIPVPHADKISWKITDPVWVDQWPLTYEKTLAAIALVQEQLAAGHIEPTNSPWNTPIFIIKKKSGSWRLLQDLRAVNKVMVPM GALQPGLPSPVAIPLNYHKIVIDLKDCFFTIPLHPEDRPYFAFSVPQINFQSPMPRYQWKVLPQGMANSPTLCQKFVAAAIAPVRSQW PEAYILHYMDDILLACDSAEAAKACYAHIISCLTSYGLKIAPDKVQVSEPFSYLGFELHHQQVFTPRVCLKTDHLKTLNDFQKLLGDIQW LRPYLKLPTSALVPLNNILKPDPNPLSVRALTPEAKQSLALINKAIQNQSVQQISYNLPLVLLLLPTPHTPTAVFWQPNGTDPTKNGSPL LWLHLPASPSKVLLTYPSLLAMLIIKGRYTGRQLFGRDPHSIIIPYTQDQLTWLLQTSDEWAIALSSFTGDIDNHYPSDPVIQFAKLHQFI FPKITKCAPIPQATLVFTDGSSNGIAAYVIDNQPISIKSPYLSAQLVELYAILQVFTVLAHQPFNLYTDSAYIAQSVPLLETVPFIKSSTNAT PLFSKLQQLILNRQHPFFIGHLRAHLNLPGPLAEGNALADAATQIFPIISD
SMRVH_P03364_2mutB	8,125	PRSRAIDIPVPHADKISWKITDPVWVDQWPLTYEKTLAAIALVQEQLAAGHIEPTNSPWNTPIFIIKKKSGSWRLLQDLRAVNKVMVPM GALQPGLPSPVAPPLNYHKIVIDLKDCFFTIPLHPEDRPYFAFSVPQINFQSPMPRYQWKVLPQGMANSPTLCQKFVAAAIAPVRSQW PEAYILHYMDDILLACDSAEAAKACYAHIISCLTSYGLKIAPDKVQVSEPFSYLGFELHHQQVFTPRVCLKTDHLKTLNDFQKLLGDIQW LRPYLKLPTSALVPLNNILKPDPNPLSVRALTPEAKQSLALINKAIQNQSVQQISYNLPLVLLLLPTPHTPTAVFWQPNGTDPTKNGSPL LWLHLPASPSKVLLTYPSLLAMLIIKGRYTGRQLFGRDPHSIIIPYTQDQLTWLLQTSDEWAIALSSFTGDIDNHYPSDPVIQFAKLHQFI FPKITKCAPIPQATLVFTDGSSNGIAAYVIDNQPISIKSPYLSAQLVELYAILQVFTVLAHQPFNLYTDSAYIAQSVPLLETVPFIKSSTNAT PLFSKLQQLILNRQHPFFIGHLRAHLNLPGPLAEGNALADAATQIFPIISD
SRV2_P51517	8,126	LATAVDILAPQRYADPITWKSDEPVWVDQWPLTQEKLAAAQQLVQEQLQAGHIIESNSPWNTPIFVIKKKSGKWRLLQDLRAVNATM VLMGALQPGLPSPVAIPQGYFKIVIDLKDCFFTIPLQPVDQKRFAFSLPSTNFKQPMKRYQWKVLPQGMANSPTLCQKYVAAAIEPVR KSWAQMYIIHYMDDILIAGKLGEQVLQCFAQLKQALTTTGLQIAPEKVQLQDPYTYLGFQINGPKITNQKAVIRRDKLQTLNDFQKLLG DINWLRPYLHLTTGDLKPLFDILKGDSNPNSPRSLSEAALASLQKVETAIAEQFVTQIDYTQPLTFLIFNTTLTPTGLFWQNNPVMWVH LPASPKKVLLPYYDAIADLIILGRDNSKKYFGLEPSTIIQPYSKSQIHWLMQNTETWPIACASYAGNIDNHYPPNKLIQFCKLHAVVFPRII SKTPLDNALLVFTDGSSTGIAAYTFEKTTVRFKTSHTSAQLVELQALIAVLSAFPHRALNVYTDSAYLAHSIPLLETVSHIKHISDTAKFFL QCQQLIYNRSIPFYLGHIRAHSGLPGPLSQGNHITDLATKVVATTLTT
SRV2_P515	8,127	LATAVDILAPQRYADPITWKSDEPVWVDQWPLTQEKLAAAQQLVQEQLQAGHIIESNSPWNTPIFVIKKKSGKWRLLQDLRAVNATM VLMGALQPGLPSPVAPPQGYFKIVIDLKDCFFTIPLQPVDQKRFAFSLPSTNFKQPMKRYQWKVLPQGMANSPTLCQKYVAAAIEPV RKSWAQMYIIHYMDDILIAGKLGEQVLQCFAQLKQALTTTGLQIAPEKVQLQDPYTYLGFQINGPKITNQKAVIRRDKLQTLNDFQKLL

RT Name	SEQ ID NO:	RT amino acid sequence
17_2mutB		GDINWLRPYLHLTTGDLKPLFDILKGDSNPNSPRSLSEAALASLQKVETAIAEQFVTQIDYTQPLTFLIFNTTLTPTGLFWQNNPVMWV HLPASPKKVLLPYYDAIADLIILGRDNSKKYFGLEPSTIIQPYSKSQIHWLMQNTETWPIACASYAGNIDNHYPPNKLIQFCKLHAVVFPR IISKTPLDNALLVFTDGSSTGIAAYTFEKTTVRFKTSHTSAQLVELQALIAVLSAFPHRALNVYTDSAYLAHSIPLLETVSHIKHISDTAKFF LQCQQLIYNRSIPFYLGHIRAHSGLPGPLSQGNHITDLATKVVATTLTT
WDSV_O92815	8,128	SCQTKNTLNIDEYLLQFPDQLWASLPTDIGRMLVPPITIKIKDNASLPSIRQYPLPKDKTEGLRPLISSLENQGILIKCHSPCNTPIFPIKKA GRDEYRMIHDLRAINNIVAPLTAVVASPTTVLSNLAPSLHWFTVIDLSNAFFSVPIHKDSQYLFAFTFEGHQYTWTVLPQGFIHSPTLFS QALYQSLHKIKFKISSEICIYMDDVLIASKDRDTNLKDTAVMLQHLASEGHKVSKKKLQLCQQEVVYLGQLLTPEGRKILPDRKVTVSQ FQQPTTIRQIRAFLGLVGYCRHWIPEFSIHSKFLEKQLKKDTAEPFQLDDQQVEAFNKLKHAITTAPVLVVPDPAKPFQLYTSHSEHASI AVLTQKHAGRTRPIAFLSSKFDAIESGLPPCLKACASIHRSLTQADSFILGAPLIIYTTHAICTLLQRDRSQLVTASRFSKWEADLLRPEL TFVACSAVSPAHLYMQSCENNIPPHDCVLLTHTISRPRPDLSDLPIPDPDMTLFSDGSYTTGRGGAAVVMHRPVTDDFIIIHQQPGGA SAQTAELLALAAACHLATDKTVNIYTDSRYAYGVVHDFGHLWMHRGFVTSAGTPIKNHKEIEYLLKQIMKPKQVSVIKIEAHTKGVSME VRGNAAADEAAKNAVFLVQR
WDSV_O92815_2mut	8,129	SCQTKNTLNIDEYLLQFPDQLWASLPTDIGRMLVPPITIKIKDNASLPSIRQYPLPKDKTEGLRPLISSLENQGILIKCHSPCNTPIFPIKKA GRDEYRMIHDLRAINNIVAPLTAVVASPTTVLSNLAPSLHWFTVIDLSNAFFSVPIHKDSQYLFAFTFEGHQYTWTVLPQGFIHSPTLFN QALYQSLHKIKFKISSEICIYMDDVLIASKDRDTNLKDTAVMLQHLASEGHKVSKKKLQLCQQEVVYLGQLLTPEGRKILPDRKVTVSQ FQQPTTIRQIRAFLGLVGYCRHWIPEFSIHSKFLEKQLKPDTAEPFQLDDQQVEAFNKLKHAITTAPVLVVPDPAKPFQLYTSHSEHASI AVLTQKHAGRTRPIAFLSSKFDAIESGLPPCLKACASIHRSLTQADSFILGAPLIIYTTHAICTLLQRDRSQLVTASRFSKWEADLLRPEL TFVACSAVSPAHLYMQSCENNIPPHDCVLLTHTISRPRPDLSDLPIPDPDMTLFSDGSYTTGRGGAAVVMHRPVTDDFIIIHQQPGGA SAQTAELLALAAACHLATDKTVNIYTDSRYAYGVVHDFGHLWMHRGFVTSAGTPIKNHKEIEYLLKQIMKPKQVSVIKIEAHTKGVSME VRGNAAADEAAKNAVFLVQR
WDSV_O92815_2mutA	8,130	SCQTKNTLNIDEYLLQFPDQLWASLPTDIGRMLVPPITIKIKDNASLPSIRQYPLPKDKTEGLRPLISSLENQGILIKCHSPCNTPIFPIKKA GRDEYRMIHDLRAINNIVAPLTAVVASPTTVLSNLAPSLHWFTVIDLSNAFFSVPIHKDSQYLFAFTFEGHQYTWTVLPQGFIHSPTLFN QALYQSLHKIKFKISSEICIYMDDVLIASKDRDTNLKDTAVMLQHLASEGHKVSKKKLQLCQQEVVYLGQLLTPEGRKILPDRKVTVSQ FQQPTTIRQIRAFLGKVGYCRHFIPEFSIHSKFLEKQLKPDTAEPFQLDDQQVEAFNKLKHAITTAPVLVVPDPAKPFQLYTSHSEHASI AVLTQKHAGRTRPIAFLSSKFDAIESGLPPCLKACASIHRSLTQADSFILGAPLIIYTTHAICTLLQRDRSQLVTASRFSKWEADLLRPEL TFVACSAVSPAHLYMQSCENNIPPHDCVLLTHTISRPRPDLSDLPIPDPDMTLFSDGSYTTGRGGAAVVMHRPVTDDFIIIHQQPGGA SAQTAELLALAAACHLATDKTVNIYTDSRYAYGVVHDFGHLWMHRGFVTSAGTPIKNHKEIEYLLKQIMKPKQVSVIKIEAHTKGVSME VRGNAAADEAAKNAVFLVQR
WMSV_P03359	8,131	VLNLEEEYRLHEKPVPSSIDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMSKEAREGIRPHIQRFLDLGVLVP CQSPWNTPLLPVKKPGTNDYRPVQDLREINKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPE KGNTGQLTWTRLPQGFKNSPTLFDEALHRDLAPFRALNPQVVLLQYVDDLLVAAPTYRDCKEGTQKLLQELSKLGYRVSAKKAQLC QKEVTYLGYLLKEGKRWLTPARKATVMKIPPPTTPRQVREFLGTAGFCRLWIPGFASLAAPLYPLTKESIPFIWTEEHQKAFDRIKEAL LSAPALALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAVAAVALLLKDADKLTLGQNVTVIASHS LESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVHRCSEILAEETGTRRDLKDQPLPGVPAWYTDGSS FIAEGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDINIYTDSRYAFATAHIHGAIYKQRGLLTSAGKDIKNKEEI LALLEAIHLPKRVAIIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKP
WMSV_P03359_3mut	8,132	VLNLEEEYRLHEKPVPSSIDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMSKEAREGIRPHIQRFLDLGVLVP CQSPWNTPLLPVKKPGTNDYRPVQDLREINKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPE KGNTGQLTWTRLPQGFKNSPTLFNEALHRDLAPFRALNPQVVLLQYVDDLLVAAPTYRDCKEGTQKLLQELSKLGYRVSAKKAQLC QKEVTYLGYLLKEGKRWLTPARKATVMKIPPPTTPRQVREFLGTAGFCRLWIPGFASLAAPLYPLTKPSIPFIWTEEHQKAFDRIKEAL LSAPALALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAVAAVALLLKDADKLTLGQNVTVIASHS LESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVHRCSEILAEETGTRRDLKDQPLPGVPAWYTDGSS FIAEGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDINIYTDSRYAFATAHIHGAIYKQRGWLTSAGKDIKNKEE ILALLEAIHLPKRVAIIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKP
WMSV_P03359_3mutA	8,133	VLNLEEEYRLHEKPVPSSIDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMSKEAREGIRPHIQRFLDLGVLVP CQSPWNTPLLPVKKPGTNDYRPVQDLREINKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPE KGNTGQLTWTRLPQGFKNSPTLFNEALHRDLAPFRALNPQVVLLQYVDDLLVAAPTYRDCKEGTQKLLQELSKLGYRVSAKKAQLC QKEVTYLGYLLKEGKRWLTPARKATVMKIPPPTTPRQVREFLGKAGFCRLFIPGFASLAAPLYPLTKPSIPFIWTEEHQKAFDRIKEALL SAPALALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAVAAVALLLKDADKLTLGQNVTVIASHSL ESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVHRCSEILAEETGTRRDLKDQPLPGVPAWYTDGSSF IAEGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDINIYTDSRYAFATAHIHGAIYKQRGWLTSAGKDIKNKEEIL ALLEAIHLPKRVAIIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKP
XMRV6_A1Z651	8,134	TLNIEDEYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVP CQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDP EMGISGQLTWTRLPQGFKNSPTLFDEALHRDLADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQ KQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKTGTLFNWGPDQQKAYQEIKQ ALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILA PHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDLTDQPIPDADYTWYT DGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGLLTSEGREI KNKNEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLL

RT Name	SEQ ID NO:	RT amino acid sequence
XMRV6_A1Z651_3mut	8,135	TLNIEDEYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVP CQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDP EMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQ KQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQ ALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILA PHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDLTDQPIPDADYTWYT DGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGR EIKNKNEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLL
XMRV6_A1Z651_3mutA	8,136	TLNIEDEYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVP CQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDP EMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQ KQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQ ALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILA PHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDLTDQPIPDADYTWYT DGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGR EIKNKNEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLL

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, 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	

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):
TLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRL
LDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRL
HPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFDEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGT
RALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFA
EMAAPLYPLTKTGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLS
KKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQF
GPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAK
ALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGLLTSEGKEIKNKDEILALLKALFLPKRL
SIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLI (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:
TLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRL
LDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRL
HPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFDEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGT
RALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFA
EMAAPLYPLTKTGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLS
KKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQF
GPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAK
ALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGLLTSEGKEIKNKDEILALLKALFLPKRL
SIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLL (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:

TLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRL
LDQGILVPCQSPWNTPLLP**VKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFC**
LRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFDEALHRDLADFRIQHPDLILLQYVDDLLLAATS
ELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTA
GFCRLWIPGFAEMAAPLYPLTKTGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKL
GPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQ
ALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAA
VTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGLLTSEGKEIKNKDEIL
ALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAA (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):

TLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRL
LDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRL
HPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGT
RALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFA
EMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLS
KKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQF
GPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAK
ALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKR
LSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLI (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).

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 as described herein.

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: 15464), 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 ("LAGLIDADG" disclosed as SEQ ID NO: 15464) with a single copy of the LAGLIDADG motif (SEQ ID NO: 15464) generally form homodimers, whereas members with two copies of the LAGLIDADG motif (SEQ ID NO: 15464) 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 x 10^{-3} – 1 x 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 x 10^8 s^{-1} M^{-1} *in vitro*. 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 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 x 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

MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRR
KNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHM
IKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLG
LTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLT
LLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGEL
HAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNE
KVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASL
GTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGK
TILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEM
ARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKD
DSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQIL
DSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKM
IAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSK
ESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKD
LIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKR
VILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQL
GGDGG (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

MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRR
KNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHM
IKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLG
LTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLT
LLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGEL
HAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNE
KVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASL
GTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGK
TILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEM
ARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKD
DSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQIL
DSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKM
IAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSK
ESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKD
LIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKR
VILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQL
GGDGGSGGSSGGSSGSETPGTSESATPESSGGSSGGSSGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQA
PLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNP
YNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLI
LLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFL
GKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRR
PVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVV
ALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAE
LIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARG
NRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE (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*	*SEQ ID NO:*	*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	MAAFKPNPINYILGLDIGIASVGWAMVEIDEEENPIRLIDLGVRVFERAEVPKTGDSLAMARRLARSVRRLTRRRAHRLLRARRLLKREGVLQAADFDENGLIKSLPNTPWQLRAAALDRKLTPLEWSAVLLHLIKHRGYLSQRKNEGETADKELGALLKGVANNAHALQTGDFRTPAELALNKFEKESGHIRNQRGDYSHTFSRKDLQAELILLFEKQKEFGNPHVSGGLKEGIETLLMTQRPALSGDAVQKMLGHCTFEPAEPKAAKNTYTAERFIWLTKLNNLRILEQGSERPLTDTERATLMDEPYRKSKLTYAQARKLLGLEDTAFFKGLRYGKDNAEASTLMEMKAYHAISRALEKEGLKDKKSPLNLSSELQDEIGTAFSLFKTDEDITGRLKDRVQPEILEALLKHISFDKFVQISLKALRRIVPLMEQGKRYDEACAEIYGDHYGKKNTEEKIYLPPIPADEIRNPVVLRALSQARKVINGVVRRYGSPARIHIETAREVGKSFKDRKEIEKRQEENRKDREKAAAKFREYFPNFVGEPKSKDILKLRLYEQQHGKCLYSGKEINLVRLNEKGYVEIDHALPFSRTWDDSFNNKVLVLGSENQNKGNQTPYEYFNGKDNSREWQEFKARVETSRFPRSKKQRILLQKFDEDGFKECNLNDTRYVNRFLCQFVADHILLTGKGKRRVFASNGQITNLLRGFWGLRKVRAENDRHHALDAVVVACSTVAMQQKITRFVRYKEMNAFDGKTIDKETGKVLHQKTHFPQPWEFFAQEVMIRVFGKPDGKPEFEEADTPEKLRTLLAEKLSSRPEAVHEYVTPLFVSRAPNRKMSGAHKDTLRSAKRFVKHNEKISVKRVWLTEIKLADLENMVNYKNGREIELYEALKARLEAYGGNAKQAFDPKDNPFYKKGGQLVKAVRVEKTQESGVLLNKKNAYTIADNGDMVRVDVFCKVDKKGKNQYFIVPIYAWQVAENILPDIDCKGYRIDDSYTFCFSLHKYDLIAFQKDEKSK	9,001	N611A	H588A	D16A

		VEFAYYINCDSSNGRFYLAWHDKGSKEQQFRISTQNLVLIQKYQVN ELGKEIRPCRLKKRPPVR				
PpnCas9	Pasteurella pneumotropic a	MQNNPLNYILGLDLGIASIGWAVVEIDEESSPIRLIDVGVRTFERAE VAKTGESLALSRRLARSSRRLIKRRAERLKKAKRLLKAEKILHSIDEKLP INVWQLRVKGLKEKLERQEWAAVLLHLSKHRGYLSQRKNEGKSDN KELGALLSGIASNHQMLQSSEYRTPAEIAVKKFQVEEGHIRNQRGS YTHTFSRLDLLAEMELLFQRQAELGNSYTSTTLLENLTALLMWQKP ALAGDAILKMLGKCTFEPSEYKAAKNSYSAERFVWLTKLNNLRILEN GTERALNDNERFALLEQPYEKSKLTYAQVRAMLALSDNAIFKGVRY LGEDKKTVESKTTLIEMKFYHQIRKTLGSAELKKEWNELKGNSDLLD EIGTAFSLYKTDDDICRYLEGKLPERVLNALLENLNFDKFIQLSLKALH QILPLMLQGQRYDEAVSAIYGDHYGKKSTETTRLLPTIPADEIRNPV VLRTLTQARKVINAVVRLYGSPARIHIETAREVGKSYQDRKKLEKQQ EDNRKQRESAVKKFKEMFPHFVGEPKGKDILKMRLYELQQAKCLYS GKSLELHRLLEKGYVEVDHALPFSRTWDDSFNNKVLVLANENQNK GNLTPYEWLDGKNNSERWQHFVVRVQTSGFSYAKKQRILNHKLD EKGFIERNLNDTRYVARFLCNFIADNMLLVGKGKRNVFASNGQITA LLRHRWGLQKVREQNDRHHALDAVVVACSTVAMQQKITRFVRY NEGNVFSGERIDRETGEIIPLHFPSPWAFFKENVEIRIFSENPKLELEN RLPDYPQYNHEWVQPLFVSRMPTRKMTGQGHMETVKSAKRLNE GLSVLKVPLTQLKLSDLERMVNRDREIALYESLKARLEQFGNDPAKA FAEPFYKKGGALVKAVRLEQTQKSGVLVRDGNGVADNASMVRVD VFTKGGKYFLVPIYTWQVAKGILPNRAATQGKDENDWDIMDEMA TFQFSLCQNDLIKLVTKKKTIFGYFNGLNRATSNINIKEHDLDKSKGK LGIYLEVGVKLAISLEKYQVDELGKNIRPCRPTKRQHVR	9,002	N605A	H582A	D13A
SauCas9	Staphylococc us aureus	MKRNYILGLDIGITSVGYGIIDYETRDVIDAGVRLFKEANVENNEGR RSKRGARRLKRRRRHRIQRVKKLLFDYNLLTDHSELSGINPYEARVK GLSQKLSEEEFSAALLHLAKRRGVHNVNEVEEDTGNELSTKEQISRN SKALEEKYVAELQLERLKKDGEVRGSINRFKTSDYVKEAKQLLKVQK AYHQLDQSFIDTYIDLLETRRTYYEGPGEGSPFGWKDIKEWYEMLM GHCTYFPEELRSVKYAYNADLYNALNDLNNLVITRDENEKLEYYEKF QIIENVFKQKKKPTLKQIAKEILVNEEDIKGYRVTSTGKPEFTNLKVY HDIKDITARKEIIENAELLDQIAKILTIYQSSEDIQEELTNLNSELTQEEI EQISNLKGYTGTHNLSLKAINLILDELWHTNDNQIAIFNRLKLVPKKV DLSQQKEIPTTLVDDFILSPVVKRSFIQSIKVINAIIKKYGLPNDIIIELA REKNSKDAQKMINEMQKRNRQTNERIEEIIRTTGKENAKYLIEKIKL HDMQEGKCLYSLEAIPLEDLLNNPFNYEVDHIIPRSVSFDNSFNNKV LVKQEENSKKGNRTPFQYLSSSDSKISYETFKKHILNLAKGKGRISKT KKEYLLEERDINRFSVQKDFINRNLVDTRYATRGLMNLLRSYFRVNN LDVKVKSINGGFTSFLRRKWKFKKERNKGYKHHAEDALIIANADFIF KEWKKLDKAKKVMENQMFEEKQAESMPEIETEQEYKEIFITPHQIK HIKDFKDYKYSHRVDKKPNRELINDTLYSTRKDDKGNTLIVNNLNGL YDKDNDKLKKLINKSPEKLLMYHHDPQTYQKLKLIMEQYGDEKNPL YKYYEETGNYLTKYSKKDNGPVIKKIKYYGNKLNAHLDITDDYPNSR NKVVKLSLKPYRFDVYLDNGVYKFVTVKNLDVIKKENYYEVNSKCYE EAKKLKKISNQAEFIASFYNNDLIKINGELYRVIGVNNDLLNRIEVNM IDITYREYLENMNDKRPPRIIKTIASKTQSIKKYSTDILGNLYEVKSKKH PQIIKKG	9,003	N580A	H557A	D10A
SauCas9-KKH	Staphylococc us aureus	MKRNYILGLDIGITSVGYGIIDYETRDVIDAGVRLFKEANVENNEGR RSKRGARRLKRRRRHRIQRVKKLLFDYNLLTDHSELSGINPYEARVK GLSQKLSEEEFSAALLHLAKRRGVHNVNEVEEDTGNELSTKEQISRN SKALEEKYVAELQLERLKKDGEVRGSINRFKTSDYVKEAKQLLKVQK	9,004	N580A	H557A	D10A

		AYHQLDQSFIDTYIDLLETRRTYYEGPGEGSPFGWKDIKEWYEMLM GHCTYFPEELRSVKYAYNADLYNALNDLNNLVITRDENEKLEYYEKF QIIENVFKQKKKPTLKQIAKEILVNEEDIKGYRVTSTGKPEFTNLKVY HDIKDITARKEIIENAELLDQIAKILTIYQSSEDIQEELTNLNSELTQEEI EQISNLKGYTGTHNLSLKAINLILDELWHTNDNQIAIFNRLKLVPKKV DLSQQKEIPTTLVDDFILSPVVKRSFIQSIKVINAIIKKYGLPNDIIIELA REKNSKDAQKMINEMQKRNRQTNERIEEIIRTTGKENAKYLIEKIKL HDMQEGKCLYSLEAIPLEDLLNNPFNYEVDHIIPRSVSFDNSFNNKV LVKQEENSKKGNRTPFQYLSSSDSKISYETFKKHILNLAKGKGRISKT KKEYLLEERDINRFSVQKDFINRNLVDTRYATRGLMNLLRSYFRVNN LDVKVKSINGGFTSFLRRKWKFKKERNKGYKHHAEDALIIANADFIF KEWKKLDKAKKVMENQMFEEKQAESMPEIETEQEYKEIFITPHQIK HIKDFKDYKYSHRVDKKPNRKLINDTLYSTRKDDKGNTLIVNNLNGL YDKDNDKLKKLINKSPEKLLMYHHDPQTYQKLKLIMEQYGDEKNPL YKYYEETGNYLTKYSKKDNGPVIKKIKYYGNKLNAHLDITDDYPNSR NKVVKLSLKPYRFDVYLDNGVYKFVTVKNLDVIKKENYYEVNSKCYE EAKKLKKISNQAEFIASFYKNDLIKINGELYRVIGVNNDLLNRIEVNM IDITYREYLENMNDKRPPHIIKTIASKTQSIKKYSTDILGNLYEVKSKK HPQIIKKG				
SauriCas9	Staphylococcus auricularis	MQENQQKQNYILGLDIGITSVGYGLIDSKTREVIDAGVRLFPEADSE NNSNRRSKRGARRLKRRRIHRLNRVKDLLADYQMIDLNNVPKSTD PYTIRVKGLREPLTKEEFAIALLHIAKRRGLHNISVSMGDEEQDNELS TKQQLQKNAQQLQDKYVCELQLERLTNINKVRGEKNRFKTEDFVK EVKQLCETQRQYHNIDDQFIQQYIDLVSTRREYFEGPGNGSPYGW DGDLLKWYEKLMGRCTYFPEELRSVKYAYSADLFNALNDLNNLVVT RDDNPKLEYYEKYHIIENVFKQKKNPTLKQIAKEIGVQDYDIRGYRIT KSGKPQFTSFKLYHDLKNIFEQAKYLEDVEMLDEIAKILTIYQDEISIK KALDQLPELLTESEKSQIAQLTGYTGTHRLSLKCIHIVIDELWESPEN QMEIFTRLNLKPKKVEMSEIDSIPTTLVDEFILSPVVKRAFIQSIKVIN AVINRFGLPEDIIIELAREKNSKDRRKFINKLQKQNEATRKKIEQLLAK YGNTNAKYMIEKIKLHDMQEGKCLYSLEAIPLEDLLSNPTHYEVDHII PRSVSFDNSLNNKVLVKQSENSKKGNRTPYQYLSSNESKISYNQFK QHILNLSKAKDRISKKKRDMLLEERDINKFEVQKEFINRNLVDTRYA TRELSNLLKTYFSTHDYAVKVKTINGGFTNHLRKVWDFKKHRNHGY KHHAEDALVIANADFLFKTHKALRRTDKILEQPGLEVNDTTVKVDT EEKYQELFETPKQVKNIKQFRDFKYSHRVDKKPNRQLINDTLYSTREI DGETYVVQTLKDLYAKDNEKVKKLFTERPQKILMYQHDPKTFEKLM TILNQYAEAKNPLAAYYEDKGEYVTKYAKKGNGPAIHKIKYIDKKLG SYLDVSNKYPETQNKLVKLSLKSFRFDIYKCEQGYKMVSIGYLDVLKK DNYYYIPKDKYEAEKQKKKIKESDLFVGSFYYNDLIMYEDELFRVIGV NSDINNLVELNMVDITYKDFCEVNNVTGEKRIKKTIGKRVVLIEKYTT DILGNLYKTPLPKKPQLIFKRGEL	9,005	N588A	H565A	D15A
SauriCas9-KKH	Staphylococcus auricularis	MQENQQKQNYILGLDIGITSVGYGLIDSKTREVIDAGVRLFPEADSE NNSNRRSKRGARRLKRRRIHRLNRVKDLLADYQMIDLNNVPKSTD PYTIRVKGLREPLTKEEFAIALLHIAKRRGLHNISVSMGDEEQDNELS TKQQLQKNAQQLQDKYVCELQLERLTNINKVRGEKNRFKTEDFVK EVKQLCETQRQYHNIDDQFIQQYIDLVSTRREYFEGPGNGSPYGW DGDLLKWYEKLMGRCTYFPEELRSVKYAYSADLFNALNDLNNLVVT RDDNPKLEYYEKYHIIENVFKQKKNPTLKQIAKEIGVQDYDIRGYRIT KSGKPQFTSFKLYHDLKNIFEQAKYLEDVEMLDEIAKILTIYQDEISIK KALDQLPELLTESEKSQIAQLTGYTGTHRLSLKCIHIVIDELWESPEN QMEIFTRLNLKPKKVEMSEIDSIPTTLVDEFILSPVVKRAFIQSIKVIN AVINRFGLPEDIIIELAREKNSKDRRKFINKLQKQNEATRKKIEQLLAK	9,006	N588A	H565A	D15A

		YGNTNAKYMIEKIKLHDMQEGKCLYSLEAIPLEDLLSNPTHYEVDHII PRSVSFDNSLNNKVLVKQSENSKKGNRTPYQYLSSNESKISYNQFK QHILNLSKAKDRISKKKRDMLLEERDINKFEVQKEFINRNLVDTRYA TRELSNLLKTYFSTHDYAVKVKTINGGFTNHLRKVWDFKKHRNHGY KHHAEDALVIANADFLFKTHKALRRTDKILEQPGLEVNDTTVKVDT EEKYQELFETPKQVKNIKQFRDFKYSHRVDKKPNRKLINDTLYSTREI DGETYVVQTLKDLYAKDNEKVKKLFTERPQKILMYQHDPKTFEKLM TILNQYAEAKNPLAAYYEDKGEYVTKYAKKGNGPAIHKIKYIDKKLG SYLDVSNKYPETQNKLVKLSLKSFRFDIYKCEQGYKMVSIGYLDVLKK DNYYYIPKDKYEAEKQKKKIKESDLFVGSFYKNDLIMYEDELFRVIGV NSDINNLVELNMVDITYKDFCEVNNVTGEKHIKKTIGKRVVLIEKYT TDILGNLYKTPLPKKPQLIFKRGEL				
ScaCas9-Sc++	Streptococcus canis	MEKKYSIGLDIGTNSVGWAVITDDYKVPSKKFKVLGNTNRKSIKKNL MGALLFDSGETAEATRLKRTARRRYTRRKNRIRYLQEIFANEMAKL DDSFFQRLEESFLVEEDKKNERHPIFGNLADEVAYHRNYPTIYHLRK KLADSPEKADLRLIYLALAHIIKFRGHFLIEGKLNAENSDVAKLFYQLI QTYNQLFEESPLDEIEVDAKGILSARLSKSKRLEKLIAVFPNEKKNGLF GNIIALALGLTPNFKSNFDLTEDAKLQLSKDTYDDDLDELLGQIGDQ YADLFSAAKNLSDAILLSDILRSNSEVTKAPLSASMVKRYDEHHQDL ALLKTLVRQQFPEKYAEIFKDDTKNGYAGYVGADKKLRKRSGKLAT EEEFYKFIKPILEKMDGAEELLAKLNRDDLLRKQRTFDNGSIPHQIHL KELHAILRRQEEFYPFLKENREKIEKILTFRIPYYVGPLARGNSRFAWL TRKSEEAITPWNFEEVVDKGASAQSFIERMTNFDEQLPNKKVLPKH SLLYEYFTVYNELTKVKYVTERMRKPEFLSGEQKKAIVDLLFKTNRKV TVKQLKEDYFKKIECFDSVEIIGVEDRFNASLGTYHDLLKIIKDKDFLD NEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRH YTGWGRLSRKMINGIRDKQSGKTILDFLKSDGFSNRNFMQLIHDD SLTFKEEIEKAQVSGQGDSLHEQIADLAGSPAIKKGILQTVKIVDELV KVMGHKPENIVIEMARENQTTTKGLQQSRERKKRIEEGIKELESQIL KENPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHI VPQSFIKDDSIDNKVLTRSVENRGKSDNVPSEEVVKKMKNYWRQL LNAKLITQRKFDNLTKAERGGLSEADKAGFIKRQLVETRQITKHVAR ILDSRMNTKRDKNDKPIREVKVITLKSKLVSDFRKDFQLYKVRDINN YHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSE QEIGKATAKRFFYSNIMNFFKTEVKLANGEIRKRPLIETNGETGEVV WNKEKDFATVRKVLAMPQVNIVKKTEVQTGGFSKESILSKRESAKLI PRKKGWDTRKYGGFGSPTVAYSILVVAKVEKGKAKKLKSVKVLVGI TIMEKGSYEKDPIGFLEAKGYKDIKKELIFKLPKYSLFELENGRRRMLA SAKELQKANELVLPQHLVRLLYYTQNISATTGSNNLGYIEQHREEFK EIFEKIIDFSEKYILKNKVNSNLKSSFDEQFAVSDSILLSNSFVSLLKYTS FGASGGFTFLDLDVKQGRLRYQTVTEVLDATLIYQSITGLYETRTDLS QLGGD	9,007	N872A	H849A	D10A
SpyCas9	Streptococcus pyogenes	MDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKN LIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVD DSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKL VDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNG LFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIG DQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQ DLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKP ILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRR QEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETI TPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFT	9,008	N863A	H840A	D10A

		VYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLK EDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENE DILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWG RLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDI QKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGR HKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEH PVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQ SFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDS RMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHA HDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGK ATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGR DFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKD WDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERS SFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGEL QKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYL DEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLT NLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQL GGD				
SpyCas9-NG	Streptococcus pyogenes	MDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKN LIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVD DSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKL VDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNG LFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIG DQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQ DLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKP ILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRR QEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETI TPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFT VYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLK EDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENE DILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWG RLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDI QKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGR HKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEH PVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQ SFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDS RMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHA HDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGK ATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGR DFATVRKVLSMPQVNIVKKTEVQTGGFSKESIRPKRNSDKLIARKKD WDPKKYGGFVSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERS SFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASARFLQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLD EIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTN LGAPRAFKYFDTTIDRKVYRSTKEVLDATLIHQSITGLYETRIDLSQLG GD	9,009	N863A	H840A	D10A
SpyCas9-SpRY	Streptococcus pyogenes	MDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKN LIGALLFDSGETAERTRLKRTARRRYTRRKNRICYLQEIFSNEMAKVD DSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKL VDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV	9,010	N863A	H840A	D10A

		QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNG LFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIG DQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQ DLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKP ILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRR QEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETI TPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFT VYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLK EDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENE DILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWG RLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDI QKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGR HKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEH PVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQ SFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDS RMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHA HDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGK ATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGR DFATVRKVLSMPQVNIVKKTEVQTGGFSKESIRPKRNSDKLIARKKD WDPKKYGGFLWPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMER SSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAKQL QKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYL DEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLT RLGAPRAFKYFDTTIDPKQYRSTKEVLDATLIHQSITGLYETRIDLSQL GGD				
St1Cas9	Streptococcus thermophilus	MSDLVLGLDIGIGSVGVGILNKVTGEIIHKNSRIFPAAQAENNLVRR TNRQGRRLARRKKHRRVRLNRLFEESGLITDFTKISINLNPYQLRVK GLTDELSNEELFIALKNMVKHRGISYLDDASDDGNSSVGDYAQIVK ENSKQLETKTPGQIQLERYQTYGQLRGDFTVEKDGKKHRLINVFPT SAYRSEALRILQTQQEFNPQITDEFINRYLEILTGKRKYYHGPGNEKS RTDYGRYRTSGETLDNIFGILIGKCTFYPDEFRAAKASYTAQEFNLLN DLNNLTVPTETKKLSKEQKNQIINYVKNEKAMGPAKLFKYIAKLLSC DVADIKGYRIDKSGKAEIHTFEAYRKMKTLETLDIEQMDRETLDKLA YVLTLNTEREGIQEALEHEFADGSFSQKQVDELVQFRKANSSIFGKG WHNFSVKLMMELIPELYETSEEQMTILTRLGKQKTTSSSNKTKYIDE KLLTEEIYNPVVAKSVRQAIKIVNAAIKEYGDFDNIVIEMARETNEDD EKKAIQKIQKANKDEKDAAMLKAANQYNGKAELPHSVFHGHKQL ATKIRLWHQQGERCLYTGKTISIHDLINNSNQFEVDHILPLSITFDDS LANKVLVYATANQEKGQRTPYQALDSMDDAWSFRELKAFVRESK TLSNKKKEYLLTEEDISKFDVRKKFIERNLVDTRYASRVVLNALQEHF RAHKIDTKVSVVRGQFTSQLRRHWGIEKTRDTYHHHAVDALIIAAS SQLNLWKKQKNTLVSYSEDQLLDIETGELISDDEYKESVFKAPYQHF VDTLKSKEFEDSILFSYQVDSKFNRKISDATIYATRQAKVGKDKADET YVLGKIKDIYTQDGYDAFMKIYKKDKSKFLMYRHDPQTFEKVIEPILE NYPNKQINEKGKEVPCNPFLKYKEEHGYIRKYSKKGNGPEIKSLKYY DSKLGNHIDITPKDSNNKVVLQSVSPWRADVYFNKTTGKYEILGLK YADLQFEKGTGTYKISQEKYNDIKKKEGVDSDSEFKFTLYKNDLLLVK DTETKEQQLFRFLSRTMPKQKHYVELKPYDKQKFEGGEALIKVLGN VANSGQCKKGLGKSNISIYKVRTDVLGNQHIIKNEGDKPKLDF	9,011	N622A	H599A	D9A
BlatCas9	Brevibacillus laterosporus	MAYTMGIDVGIASCGWAIVDLERQRIIDIGVRTFEKAENPKNGEAL AVPRREARSSRRRLRRKKHRIERLKHMFVRNGLAVDIQHLEQTLRS QNEIDVWQLRVDGLDRMLTQKEWLRVLIHLAQRRGFQSNRKTDG	9,012	N607A	H584A	D8A

		SSEDGQVLVNVTENDRLMEEKDYRTVAEMMVKDEKFSDHKRNK NGNYHGVVSRSSLLVEIHTLFETQRQHHNSLASKDFELEYVNIWSA QRPVATKDQIEKMIGTCTFLPKEKRAPKASWHFQYFMLLQTINHIR ITNVQGTRSLNKEEIEQVVNMALTKSKVSYHDTRKILDLSEEYQFVG LDYGKEDEKKKVESKETIIKLDDYHKLNKIFNEVELAKGETWEADDY DTVAYALTFFKDDEDIRDYLQNKYKDSKNRLVKNLANKEYTNELIGK VSTLSFRKVGHLSLKALRKIIPFLEQGMTYDKACQAAGFDFQGISKK KRSVVLPVIDQISNPVVNRALTQTRKVINALIKKYGSPETIHIETAREL SKTFDERKNITKDYKENRDKNEHAKKHLSELGIINPTGLDIVKYKLW CEQQGRCMYSNQPISFERLKESGYTEVDHIIPYSRSMNDSYNNRVL VMTRENREKGNQTPFEYMGNDTQRWYEFEQRVTTNPQIKKEKR QNLLLKGFTNRRELEMLERNLNDTRYITKYLSHFISTNLEFSPSDKKK KVVNTSGRITSHLRSRWGLEKNRGQNDLHHAMDAIVIAVTSDSFI QQVTNYYKRKERRELNGDDKFPLPWKFFREEVIARLSPNPKEQIEAL PNHFYSEDELADLQPIFVSRMPKRSITGEAHQAQFRRVVGKTKEGK NITAKKTALVDISYDKNGDFNMYGRETDPATYEAIKERYLEFGGNV KKAFSTDLHKPKKDGTKGPLIKSVRIMENKTLVHPVNKGKGVVYNS SIVRTDVFQRKEKYYLLPVYVTDVTKGKLPNKVIVAKKGYHDWIEVD DSFTFLFSLYPNDLIFIRQNPKKKISLKKRIESHSISDSKEVQEIHAYYK GVDSSTAAIEFIIHDGSYYAKGVGVQNLDCFEKYQVDILGNYFKVKG EKRLELETSDSNHKGKDVNSIKSTSR				
cCas9-v16	Staphylococcus aureus	MKRNYILGLDIGITSVGYGIIDYETRDVIDAGVRLFKEANVENNEGR RSKRGARRLKRRRRHRIQRVKKLLFDYNLLTDHSELSGINPYEARVK GLSQKLSEEEFSAALLHLAKRRGVHNVNEVEEDTGNELSTKEQISRN SKALEEKYVAELQLERLKKDGEVRGSINRFKTSDYVKEAKQLLKVQK AYHQLDQSFIDTYIDLLETRRTYYEGPGEGSPFGWKDIKEWYEMLM GHCTYFPEELRSVKYAYNADLYNALNDLNNLVITRDENEKLEYYEKF QIIENVFKQKKKPTLKQIAKEILVNEEDIKGYRVTSTGKPEFTNLKVY HDIKDITARKEIIENAELLDQIAKILTIYQSSEDIQEELTNLNSELTQEEI EQISNLKGYTGTHNLSLKAINLILDELWHTNDNQIAIFNRLKLVPKKV DLSQQKEIPTTLVDDFILSPVVKRSFIQSIKVINAIIKKYGLPNDIIIELA REKNSKDAQKMINEMQKRNRQTNERIEEIIRTTGKENAKYLIEKIKL HDMQEGKCLYSLEAIPLEDLLNNPFNYEVDHIIPRSVSFDNSFNNKV LVKQEENSKKGNRTPFQYLSSSDSKISYETFKKHILNLAKGKGRISKT KKEYLLEERDINRFSVQKDFINRNLVDTRYATRGLMNLLRSYFRVNN LDVKVKSINGGFTSFLRRKWKFKKERNKGYKHHAEDALIIANADFIF KEWKKLDKAKKVMENQMFEEKQAESMPEIETEQEYKEIFITPHQIK HIKDFKDYKYSHRVDKKPNRKLINDTLYSTRKDDKGNTLIVNNLNGL YDKDNDKLKKLINKSPEKLLMYHHDPQTYQKLKLIMEQYGDEKNPL YKYYEETGNYLTKYSKKDNGPVIKKIKYYGNKLNAHLDITDDYPNSR NKVVKLSLKPYRFDVYLDNGVYKFVTVKNLDVIKKENYYEVNSKCYE EAKKLKKISNQAEFIASFYKNDLIKINGELYRVIGVNSDKNNLIEVNM IDITYREYLENMNDKRPPHIIKTIASKTQSIKKYSTDILGNLYEVKSKK HPQIIKKG	9,013	N580A	H557A	D10A
cCas9-v17	Staphylococcus aureus	MKRNYILGLDIGITSVGYGIIDYETRDVIDAGVRLFKEANVENNEGR RSKRGARRLKRRRRHRIQRVKKLLFDYNLLTDHSELSGINPYEARVK GLSQKLSEEEFSAALLHLAKRRGVHNVNEVEEDTGNELSTKEQISRN SKALEEKYVAELQLERLKKDGEVRGSINRFKTSDYVKEAKQLLKVQK AYHQLDQSFIDTYIDLLETRRTYYEGPGEGSPFGWKDIKEWYEMLM GHCTYFPEELRSVKYAYNADLYNALNDLNNLVITRDENEKLEYYEKF QIIENVFKQKKKPTLKQIAKEILVNEEDIKGYRVTSTGKPEFTNLKVY HDIKDITARKEIIENAELLDQIAKILTIYQSSEDIQEELTNLNSELTQEEI EQISNLKGYTGTHNLSLKAINLILDELWHTNDNQIAIFNRLKLVPKKV	9,014	N580A	H557A	D10A

		DLSQQKEIPTTLVDDFILSPVVKRSFIQSIKVINAIIKKYGLPNDIIIELA REKNSKDAQKMINEMQKRNRQTNERIEEIIRTTGKENAKYLIEKIKL HDMQEGKCLYSLEAIPLEDLLNNPFNYEVDHIIPRSVSFDNSFNNKV LVKQEENSKKGNRTPFQYLSSSDSKISYETFKKHILNLAKGKGRISKT KKEYLLEERDINRFSVQKDFINRNLVDTRYATRGLMNLLRSYFRVNN LDVKVKSINGGFTSFLRRKWKFKKERNKGYKHHAEDALIIANADFIF KEWKKLDKAKKVMENQMFEEKQAESMPEIETEQEYKEIFITPHQIK HIKDFKDYKYSHRVDKKPNRKLINDTLYSTRKDDKGNTLIVNNLNGL YDKDNDKLKKLINKSPEKLLMYHHDPQTYQKLKLIMEQYGDEKNPL YKYYEETGNYLTKYSKKDNGPVIKKIKYYGNKLNAHLDITDDYPNSR NKVVKLSLKPYRFDVYLDNGVYKFVTVKNLDVIKKENYYEVNSKCYE EAKKLKKISNQAEFIASFYKNDLIKINGELYRVIGVNNSTRNIVELNMI DITYREYLENMNDKRPPHIIKTIASKTQSIKKYSTDILGNLYEVKSKKH PQIIKKG				
cCas9-v21	Staphylococcus aureus	MKRNYILGLDIGITSVGYGIIDYETRDVIDAGVRLFKEANVENNEGR RSKRGARRLKRRRRHRIQRVKKLLFDYNLLTDHSELSGINPYEARVK GLSQKLSEEEFSAALLHLAKRRGVHNVNEVEEDTGNELSTKEQISRN SKALEEKYVAELQLERLKKDGEVRGSINRFKTSDYVKEAKQLLKVQK AYHQLDQSFIDTYIDLLETRRTYYEGPGEGSPFGWKDIKEWYEMLM GHCTYFPEELRSVKYAYNADLYNALNDLNNLVITRDENEKLEYYEKF QIIENVFKQKKKPTLKQIAKEILVNEEDIKGYRVTSTGKPEFTNLKVY HDIKDITARKEIIENAELLDQIAKILTIYQSSEDIQEELTNLNSELTQEEI EQISNLKGYTGTHNLSLKAINLILDELWHTNDNQIAIFNRLKLVPKKV DLSQQKEIPTTLVDDFILSPVVKRSFIQSIKVINAIIKKYGLPNDIIIELA REKNSKDAQKMINEMQKRNRQTNERIEEIIRTTGKENAKYLIEKIKL HDMQEGKCLYSLEAIPLEDLLNNPFNYEVDHIIPRSVSFDNSFNNKV LVKQEENSKKGNRTPFQYLSSSDSKISYETFKKHILNLAKGKGRISKT KKEYLLEERDINRFSVQKDFINRNLVDTRYATRGLMNLLRSYFRVNN LDVKVKSINGGFTSFLRRKWKFKKERNKGYKHHAEDALIIANADFIF KEWKKLDKAKKVMENQMFEEKQAESMPEIETEQEYKEIFITPHQIK HIKDFKDYKYSHRVDKKPNRKLINDTLYSTRKDDKGNTLIVNNLNGL YDKDNDKLKKLINKSPEKLLMYHHDPQTYQKLKLIMEQYGDEKNPL YKYYEETGNYLTKYSKKDNGPVIKKIKYYGNKLNAHLDITDDYPNSR NKVVKLSLKPYRFDVYLDNGVYKFVTVKNLDVIKKENYYEVNSKCYE EAKKLKKISNQAEFIASFYKNDLIKINGELYRVIGVNSDDRNIIELNMI DITYREYLENMNDKRPPHIIKTIASKTQSIKKYSTDILGNLYEVKSKKH PQIIKKG	9,015	N580A	H557A	D10A
cCas9-v42	Staphylococcus aureus	MKRNYILGLDIGITSVGYGIIDYETRDVIDAGVRLFKEANVENNEGR RSKRGARRLKRRRRHRIQRVKKLLFDYNLLTDHSELSGINPYEARVK GLSQKLSEEEFSAALLHLAKRRGVHNVNEVEEDTGNELSTKEQISRN SKALEEKYVAELQLERLKKDGEVRGSINRFKTSDYVKEAKQLLKVQK AYHQLDQSFIDTYIDLLETRRTYYEGPGEGSPFGWKDIKEWYEMLM GHCTYFPEELRSVKYAYNADLYNALNDLNNLVITRDENEKLEYYEKF QIIENVFKQKKKPTLKQIAKEILVNEEDIKGYRVTSTGKPEFTNLKVY HDIKDITARKEIIENAELLDQIAKILTIYQSSEDIQEELTNLNSELTQEEI EQISNLKGYTGTHNLSLKAINLILDELWHTNDNQIAIFNRLKLVPKKV DLSQQKEIPTTLVDDFILSPVVKRSFIQSIKVINAIIKKYGLPNDIIIELA REKNSKDAQKMINEMQKRNRQTNERIEEIIRTTGKENAKYLIEKIKL HDMQEGKCLYSLEAIPLEDLLNNPFNYEVDHIIPRSVSFDNSFNNKV LVKQEENSKKGNRTPFQYLSSSDSKISYETFKKHILNLAKGKGRISKT KKEYLLEERDINRFSVQKDFINRNLVDTRYATRGLMNLLRSYFRVNN LDVKVKSINGGFTSFLRRKWKFKKERNKGYKHHAEDALIIANADFIF KEWKKLDKAKKVMENQMFEEKQAESMPEIETEQEYKEIFITPHQIK	9,016	N580A	H557A	D10A

		HIKDFKDYKYSHRVDKKPNRKLINDTLYSTRKDDKGNTLIVNNLNGL YDKDNDKLKKLINKSPEKLLMYHHDPQTYQKLKLIMEQYGDEKNPL YKYYEETGNYLTKYSKKDNGPVIKKIKYYGNKLNAHLDITDDYPNSR NKVVKLSLKPYRFDVYLDNGVYKFVTVKNLDVIKKENYYEVNSKCYE EAKKLKKISNQAEFIASFYKNDLIKINGELYRVIGVNNNRLNKIELNMI DITYREYLENMNDKRPPHIIKTIASKTQSIKKYSTDILGNLYEVKSKKH PQIIKKG				
CdiCas9	Corynebacterium diphtheriae	MKYHVGIDVGTFSVGLAAIEVDDAGMPIKTLSLVSHIHDSGLDPDEI KSAVTRLASSGIARRTRRLYRRKRRRLQQLDKFIQRQGWPVIELEDY SDPLYPWKVRAELAASYIADEKERGEKLSVALRHIARHRGWRNPYA KVSSLYLPDGPSDAFKAIREEIKRASGQPVPETATVGQMVTLCELGT LKLRGEGGVLSARLQQSDYAREIQEICRMQEIGQELYRKIIDVVFAA ESPKGSASSRVGKDPLQPGKNRALKASDAFQRYRIAALIGNLRVRV DGEKRILSVEEKNLVFDHLVNLTPKKEPEWVTIAEILGIDRGQLIGTA TMTDDGERAGARPPTHDTNRSIVNSRIAPLVDWWKTASALEQHA MVKALSNAEVDDFDSPEGAKVQAFFADLDDDVHAKLDSLHLPVG RAAYSEDTLVRLTRRMLSDGVDLYTARLQEFGIEPSWTPPTPRIGEP VGNPAVDRVLKTVSRWLESATKTWGAPERVIIEHVREGFVTEKRA REMDGDMRRRAARNAKLFQEMQEKLNVQGKPSRADLWRYQSV QRQNCQCAYCGSPITFSNSEMDHIVPRAGQGSTNTRENLVAVCH RCNQSKGNTPFAIWAKNTSIEGVSVKEAVERTRHWVTDTGMRST DFKKFTKAVVERFQRATMDEEIDARSMESVAWMANELRSRVAQH FASHGTTVRVYRGSLTAEARRASGISGKLKFFDGVGKSRLDRRHHAI DAAVIAFTSDYVAETLAVRSNLKQSQAHRQEAPQWREFTGKDAEH RAAWRVWCQKMEKLSALLTEDLRDDRVVVMSNVRLRLGNGSAH KETIGKLSKVKLSSQLSVSDIDKASSEALWCALTREPGFDPKEGLPAN PERHIRVNGTHVYAGDNIGLFPVSAGSIALRGGYAELGSSFHHARV YKITSGKKPAFAMLRVYTIDLLPYRNQDLFSVELKPQTMSMRQAEK KLRDALATGNAEYLGWLVVDDELVVDTSKIATDQVKAVEAELGTIR RWRVDGFFSPSKLRLRPLQMSKEGIKKESAPELSKIIDRPGWLPAV NKLFSDGNVTVVRRDSLGRVRLESTAHLPVTWKVQ	9,017	N597A	H573A	D8A
CjeCas9	Campylobacter jejuni	MARILAFDIGISSIGWAFSENDELKDCGVRIFTKVENPKTGESLALPR RLARSARKRLARRKARLNHLKHLIANEFKLNYEDYQSFDESLAKAYK GSLISPYELRFRALNELLSKQDFARVILHIAKRRGYDDIKNSDDKEKG AILKAIKQNEEKLANYQSVGEYLYKEYFQKFKENSKEFTNVRNKKES YERCIAQSFLKDELKLIFKKQREFGFSFSKKFEEEVLSVAFYKRALKDF SHLVGNCSFFTDEKRAPKNSPLAFMFVALTRIINLLNNLKNTEGILYT KDDLNALLNEVLKNGTLTYKQTKKLLGLSDDYEFKGEKGTYFIEFKKY KEFIKALGEHNLSQDDLNEIAKDITLIKDEIKLKKALAKYDLNQNQIDS LSKLEFKDHLNISFKALKLVTPLMLEGKKYDEACNELNLKVAINEDKK DFLPAFNETYYKDEVTNPVVLRAIKEYRKVLNALLKKYGKVHKINIEL AREVGKNHSQRAKIEKEQNENYKAKKDAELECEKLGLKINSKNILKL RLFKEQKEFCAYSGEKIKISDLQDEKMLEIDHIYPYSRSFDDSYMNKV LVFTKQNQEKLNQTPFEAFGNDSAKWQKIEVLAKNLPTKKQKRILD KNYKDKEQKNFKDRNLNDTRYIARLVLNYTKDYLDFLPLSDDENTKL NDTQKGSKVHVEAKSGMLTSALRHTWGFSAKDRNNHLHHAIDAV IIAYANNSIVKAFSDFKKEQESNSAELYAKKISELDYKNKRKFFEPFSG FRQKVLDKIDEIFVSKPERKKPSGALHEETFRKEEEFYQSYGGKEGVL KALELGKIRKVNGKIVKNGDMFRVDIFKHKKTNKFYAVPIYTMDFA LKVLPNKAVARSKKGEIKDWILMDENYEFCFSLYKDSLILIQTKDMQ EPEFVYYNAFTSSTVSLIVSKHDNKFETLSKNQKILFKNANEKEVIAKS IGIQNLKVFEKYIVSALGEVTKAEFRQREDFKK	9,018	N582A	H559A	D8A

GeoCas9	Geobacillus stearothermophilus	MRYKIGLDIGITSVGWAVMNLDIPRIEDLGVRIFDRAENPQTGESL ALPRRLARSARRRLRRRKHRLERIRRLVIREGILTKEELDKLFEEKHEI DVWQLRVEALDRKLNNDELARVLLHLAKRRGFKSNRKSERSNKEN STMLKHIEENRAILSSYRTVGEMIVKDPKFALHKRNKGENYTNTIAR DDLEREIRLIFSKQREFGNMSCTEEFENEYITIWASQRPVASKDDIEK KVGFCTFEPKEKRAPKATYTFQSFIAWEHINKLRLISPSGARGLTDEE RRLLYEQAFQKNKITYHDIRTLLHLPDDTYFKGIVYDRGESRKQNENI RFLELDAYHQIRKAVDKVYGKGKSSSFLPIDFDTFGYALTLFKDDADI HSYLRNEYEQNGKRMPNLANKVYDNELIEELLNLSFTKFGHLSLKAL RSILPYMEQGEVYSSACERAGYTFTGPKKKQKTMLLPNIPPIANPVV MRALTQARKVVNAIIKKYGSPVSIHIELARDLSQTFDERRKTKKEQD ENRKKNETAIRQLMEYGLTLNPTGHDIVKFKLWSEQNGRCAYSLQ PIEIERLLEPGYVEVDHVIPYSRSLDDSYTNKVLVLTRENREKGNRIPA EYLGVGTERWQQFETFVLTNKQFSKKKRDRLLRLHYDENEETEFKN RNLNDTRYISRFFANFIREHLKFAESDDKQKVYTVNGRVTAHLRSR WEFNKNREESDLHHAVDAVIVACTTPSDIAKVTAFYQRREQNKEL AKKTEPHFPQPWPHFADELRARLSKHPKESIKALNLGNYDDQKLES LQPVFVSRMPKRSVTGAAHQETLRRYVGIDERSGKIQTVVKTKLSEI KLDASGHFPMYGKESDPRTYEAIRQRLLEHNNDPKKAFQEPLYKPK KNGEPGPVIRTVKIIDTKNQVIPLNDGKTVAYNSNIVRVDVFEKDGK YYCVPVYTMDIMKGILPNKAIEPNKPYSEWKEMTEDYTFRFSLYPN DLIRIELPREKTVKTAAGEEINVKDVFVYYKTIDSANGGLELISHDHRF SLRGVGSRTLKRFEKYQVDVLGNIYKVRGEKRVGLASSAHSKPGKTI RPLQSTRD	9,019	N605A	H582A	D8A
iSpyMacCas9	Streptococcus spp.	MDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKN LIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVD DSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKL VDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRKLENLIAQLPGEKKNG LFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIG DQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQ DLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKP ILEKMDGTEELLVKLKREDLLRKQRTFDNGSIPHQIHLGELHAILRRQ EDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETIT PWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTV YNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKE DYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDI LEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQ KAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRH KPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPV ENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFL KDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLI TQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSR MNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAH DAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKA TAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDF ATVRKVLSMPQVNIVKKTEIQTVGQNGGLFDDNPKSPLEVTPSKLV PLKKELNPKKYGGYQKPTTAYPVLLITDTKQLIPISVMNKKQFEQNP VKFLRDRGYQQVGKNDFIKLPKYTLVDIGDGIKRLWASSKEIHKGN QLVVSKKSQILLYHAHHLDSDLSNDYLQNHNQQFDVLFNEIISFSKK CKLGKEHIQKIENVYSNKKNSASIEELAESFIKLLGFTQLGATSPFNFL	9,020	N863A	H840A	D10A

		GVKLNQKQYKGKKDYILPCTEGTLIRQSITGLYETRVDLSKIGEDSGG SGGSKRTADGSEFES				
NmeCas9	Neisseria meningitidis	MAAFKPNSINYILGLDIGIASVGWAMVEIDEEENPIRLIDLGVRVFE RAEVPKTGDSLAMARRLARSVRRLTRRRAHRLLRTRRLLKREGVLQ AANFDENGLIKSLPNTPWQLRAAALDRKLTPLEWSAVLLHLIKHRG YLSQRKNEGETADKELGALLKGVAGNAHALQTGDFRTPAELALNK FEKESGHIRNQRSDYSHTFSRKDLQAELILLFEKQKEFGNPHVSGGL KEGIETLLMTQRPALSGDAVQKMLGHCTFEPAEPKAAKNTYTAERF IWLTKLNNLRILEQGSERPLTDTERATLMDEPYRKSKLTYAQARKLL GLEDTAFFKGLRYGKDNAEASTLMEMKAYHAISRALEKEGLKDKKS PLNLSPELQDEIGTAFSLFKTDEDITGRLKDRIQPEILEALLKHISFDKF VQISLKALRRIVPLMEQGKRYDEACAEIYGDHYGKKNTEEKIYLPPIP ADEIRNPVVLRALSQARKVINGVVRRYGSPARIHIETAREVGKSFKD RKEIEKRQEENRKDREKAAAKFREYFPNFVGEPKSKDILKLRLYEQQ HGKCLYSGKEINLGRLNEKGYVEIDHALPFSRTWDDSFNNKVLVLG SENQNKGNQTPYEYFNGKDNSREWQEFKARVETSRFPRSKKQRIL LQKFDEDGFKERNLNDTRYVNRFLCQFVADRMRLTGKGKKRVFAS NGQITNLLRGFWGLRKVRAENDRHHALDAVVVACSTVAMQQKIT RFVRYKEMNAFDGKTIDKETGEVLHQKTHFPQPWEFFAQEVMIRV FGKPDGKPEFEEADTLEKLRTLLAEKLSSRPEAVHEYVTPLFVSRAPN RKMSGQGHMETVKSAKRLDEGVSVLRVPLTQLKLKDLEKMVNRE REPKLYEALKARLEAHKDDPAKAFAEPFYKYDKAGNRTQQVKAVR VEQVQKTGVWVRNHNGIADNATMVRVDVFEKGDKYYLVPIYSW QVAKGILPDRAVVQGKDEEDWQLIDDSFNFKFSLHPNDLVEVITKK ARMFGYFASCHRGTGNINIRIHDLDHKIGKNGILEGIGVKTALSFQK YQIDELGKEIRPCRLKKRPPVR	9,021	N611A	H588A	D16A
ScaCas9	Streptococcus canis	MEKKYSIGLDIGTNSVGWAVITDDYKVPSKKFKVLGNTNRKSIKKNL MGALLFDSGETAEATRLKRTARRRYTRRKNRIRYLQEIFANEMAKL DDSFFQRLEESFLVEEDKKNERHPIFGNLADEVAYHRNYPTIYHLRK KLADSPEKADLRLIYLALAHIIKFRGHFLIEGKLNAENSDVAKLFYQLI QTYNQLFEESPLDEIEVDAKGILSARLSKSKRLEKLIAVFPNEKKNGLF GNIIALALGLTPNFKSNFDLTEDAKLQLSKDTYDDDLDELLGQIGDQ YADLFSAAKNLSDAILLSDILRSNSEVTKAPLSASMVKRYDEHHQDL ALLKTLVRQQFPEKYAEIFKDDTKNGYAGYVGIGIKHRKRTTKLATQ EEFYKFIKPILEKMDGAEELLAKLNRDDLLRKQRTFDNGSIPHQIHLK ELHAILRRQEEFYPFLKENREKIEKILTFRIPYYVGPLARGNSRFAWLT RKSEEAITPWNFEEVVDKGASAQSFIERMTNFDEQLPNKKVLPKHS LLYEYFTVYNELTKVKYVTERMRKPEFLSGEQKKAIVDLLFKTNRKVT VKQLKEDYFKKIECFDSVEIIGVEDRFNASLGTYHDLLKIIKDKDFLDN EENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRHYT GWGRLSRKMINGIRDKQSGKTILDFLKSDGFSNRNFMQLIHDDSLT FKEEIEKAQVSGQGDSLHEQIADLAGSPAIKKGILQTVKIVDELVKV MGHKPENIVIEMARENQTTTKGLQQSRERKKRIEEGIKELESQILKE NPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVP QSFIKDDSIDNKVLTRSVENRGKSDNVPSEEVVKKMKNYWRQLLN AKLITQRKFDNLTKAERGGLSEADKAGFIKRQLVETRQITKHVARILD SRMNTKRDKNDKPIREVKVITLKSKLVSDFRKDFQLYKVRDINNYH HAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEI GKATAKRFFYSNIMNFFKTEVKLANGEIRKRPLIETNGETGEVVWN KEKDFATVRKVLAMPQVNIVKKTEVQTGGFSKESILSKRESAKLIPR KKGWDTRKYGGFGSPTVAYSILVVAKVEKGKAKKLKSVKVLVGITI MEKGSYEKDPIGFLEAKGYKDIKKELIFKLPKYSLFELENGRRRMLAS ATELQKANELVLPQHLVRLLYYTQNISATTGSNNLGYIEQHREEFKEI	9,022	N872A	H849A	D10A

		FEKIIDFSEKYILKNKVNSNLKSSFDEQFAVSDSILLSNSFVSLLKYTSF GASGGFTFLDLDVKQGRLRYQTVTEVLDATLIYQSITGLYETRTDLS QLGGD				
ScaCas9-HiFi-Sc++	Streptococcus canis	MEKKYSIGLDIGTNSVGWAVITDDYKVPSKKFKVLGNTNRKSIKKNL MGALLFDSGETAEATRLKRTARRRYTRRKNRIRYLQEIFANEMAKL DDSFFQRLEESFLVEEDKKNERHPIFGNLADEVAYHRNYPTIYHLRK KLADSPEKADLRLIYLALAHIIKFRGHFLIEGKLNAENSDVAKLFYQLI QTYNQLFEESPLDEIEVDAKGILSARLSKSKRLEKLIAVFPNEKKNGLF GNIIALALGLTPNFKSNFDLTEDAKLQLSKDTYDDDLDELLGQIGDQ YADLFSAAKNLSDAILLSDILRSNSEVTKAPLSASMVKRYDEHHQDL ALLKTLVRQQFPEKYAEIFKDDTKNGYAGYVGADKKLRKRSGKLAT EEEFYKFIKPILEKMDGAEELLAKLNRDDLLRKQRTFDNGSIPHQIHL KELHAILRRQEEFYPFLKENREKIEKILTFRIPYYVGPLARGNSRFAWL TRKSEEAITPWNFEEVVDKGASAQSFIERMTNFDEQLPNKKVLPKH SLLYEYFTVYNELTKVKYVTERMRKPEFLSGEQKKAIVDLLFKTNRKV TVKQLKEDYFKKIECFDSVEIIGVEDRFNASLGTYHDLLKIIKDKDFLD NEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRH YTGWGRLSRKMINGIRDKQSGKTILDFLKSDGFSNANFMQLIHDD SLTFKEEIEKAQVSGQGDSLHEQIADLAGSPAIKKGILQTVKIVDELV KVMGHKPENIVIEMARENQTTTKGLQQSRERKKRIEEGIKELESQIL KENPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHI VPQSFIKDDSIDNKVLTRSVENRGKSDNVPSEEVVKKMKNYWRQL LNAKLITQRKFDNLTKAERGGLSEADKAGFIKRQLVETRQITKHVAR ILDSRMNTKRDKNDKPIREVKVITLKSKLVSDFRKDFQLYKVRDINN YHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSE QEIGKATAKRFFYSNIMNFFKTEVKLANGEIRKRPLIETNGETGEVV WNKEKDFATVRKVLAMPQVNIVKKTEVQTGGFSKESILSKRESAKLI PRKKGWDTRKYGGFGSPTVAYSILVVAKVEKGKAKKLKSVKVLVGI TIMEKGSYEKDPIGFLEAKGYKDIKKELIFKLPKYSLFELENGRRRMLA SAKELQKANELVLPQHLVRLLYYTQNISATTGSNNLGYIEQHREEFK EIFEKIIDFSEKYILKNKVNSNLKSSFDEQFAVSDSILLSNSFVSLLKYTS FGASGGFTFLDLDVKQGRLRYQTVTEVLDATLIYQSITGLYETRTDLS QLGGD	9,023	N872A	H849A	D10A
SpyCas9-3var-NRRH	Streptococcus pyogenes	MDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKN LIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVD DSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKL VDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNG LFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIG DQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMVKRYDEHHQ DLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKP ILEKMDGTEELLVKLNREDLLRKQRTFDNGIIPHQIHLGELHAILRRQ GDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETIT PWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTV YNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKE DYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDI LEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRLRYTGWGRL SRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQ KAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGGH KPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPV ENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFL KDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLI TQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSR	9,024	N863A	H840A	D10A

		MNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAH DAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKA TAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDF ATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKGNSDKLIARKKDW DPKKYGGFNSPTAAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSF EKNPIGFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGVLHK GNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEI IEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNL GVPAAFKYFDTTIDKKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGG D				
SpyCas9-3var-NRTH	Streptococcus pyogenes	MDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKN LIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVD DSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKL VDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNG LFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIG DQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMVKRYDEHHQ DLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKP ILEKMDGTEELLVKLNREDLLRKQRTFDNGIIPHQIHLGELHAILRRQ GDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETIT PWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTV YNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKE DYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDI LEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRLRYTGWGRL SRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQ KAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGGH KPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPV ENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFL KDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLI TQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSR MNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAH DAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKA TAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDF ATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKGNSDKLIARKKDW DPKKYGGFNSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSF EKNPIGFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASASVLHK GNELALPSKYVNFLYLASHYEKLKGSSEDNKQKQLFVEQHKHYLDEI IEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNL GASAAFKYFDTTIGRKLYTSTKEVLDATLIHQSITGLYETRIDLSQLGG D	9,025	N863A	H840A	D10A
SpyCas9-3var-NRCH	Streptococcus pyogenes	MDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKN LIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVD DSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKL VDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNG LFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIG DQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMVKRYDEHHQ DLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKP ILEKMDGTEELLVKLNREDLLRKQRTFDNGIIPHQIHLGELHAILRRQ GDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETIT PWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTV YNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKE DYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDI	9,026	N863A	H840A	D10A

		LEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRLRYTGWGRL SRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQ KAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGGH KPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPV ENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFL KDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLI TQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSR MNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAH DAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKA TAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDF ATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKGNSDKLIARKKDW DPKKYGGFNSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSF EKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGVLQK GNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEI IEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNL GAPAAFKYFDTTINRKQYNTTKEVLDATLIRQSITGLYETRIDLSQLG GD				
SpyCas9-HF1	Streptococcus pyogenes	MDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKN LIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVD DSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKL VDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNG LFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIG DQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQ DLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKP ILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRR QEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETI TPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFT VYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLK EDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENE DILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWG RLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDI QKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGR HKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEH PVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQ SFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDS RMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHA HDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGK ATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGR DFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKD WDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERS SFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGEL QKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYL DEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLT NLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQL GGD	9,027	N863A	H840A	D10A
SpyCas9-QQR1	Streptococcus pyogenes	MDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKN LIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVD DSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKL VDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNG LFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIG	9,028	N863A	H840A	D10A

		DQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQ DLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKP ILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRR QEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETI TPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFT VYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLK EDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENE DILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWG RLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDI QKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGR HKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEH PVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQ SFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDS RMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHA HDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGK ATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGR DFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKD WDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERS SFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASARELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLD EIIEQISEFSKRVILADAQLDKVLSAYNKHRDKPIREQAENIIHLFTLTN LGAPAAFKYFDTTFKQKQYRSTKEVLDATLIHQSITGLYETRIDLSQL GGD				
SpyCas9-SpG	Streptococcus pyogenes	MDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKN LIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVD DSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKL VDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNG LFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIG DQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQ DLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKP ILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRR QEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETI TPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFT VYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLK EDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENE DILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWG RLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDI QKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGR HKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEH PVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQ SFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDS RMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHA HDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGK ATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGR DFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKD WDPKKYGGFLWPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMER SSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAKQL QKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYL DEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLT	9,029	N863A	H840A	D10A

		NLGAPAAFKYFDTTIDRKQYRSTKEVLDATLIHQSITGLYETRIDLSQL GGD				
SpyCas9-VQR	Streptococcus pyogenes	MDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKN LIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVD DSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKL VDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNG LFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIG DQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQ DLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKP ILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRR QEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETI TPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFT VYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLK EDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENE DILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWG RLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDI QKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGR HKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEH PVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQ SFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDS RMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHA HDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGK ATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGR DFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKD WDPKKYGGFVSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERS SFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGEL QKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYL DEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLT NLGAPAAFKYFDTTIDRKQYRSTKEVLDATLIHQSITGLYETRIDLSQL GGD	9,030	N863A	H840A	D10A
SpyCas9-VRER	Streptococcus pyogenes	MDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKN LIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVD DSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKL VDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNG LFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIG DQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQ DLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKP ILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRR QEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETI TPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFT VYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLK EDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENE DILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWG RLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDI QKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGR HKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEH PVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQ SFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDS RMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHA	9,031	N863A	H840A	D10A

		HDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGK ATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGR DFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKD WDPKKYGGFVSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERS SFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASARELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLD EIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTN LGAPAAFKYFDTTIDRKEYRSTKEVLDATLIHQSITGLYETRIDLSQLG GD				
SpyCas9-xCas	Streptococcus pyogenes	MDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKN LIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVD DSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKL VDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNG LFGNLIALSLGLTPNFKSNFDLAEDTKLQLSKDTYDDDLDNLLAQIG DQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKLYDEHHQD LTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPIL EKMDGTEELLVKLNREDLLRKQRTFDNGIIPHQIHLGELHAILRRQE DFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITP WNFEKVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVY NELTKVKYVTEGMRKPAFLSGDQKKAIVDLLFKTNRKVTVKQLKED YFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDIL EDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRL SRKLINGIRDKQSGKTILDFLKSDGFANRNFIQLIHDDSLTFKEDIQK AQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHK PENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVE NTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFL KDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLI TQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSR MNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAH DAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKA TAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDF ATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDW DPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSF EKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGVLQK GNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEI IEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNL GAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGG D	9,032	N863A	H840A	D10A
SpyCas9-xCas-NG	Streptococcus pyogenes	MDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKN LIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVD DSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKL VDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNG LFGNLIALSLGLTPNFKSNFDLAEDTKLQLSKDTYDDDLDNLLAQIG DQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKLYDEHHQD LTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPIL EKMDGTEELLVKLNREDLLRKQRTFDNGIIPHQIHLGELHAILRRQE DFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITP WNFEKVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVY NELTKVKYVTEGMRKPAFLSGDQKKAIVDLLFKTNRKVTVKQLKED YFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDIL EDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRL	9,033	N863A	H840A	D10A

		SRKLINGIRDKQSGKTILDFLKSDGFANRNFIQLIHDDSLTFKEDIQK AQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHK PENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVE NTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFL KDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLI TQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSR MNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAH DAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKA TAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDF ATVRKVLSMPQVNIVKKTEVQTGGFSKESIRPKRNSDKLIARKKDW DPKKYGGFVSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSF EKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASARFLQK GNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEI IEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNL GAPRAFKYFDTTIDRKVYRSTKEVLDATLIHQSITGLYETRIDLSQLG GD				
St1Cas9-CNRZ1066	Streptococcus thermophilus	MSDLVLGLDIGIGSVGVGILNKVTGEIIHKNSRIFPAAQAENNLVRR TNRQGRRLARRKKHRRVRLNRLFEESGLITDFTKISINLNPYQLRVK GLTDELSNEELFIALKNMVKHRGISYLDDASDDGNSSVGDYAQIVK ENSKQLETKTPGQIQLERYQTYGQLRGDFTVEKDGKKHRLINVFPT SAYRSEALRILQTQQEFNPQITDEFINRYLEILTGKRKYYHGPGNEKS RTDYGRYRTSGETLDNIFGILIGKCTFYPDEFRAAKASYTAQEFNLLN DLNNLTVPTETKKLSKEQKNQIINYVKNEKAMGPAKLFKYIAKLLSC DVADIKGYRIDKSGKAEIHTFEAYRKMKTLETLDIEQMDRETLDKLA YVLTLNTEREGIQEALEHEFADGSFSQKQVDELVQFRKANSSIFGKG WHNFSVKLMMELIPELYETSEEQMTILTRLGKQKTTSSSNKTKYIDE KLLTEEIYNPVVAKSVRQAIKIVNAAIKEYGDFDNIVIEMARETNEDD EKKAIQKIQKANKDEKDAAMLKAANQYNGKAELPHSVFHGHKQL ATKIRLWHQQGERCLYTGKTISIHDLINNSNQFEVDHILPLSITFDDS LANKVLVYATANQEKGQRTPYQALDSMDDAWSFRELKAFVRESK TLSNKKKEYLLTEEDISKFDVRKKFIERNLVDTRYASRVVLNALQEHF RAHKIDTKVSVVRGQFTSQLRRHWGIEKTRDTYHHHAVDALIIAAS SQLNLWKKQKNTLVSYSEEQLLDIETGELISDDEYKESVFKAPYQHF VDTLKSKEFEDSILFSYQVDSKFNRKISDATIYATRQAKVGKDKKDET YVLGKIKDIYTQDGYDAFMKIYKKDKSKFLMYRHDPQTFEKVIEPILE NYPNKQMNEKGKEVPCNPFLKYKEEHGYIRKYSKKGNGPEIKSLKY YDSKLLGNPIDITPENSKNKVVLQSLKPWRTDVYFNKATGKYEILGL KYADLQFEKGTGTYKISQEKYNDIKKKEGVDSDSEFKFTLYKNDLLLV KDTETKEQQLFRFLSRTLPKQKHYVELKPYDKQKFEGGEALIKVLGN VANGGQCIKGLAKSNISIYKVRTDVLGNQHIIKNEGDKPKLDF	9,034	N622A	H599A	D9A
St1Cas9-LMG1831	Streptococcus thermophilus	MSDLVLGLDIGIGSVGVGILNKVTGEIIHKNSRIFPAAQAENNLVRR TNRQGRRLARRKKHRRVRLNRLFEESGLITDFTKISINLNPYQLRVK GLTDELSNEELFIALKNMVKHRGISYLDDASDDGNSSVGDYAQIVK ENSKQLETKTPGQIQLERYQTYGQLRGDFTVEKDGKKHRLINVFPT SAYRSEALRILQTQQEFNPQITDEFINRYLEILTGKRKYYHGPGNEKS RTDYGRYRTSGETLDNIFGILIGKCTFYPDEFRAAKASYTAQEFNLLN DLNNLTVPTETKKLSKEQKNQIINYVKNEKAMGPAKLFKYIAKLLSC DVADIKGYRIDKSGKAEIHTFEAYRKMKTLETLDIEQMDRETLDKLA YVLTLNTEREGIQEALEHEFADGSFSQKQVDELVQFRKANSSIFGKG WHNFSVKLMMELIPELYETSEEQMTILTRLGKQKTTSSSNKTKYIDE KLLTEEIYNPVVAKSVRQAIKIVNAAIKEYGDFDNIVIEMARETNEDD EKKAIQKIQKANKDEKDAAMLKAANQYNGKAELPHSVFHGHKQL ATKIRLWHQQGERCLYTGKTISIHDLINNSNQFEVDHILPLSITFDDS	9,035	N622A	H599A	D9A

		LANKVLVYATANQEKGQRTPYQALDSMDDAWSFRELKAFVRESK TLSNKKKEYLLTEEDISKFDVRKKFIERNLVDTRYASRVVLNALQEHF RAHKIDTKVSVVRGQFTSQLRRHWGIEKTRDTYHHHAVDALIIAAS SQLNLWKKQKNTLVSYSEEQLLDIETGELISDDEYKESVFKAPYQHF VDTLKSKEFEDSILFSYQVDSKFNRKISDATIYATRQAKVGKDKKDET YVLGKIKDIYTQDGYDAFMKIYKKDKSKFLMYRHDPQTFEKVIEPILE NYPNKQMNEKGKEVPCNPFLKYKEEHGYIRKYSKKGNGPEIKSLKY YDSKLLGNPIDITPENSKNKVVLQSLKPWRTDVYFNKNTGKYEILGL KYADLQFEKKTGTYKISQEKYNGIMKEEGVDSDSEFKFTLYKNDLLL VKDTETKEQQLFRFLSRTMPNVKYYVELKPYSKDKFEKNESLIEILGS ADKSGRCIKGLGKSNISIYKVRTDVLGNQHIIKNEGDKPKLDF				
St1Cas9-MTH17CL396	Streptococcus thermophilus	MSDLVLGLDIGIGSVGVGILNKVTGEIIHKNSRIFPAAQAENNLVRR TNRQGRRLARRKKHRRVRLNRLFEESGLITDFTKISINLNPYQLRVK GLTDELSNEELFIALKNMVKHRGISYLDDASDDGNSSVGDYAQIVK ENSKQLETKTPGQIQLERYQTYGQLRGDFTVEKDGKKHRLINVFPT SAYRSEALRILQTQQEFNPQITDEFINRYLEILTGKRKYYHGPGNEKS RTDYGRYRTSGETLDNIFGILIGKCTFYPDEFRAAKASYTAQEFNLLN DLNNLTVPTETKKLSKEQKNQIINYVKNEKAMGPAKLFKYIAKLLSC DVADIKGYRIDKSGKAEIHTFEAYRKMKTLETLDIEQMDRETLDKLA YVLTLNTEREGIQEALEHEFADGSFSQKQVDELVQFRKANSSIFGKG WHNFSVKLMMELIPELYETSEEQMTILTRLGKQKTTSSSNKTKYIDE KLLTEEIYNPVVAKSVRQAIKIVNAAIKEYGDFDNIVIEMARETNEDD EKKAIQKIQKANKDEKDAAMLKAANQYNGKAELPHSVFHGHKQL ATKIRLWHQQGERCLYTGKTISIHDLINNSNQFEVDHILPLSITFDDS LANKVLVYATANQEKGQRTPYQALDSMDDAWSFRELKAFVRESK TLSNKKKEYLLTEEDISKFDVRKKFIERNLVDTRYASRVVLNALQEHF RAHKIDTKVSVVRGQFTSQLRRHWGIEKTRDTYHHHAVDALIIAAS SQLNLWKKQKNTLVSYSEDQLLDIETGELISDDEYKESVFKAPYQHF VDTLKSKEFEDSILFSYQVDSKFNRKISDATIYATRQAKVGKDKADET YVLGKIKDIYTQDGYDAFMKIYKKDKSKFLMYRHDPQTFEKVIEPILE NYPNKQINEKGKEVPCNPFLKYKEEHGYIRKYSKKGNGPEIKSLKYY DSKLGNHIDITPKDSNNKVVLQSLKPWRTDVYFNKNTGKYEILGLKY SDMQFEKGTGKYSISKEQYENIKVREGVDENSEFKFTLYKNDLLLLK DSENGEQILLRFTSRNDTSKHYVELKPYNRQKFEGSEYLIKSLGTVAK GGQCIKGLGKSNISIYKVRTDVLGNQHIIKNEGDKPKLDF	9,036	N622A	H599A	D9A
St1Cas9-TH1477	Streptococcus thermophilus	MSDLVLGLDIGIGSVGVGILNKVTGEIIHKNSRIFPAAQAENNLVRR TNRQGRRLARRKKHRRVRLNRLFEESGLITDFTKISINLNPYQLRVK GLTDELSNEELFIALKNMVKHRGISYLDDASDDGNSSVGDYAQIVK ENSKQLETKTPGQIQLERYQTYGQLRGDFTVEKDGKKHRLINVFPT SAYRSEALRILQTQQEFNPQITDEFINRYLEILTGKRKYYHGPGNEKS RTDYGRYRTSGETLDNIFGILIGKCTFYPDEFRAAKASYTAQEFNLLN DLNNLTVPTETKKLSKEQKNQIINYVKNEKAMGPAKLFKYIAKLLSC DVADIKGYRIDKSGKAEIHTFEAYRKMKTLETLDIEQMDRETLDKLA YVLTLNTEREGIQEALEHEFADGSFSQKQVDELVQFRKANSSIFGKG WHNFSVKLMMELIPELYETSEEQMTILTRLGKQKTTSSSNKTKYIDE KLLTEEIYNPVVAKSVRQAIKIVNAAIKEYGDFDNIVIEMARETNEDD EKKAIQKIQKANKDEKDAAMLKAANQYNGKAELPHSVFHGHKQL ATKIRLWHQQGERCLYTGKTISIHDLINNSNQFEVDHILPLSITFDDS LANKVLVYATANQEKGQRTPYQALDSMDDAWSFRELKAFVRESK TLSNKKKEYLLTEEDISKFDVRKKFIERNLVDTRYASRVVLNALQEHF RAHKIDTKVSVVRGQFTSQLRRHWGIEKTRDTYHHHAVDALIIAAS SQLNLWKKQKNTLVSYSEDQLLDIETGELISDDEYKESVFKAPYQHF VDTLKSKEFEDSILFSYQVDSKFNRKISDATIYATRQAKVGKDKADET	9,037	N622A	H599A	D9A

		YVLGKIKDIYTQDGYDAFMKIYKKDKSKFLMYRHDPQTFEKVIEPILE NYPNKQINEKGKEVPCNPFLKYKEEHGYIRKYSKKGNGPEIKSLKYY DSKLGNHIDITPKDSNNKVVLQSLKPWRTDVYFNKNTGKYEILGLKY SDMQFEKGTGKYSISKEQYENIKVREGVDENSEFKFTLYKNDLLLLK DSENGEQILLRFTSRNDTSKHYVELKPYNRQKFEGSEYLIKSLGTVVK GGRCIKGLGKSNISIYKVRTDVLGNQHIIKNEGDKPKLDF				
sRGN3.1	Staphylococcus spp.	MNQKFILGLDIGITSVGYGLIDYETKNIIDAGVRLFPEANVENNEGR RSKRGSRRLKRRRIHRLERVKLLLTEYDLINKEQIPTSNNPYQIRVKGL SEILSKDELAIALLHLAKRRGIHNVDVAADKEETASDSLSTKDQINKN AKFLESRYVCELQKERLENEGHVRGVENRFLTKDIVREAKKIIDTQM QYYPEIDETFKEKYISLVETRREYFEGPGQGSPFGWNGDLKKWYEM LMGHCTYFPQELRSVKYAYSADLFNALNDLNNLIIQRDNSEKLEYHE KYHIIENVFKQKKKPTLKQIAKEIGVNPEDIKGYRITKSGTPEFTSFKLF HDLKKVVKDHAILDDIDLLNQIAEILTIYQDKDSIVAELGQLEYLMSE ADKQSISELTGYTGTHSLSLKCMNMIIDELWHSSMNQMEVFTYLN MRPKKYELKGYQRIPTDMIDDAILSPVVKRTFIQSINVINKVIEKYGIP EDIIIELARENNSDDRKKFINNLQKKNEATRKRINEIIGQTGNQNAKR IVEKIRLHDQQEGKCLYSLESIPLEDLLNNPNHYEVDHIIPRSVSFDNS YHNKVLVKQSENSKKSNLTPYQYFNSGKSKLSYNQFKQHILNLSKSQ DRISKKKKEYLLEERDINKFEVQKEFINRNLVDTRYATRELTNYLKAYF SANNMNVKVKTINGSFTDYLRKVWKFKKERNHGYKHHAEDALIIA NADFLFKENKKLKAVNSVLEKPEIETKQLDIQVDSEDNYSEMFIIPKQ VQDIKDFRNFKYSHRVDKKPNRQLINDTLYSTRKKDNSTYIVQTIKDI YAKDNTTLKKQFDKSPEKFLMYQHDPRTFEKLEVIMKQYANEKNPL AKYHEETGEYLTKYSKKNNGPIVKSLKYIGNKLGSHLDVTHQFKSST KKLVKLSIKNYRFDVYLTEKGYKFVTIAYLNVFKKDNYYYIPKDKYQEL KEKKKIKDTDQFIASFYKNDLIKLNGDLYKIIGVNSDDRNIIELDYYDIK YKDYCEINNIKGEPRIKKTIGKKTESIEKFTTDVLGNLYLHSTEKAPQLI FKRGL	9,038	N585A	H562A	D10A
sRGN3.3	Staphylococcus spp.	MNQKFILGLDIGITSVGYGLIDYETKNIIDAGVRLFPEANVENNEGR RSKRGSRRLKRRRIHRLERVKLLLTEYDLINKEQIPTSNNPYQIRVKGL SEILSKDELAIALLHLAKRRGIHNVDVAADKEETASDSLSTKDQINKN AKFLESRYVCELQKERLENEGHVRGVENRFLTKDIVREAKKIIDTQM QYYPEIDETFKEKYISLVETRREYFEGPGQGSPFGWNGDLKKWYEM LMGHCTYFPQELRSVKYAYSADLFNALNDLNNLIIQRDNSEKLEYHE KYHIIENVFKQKKKPTLKQIAKEIGVNPEDIKGYRITKSGTPEFTSFKLF HDLKKVVKDHAILDDIDLLNQIAEILTIYQDKDSIVAELGQLEYLMSE ADKQSISELTGYTGTHSLSLKCMNMIIDELWHSSMNQMEVFTYLN MRPKKYELKGYQRIPTDMIDDAILSPVVKRTFIQSINVINKVIEKYGIP EDIIIELARENNSDDRKKFINNLQKKNEATRKRINEIIGQTGNQNAKR IVEKIRLHDQQEGKCLYSLESIPLEDLLNNPNHYEVDHIIPRSVSFDNS YHNKVLVKQSENSKKSNLTPYQYFNSGKSKLSYNQFKQHILNLSKSQ DRISKKKKEYLLEERDINKFEVQKEFINRNLVDTRYATRELTSYLKAYF SANNMDVKVKTINGSFTNHLRKVWRFDKYRNHGYKHHAEDALIIA NADFLFKENKKLQNTNKILEKPTIENNTKKVTVEKEEDYNNVFETPK LVEDIKQYRDYKFSHRVDKKPNRQLINDTLYSTRMKDEHDYIVQTIT DIYGKDNTNLKKQFNKNPEKFLMYQNDPKTFEKLSIIMKQYSDEKN PLAKYYEETGEYLTKYSKKNNGPIVKKIKLLGNKVGNHLDVTNKYEN STKKLVKLSIKNYRFDVYLTEKGYKFVTIAYLNVFKKDNYYYIPKDKYQ ELKEKKKIKDTDQFIASFYKNDLIKLNGDLYKIIGVNSDDRNIIELDYY DIKYKDYCEINNIKGEPRIKKTIGKKTESIEKFTTDVLGNLYLHSTEKAP QLIFKRGL	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 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.

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):

DKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRY
TRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVD
STDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLS
KSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYAD
LFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYA
GYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFL
KDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNE
KVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECF
DSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVM
KQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDS
LHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKE
LGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSD
KNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHV
AQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYP
KLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVW
DKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVL
VVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLAS
AGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLD
KVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDL
SQLGGD (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:

SMDKKYSIGLAIGTNSVGWAVITDDYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARR
RYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKL
VDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSA
RLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQY
ADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNG
YAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYP
FLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLP
NEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIE
CFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDK
VMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQG
DSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGI
KELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTR
SDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITK
HVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEI
VWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYS
VLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRML

ASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADAN
LDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRI
DLSQLGGD (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	NN	GN	SN	VN	LN	DN	QN	EN	HN	RH	NK	AN	FN
C	HD	RD	KD	ND	AD								
T	NG	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 1 or 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%, 75%, 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. In some embodiments, a gene modifying polypeptide comprises an amino acid sequence as listed in Table A1, or or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto.

Table 10. Exemplary linker sequences

Amino Acid Sequence	SEQ ID NO
GGS	
GGSGGS	5102
GGSGGSGGS	5103
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

Amino Acid Sequence	SEQ ID NO
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
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

Amino Acid Sequence	SEQ ID NO
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
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

Amino Acid Sequence	SEQ ID NO
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
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 8**, 2) a peptide linker, e.g., a sequence from **Table 1 or 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 1 or 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 8, a peptide linker of Table 10 and an RT of Table 6, for example a Cas-linker-RT fusion as in **Table 1**; (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 as listed in Example 7.

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 1, 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

1, 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 1, 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 1, 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 1, 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 1, 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 of a SEQ ID NO as listed in Table D1, 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 a SEQ ID NO as listed in Table D2, 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 a SEQ ID NO as listed in Table D3, 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 a SEQ ID NO

as listed in Table D4, 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 a SEQ ID NO as listed in Table D5, 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 a SEQ ID NO as listed in Table D6, 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 a SEQ ID NO as listed in Table D7, 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 a SEQ ID NO as listed in Table D8, 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 a SEQ ID NO as listed in Table D9, 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 a SEQ ID NO as listed in Table D10, 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 a SEQ ID NO as listed in Table D11, 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 a SEQ ID NO as listed in Table D12, 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	AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAA KEAAAKEAAAKA	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	AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKEAAAKA	15,453	AVIRE_P03360_3mutA
1197	AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKEAAAKA	15,454	FLV_P10273_3mutA
2611	AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKEAAAKA	15,455	MLVMS_P03355_PLV919
2784	AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKEAAAKA	15,456	MLVMS_P03355_3mutA_WS
480	AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKEAAAKA	15,457	SFV1_P23074_2mutA
647	AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKEAAAKA	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, T2, or D1-D12, 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, T2, or D1-D12, 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, T2, or D1-D12, 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, T2, or D1-D12, 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, T2, or D1-D12, 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, T2, or D1-D12,

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, T2, or D1-D12, 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, T2, or D1-D12, 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:

DKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNR
ICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIY
LALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGE
KKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVN
TEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGT
EELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFA
WMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFL
SGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILE
DIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFM
QLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQ
KGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLK
DDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETR
QITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYP

KLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRD
FATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKK
LKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYV
NFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENII
HLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGD (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, T2, or D1-D12, 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 1 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, T2, or D1-D12, 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 1 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, T2, or D1-D12. 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 Table A1, 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 having the amino acid sequence of a SEQ ID NO: listed in Table T1, 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 having the amino acid sequence of a SEQ ID NO: listed in Table 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 a linker sequence of a gene modifying polypeptide having the amino acid sequence of a SEQ ID NO: listed in Table D1, 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 having the amino acid sequence of a SEQ ID NO: listed in Table D2, 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 having the amino acid sequence of a SEQ ID NO: listed in Table D3, 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 having the amino acid sequence of a SEQ ID NO: listed in Table D4, 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 having the amino acid sequence of a SEQ ID NO: listed in Table D5, 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 having the amino acid sequence of a SEQ ID NO: listed in Table D6, 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 having the amino acid sequence of a SEQ ID NO: listed in Table D7, 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 having the amino acid sequence of a SEQ ID NO: listed in Table D8, 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 having the amino acid sequence of a SEQ ID NO: listed in Table D9, 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 having the amino acid sequence of a SEQ ID NO: listed in Table D10, 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 having the amino acid sequence of a SEQ ID NO: listed in Table D11, 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 having the amino acid sequence of a SEQ ID NO: listed in Table D12, 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 Table A1, 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 having the amino acid sequence of a SEQ ID NO: listed in Table T1, 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 having the amino acid sequence of a SEQ ID NO: listed in Table 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 a RT domain sequence of a gene modifying polypeptide having the amino acid sequence of a SEQ ID NO: listed in Table D1, 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 having the amino acid sequence of a SEQ ID NO: listed in Table D2, 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 having the amino acid sequence of a SEQ ID NO: listed in Table D3, 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 having the amino acid sequence of a SEQ ID NO: listed in Table D4, 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 having the amino acid sequence of a SEQ ID NO: listed in Table D5, 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 having the amino acid sequence of a SEQ ID NO: listed in Table D6, 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 having the amino acid sequence of a SEQ ID NO: listed in Table D7, 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 having the amino acid sequence of a SEQ ID NO: listed in Table D8, 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 having the amino acid sequence of a SEQ ID NO: listed in Table D9, 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 having the amino acid sequence of a SEQ ID NO: listed in Table D10, 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 having the amino acid sequence of a SEQ ID NO: listed in Table D11, 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 having the amino acid sequence of a SEQ ID NO: listed in Table D12, 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, T2, or D1-D12, 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, T2, or D1-D12, 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, T2, or D1-D12 (e.g., from a single exemplary gene modifying polypeptide as listed in any of Tables A1, T1, T2, or D1-D12).

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, T2, or D1-D12.

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 (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 (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: 15465) (e.g., at the C-terminus).

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

RT-linker filing (MLVMS)	Corresponding AVIRE	MLVMS (PLV4921)	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: 15465) 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, T2, or D1-D12, 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, T2, or D1-D12, 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, T2, or D1-D12, 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, T2, or D1-D12, 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, T2, or D1-D12, 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, T2, or D1-D12, 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, T2, or D1-D12, 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, T2, or D1-D12, 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	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGSSGGLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKE AQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTG QLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPA PTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASG WPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGE VLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKR LAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
35	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSPAPGGLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPL SKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTG RTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQ IPAPTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPV

	ASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPL TGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHL PKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
35	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSPAPGGLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPL SKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTG RTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQ IPAPTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPV ASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPL TGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHL PKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
36	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKAGGLDDEYRLYSPLVKPDQNIQFWLEQFPQ AWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQR SWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRAS AKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFT LYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNP ATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATA HVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
36	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS

	ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKEAAAKAGGLDDEYRLYSPLVKPDQNIQFWLEQFPQ AWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQR SWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRAS AKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFT LYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNP ATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATA HVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
37	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKGGLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVR QYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKK TVVQIPAPTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKK LDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLT DIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLE ALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
38	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG

	QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGSSPAPGGLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSK EAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRT GQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIP APTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVAS GWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTG EVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPK RLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
39	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAAKEAAAKGGLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQL KASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTS QPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDG QRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPW RRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLI EETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIK NKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
40	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR

	KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGGEAAAKGGLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPL SKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTG RTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQ IPAPTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPV ASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPL TGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHL PKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
40	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGGEAAAKGGLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPL SKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTG RTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQ IPAPTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPV ASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPL TGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHL PKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
41	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGSSGSSGSSGGLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYP LSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGT GRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVV QIPAPTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDP VASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIP

	LTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALH LPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
41	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGSSGSSGSSGGLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYP LSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGT GRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVV QIPAPTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDP VASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIP LTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALH LPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
43	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSSPAPGGLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSK EAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRT GQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIP APTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVAS GWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTG EVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPK RLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
47	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY

	DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSPAPGGLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQ EGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQL TWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPT TAKQVREFLGKAGFCRLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWP VCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVL TWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRLA IIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
48	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGGLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKE AQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTG QLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPA PTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASG WPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGE VLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKR LAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
49	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ

	LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSEAAAKPAPGGLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPL SKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTG RTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQ IPAPTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPV ASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPL TGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHL PKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
51	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSGGGGSGGGGSGGLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVR QYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKK TVVQIPAPTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKK LDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLT DIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLE ALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
62	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPAPGGLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPL

	SKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTG RTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQ IPAPTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPV ASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPL TGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHL PKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
65	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGEAAAKGGSGGLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLLKASATPVSVRQYPL SKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTG RTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQ IPAPTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPV ASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPL TGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHL PKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
83	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGSSGGSGGLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLLKASATPVSVRQYPL SKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTG RTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQ IPAPTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPV ASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPL

	TGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHL PKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
90	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGSGSETPGTSESATPESGGLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSV RQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWR DPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARK KTVVQIPAPTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSK KLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDL TDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLL EALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
97	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGSEAAAKGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPV SVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFE WRDPGTGRTGQLTWTRLPQGFKNSPTIFDEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEA RKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKEKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYL SKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRK DLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGLLTSAGREIKNKEEILS LLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
112	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY

	DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGPAPGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQ YPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDP GTGRTGQLTWTRLPQGFKNSPTIFDEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKT VVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKEKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKL DPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTD IPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGLLTSAGREIKNKEEILSLLEA LHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
113	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGSSGSSGSSGSSGSSGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASA TPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLF AFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWL TEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPV AYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETG VRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEE ILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
113	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ

	LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGSSGSSGSSGSSGSSGSSGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASA TPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLF AFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWL TEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPV AYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETG VRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEE ILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
117	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAAKEAAAKEAAAKEAAAKGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQ VPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFF CLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTY LGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGV LTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVT HDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWL TSAGREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
117	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAAKEAAAKEAAAKEAAAKGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQ

	VPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFF CLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTY LGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGV LTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVT HDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWL TSAGREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
121	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSSEAAAKGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQ YPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDP GTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKT VVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKL DPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTD IPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEA LHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
121	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSSEAAAKGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQ YPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDP GTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKT VVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKL DPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTD

	IPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEA LHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
122	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGSGSETPGTSESATPESGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATP VSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAF EWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTE ARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAY LSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVR KDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEIL SLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
123	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGSSGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSK EAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRT GQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIP APTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVAS GWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTG EVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPK RLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
124	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY

	DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPEAAAKGGGGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQ YPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDP GTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKT VVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKL DPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTD IPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEA LHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
126	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPL SKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTG RTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQ IPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPV ASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPL TGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHL PKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
127	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ

	LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGGEAAAKGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQ YPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDP GTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKT VVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKL DPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTD IPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEA LHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
133	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSEAAAKGGGGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQ YPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDP GTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKT VVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKL DPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTD IPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEA LHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
138	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGSEAAAKGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQ

	YPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDP GTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKT VVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKL DPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTD IPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEA LHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
139	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGSSEAAAKGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQ YPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDP GTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKT VVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKL DPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTD IPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEA LHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
140	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGSGGSSGGSSGSETPGTSESATPESSGGSSGGSSGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGL AKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKD AFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRRE VTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVA RGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDE

	PVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQR GWLTSAGREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
141	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSPAPGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQ YPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDP GTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKT VVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKL DPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTD IPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEA LHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
142	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGSGGSGGSGGSGGSGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASA TPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLF AFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWL TEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPV AYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETG VRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEE ILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
142	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY

	DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGSGGSGGSGGSGGSGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASA TPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLF AFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWL TEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPV AYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETG VRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEE ILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
144	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGSSGGGGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYP LSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGT GRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVV QIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDP VASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIP LTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALH LPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
147	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ

	LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKE AQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTG QLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPA PTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASG WPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGE VLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKR LAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
151	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKE AQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTG QLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPA PTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASG WPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGE VLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKR LAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
156	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKAGGTLQLDDEYRLYSPLVKPDQNIQFWLEQ

	FPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALP PQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGY RASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTK PFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAA LNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAF ATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
156	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKEAAAKAGGTLQLDDEYRLYSPLVKPDQNIQFWLEQ FPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALP PQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGY RASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTK PFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAA LNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAF ATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
157	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPAPAPGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSV RQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWR DPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARK KTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSK KLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDL

	TDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLL EALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
164	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSPAPEAAAKGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQ YPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDP GTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKT VVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKL DPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTD IPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEA LHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
168	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKPAPGGSGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQ YPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDP GTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKT VVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKL DPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTD IPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEA LHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
173	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY

	DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGGGGSGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYP LSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGT GRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVV QIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDP VASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIP LTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALH LPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
190	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKEAAAKAGGLDDEYRLYSPLVKPDQNIQFWLEQFPQ AWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQR SWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRAS AKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFT LYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNP ATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATA HVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
190	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ

	LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKEAAAKAGGLDDEYRLYSPLVKPDQNIQFWLEQFPQ AWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQR SWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRAS AKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFT LYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNP ATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATA HVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
191	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGSGGSGGSGGSGGSGGLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPV SVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFE WRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEA RKKTVVQIPAPTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYL SKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRK DLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILS LLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
192	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPEAAAKGGGGGLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPL

	SKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTG RTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQ IPAPTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPV ASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPL TGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHL PKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
193	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAAKEAAAKEAAAKGGLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPP QVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLR LHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGY SLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQ TLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDC HQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSA GREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
195	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSPAPGGLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPL SKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTG RTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQ IPAPTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPV ASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPL

	TGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHL PKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
195	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSPAPGGLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLLKASATPVSVRQYPL SKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTG RTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQ IPAPTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPV ASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPL TGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHL PKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
196	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGSGSETPGTSESATPESGGLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSV RQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWR DPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARK KTVVQIPAPTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSK KLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDL TDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLL EALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
199	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY

	DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGGEAAAKGGLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPL SKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTG RTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQ IPAPTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPV ASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPL TGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHL PKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
199	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGGEAAAKGGLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPL SKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTG RTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQ IPAPTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPV ASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPL TGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHL PKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
202	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ

	LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGSSGSSGSSGGLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVR QYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKK TVVQIPAPTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKK LDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLT DIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLE ALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
207	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSSPAPGGLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSK EAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRT GQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIP APTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVAS GWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTG EVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPK RLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
208	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGSSGSSGGLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSK

	EAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRT GQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIP APTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVAS GWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTG EVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPK RLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
212	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGSSGGLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQ EGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQL TWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPT TAKQVREFLGKAGFCRLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWP VCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVL TWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRLA IIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
213	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGGPAPGGLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSK EAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRT GQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIP APTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVAS GWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTG

	EVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPK RLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
216	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSGGGGSGGGGSGGLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVR QYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKK TVVQIPAPTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKK LDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLT DIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLE ALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
217	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGSEAAAKGGLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPL SKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTG RTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQ IPAPTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPV ASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPL TGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHL PKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
219	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY

	DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGGLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKE AQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTG QLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPA PTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASG WPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGE VLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKR LAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
223	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSPAPGGLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQ EGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQL TWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPT TAKQVREFLGKAGFCRLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWP VCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVL TWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRLA IIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
224	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ

	LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKPAPGSSGGLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPL SKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTG RTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQ IPAPTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPV ASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPL TGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHL PKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
225	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGSSEAAAKGGLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPL SKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTG RTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQ IPAPTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPV ASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPL TGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHL PKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
228	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGSSGSSGSSGGLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYP

	LSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGT GRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVV QIPAPTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDP VASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIP LTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALH LPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
228	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGSSGSSGSSGGLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYP LSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGT GRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVV QIPAPTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDP VASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIP LTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALH LPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
229	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGEAAAKGGSGGLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPL SKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTG RTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQ IPAPTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPV ASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPL

	TGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHL PKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
232	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAAKEAAAKGGLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQL KASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTS QPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDG QRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPW RRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLI EETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIK NKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
235	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGSSGGLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQ EGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQL TWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPT TAKQVREFLGKAGFCRLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWP VCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVL TWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRLA IIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
239	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY

	DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSEAAAKPAPGGLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPL SKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTG RTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQ IPAPTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPV ASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPL TGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHL PKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
252	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGSGGLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQ EGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQL TWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPT TAKQVREFLGKAGFCRLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWP VCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVL TWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRLA IIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
258	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ

	LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSEAAAKGGSGGLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPL SKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTG RTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQ IPAPTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPV ASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPL TGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHL PKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
268	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGSSPAPGGLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSK EAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRT GQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIP APTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVAS GWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTG EVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPK RLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
278	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGPAPGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQ

	YPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDP GTGRTGQLTWTRLPQGFKNSPTIFDEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKT VVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKEKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKL DPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTD IPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGLLTSAGREIKNKEEILSLLEA LHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
279	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPV SVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFE WRDPGTGRTGQLTWTRLPQGFKNSPTIFDEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEA RKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKEKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYL SKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRK DLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGLLTSAGREIKNKEEILS LLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
280	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAAKEAAAKEAAAKGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQ VPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFF CLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFDEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTY LGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKEKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGV LTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVT

	HDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGLL TSAGREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
298	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPV SVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFE WRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEA RKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYL SKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRK DLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILS LLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
299	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSGGGGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQ YPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDP GTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKT VVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKL DPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTD IPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEA LHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
300	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID

	GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGAEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKAGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQE GIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPT IFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAA PLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQP PDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRL AEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
300	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGAEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKAGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQE GIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPT IFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAA PLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQP PDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRL AEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
302	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGGGSPAPEAAAKGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTN DYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGAT KQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPAL ALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATL

	LPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSA GREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
303	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGSGGSSGGSSGSETPGTSESATPESSGGSSGGSSGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQG ILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANF RIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFS WAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHY QSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSR YAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
304	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGEAAAKPAPGSSGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTN DYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGAT KQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPAL ALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATL LPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSA GREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
305	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ

	LGGDGGPAPGGGEAAAKGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTN DYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGAT KQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPAL ALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATL LPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSA GREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
306	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGEAAAKGGGGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYR PVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQD CLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALP DVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPE ETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGRE IKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
307	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGGGGGSSPAPGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDY RPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQ DCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALAL PDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLP EETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGR EIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
308	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR

	GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGEAAAKGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQ DLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLE GTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVT KPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETD EPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKN KEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
309	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGPAPAPAPAPAPGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPG TNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAG ATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAP ALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPA TLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLT SAGREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
311	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGGGGGGSEAAAKGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTN DYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGAT KQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPAL ALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATL LPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSA GREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
313	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID

	GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGEAAAKEAAAKEAAAKEAAAKEAAAKEAAAKGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILV PVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQ HPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAP EHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSL LLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAF ATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
313	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGEAAAKEAAAKEAAAKEAAAKEAAAKEAAAKGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILV PVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQ HPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAP EHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSL LLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAF ATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
314	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGGGGPAPGSSGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDY RPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQ DCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALAL PDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLP

	EETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGR EIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
316	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGGGSGGSGGSGGSGGSGGSGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLP VRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDD LLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKA LLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPA ALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQ RGWLTSAGREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
316	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGGGSGGSGGSGGSGGSGGSGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLP VRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDD LLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKA LLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPA ALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQ RGWLTSAGREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
317	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ

	LGGDGGGSSGGGEAAAKGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTN DYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGAT KQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPAL ALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATL LPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSA GREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
317	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGGSSGGGEAAAKGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTN DYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGAT KQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPAL ALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATL LPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSA GREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
318	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGGSSGGGEAAAKGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTN DYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGAT KQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPAL ALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATL LPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSA GREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
318	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR

	GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGGGGGSSEAAAKGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTN DYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGAT KQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPAL ALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATL LPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSA GREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
319	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGPAPEAAAKGGGGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTN DYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGAT KQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPAL ALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATL LPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSA GREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
320	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGGGGGGSGSSGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDY RPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQ DCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALAL PDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLP EETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGR EIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
320	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID

	GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGGGGGGSGSSGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDY RPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQ DCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALAL PDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLP EETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGR EIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
321	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGPAPGGSEAAAKGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTN DYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGAT KQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPAL ALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATL LPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSA GREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
322	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGGGGEAAAKGGSGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTN DYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGAT KQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPAL ALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATL

	LPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSA GREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
324	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGGGGEAAAKPAPGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTN DYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGAT KQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPAL ALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATL LPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSA GREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
328	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGSGSETPGTSESATPESGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVR KPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLL LAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALL SAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAAL NPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRG WLTSAGREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
332	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ

	LGGDGGPAPGGGGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPV QDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCL EGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDV TKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEET DEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIK NKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
340	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGPAPGGGGGSGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDY RPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQ DCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALAL PDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLP EETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGR EIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
341	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGEAAAKGGSPAPGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTN DYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGAT KQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPAL ALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATL LPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSA GREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
346	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR

	GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGGGGPAPEAAAKGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTN DYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGAT KQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPAL ALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATL LPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSA GREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
352	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGGGSEAAAKGGGGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTN DYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGAT KQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPAL ALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATL LPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSA GREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
352	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGGGSEAAAKGGGGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTN DYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGAT KQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPAL ALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATL LPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSA GREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
358	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID

	GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGEAAAKPAPGGGGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTN DYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGAT KQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPAL ALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATL LPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSA GREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
363	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGGGSGSSEAAAKGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTN DYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGAT KQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPAL ALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATL LPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSA GREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
365	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGGSSEAAAKGGGGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTN DYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGAT KQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPAL ALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATL

	LPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSA GREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
384	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGGGSGSSGGGGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDY RPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQ DCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALAL PDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLP EETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGR EIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
386	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGSSGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSK EAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRT GQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIP APTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVAS GWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTG EVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPK RLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
392	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR

	LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKE AQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTG QLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPA PTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASG WPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGE VLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKR LAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
396	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGSSGSSGSSGSSGSSGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASA TPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLF AFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWL TEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPV AYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETG VRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEE ILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
396	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ

	KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGSSGSSGSSGSSGSSGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASA TPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLF AFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWL TEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPV AYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETG VRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEE ILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
480	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKEAAAKAGGMDPLQLLQPLEAEIKGTKLKAHWNSGA TITCVPEAFLEDERPIQTMLIKTIHGEKQQDVYYLTFKVQGRKVEAEVLASPYDYILLNPSDVPWLMKKPLQLTVLVPLHEYQERLLQQTALPKEQKELLQKLFLKYDALWQ HWENQVGHRRIKPHNIATGTLAPRPQKQYPINPKAKPSIQIVIDDLLKQGVLIQQNSTMNTPVYPVPKPDGKWRMVLDYREVNKTIPLIAAQNQHSAGILSSIYRGKYKTTL DLTNGFWAHPITPESYWLTAFTWQGKQYCWTRLPQGFLNSPALFNADVVDLLKEIPNVQAYVDDIYISHDDPQEHLEQLEKIFSILLNAGYVVSLKKSEIAQREVEFLGFNI TKEGRGLTDTFKQKLLNITPPKDLKQLQSILGKLNFARNFIPNYSELVKPLYTIVAPANGKFISWTEDNSNQLQHIISVLNQADNLEERNPETRLIIKVNSSPSAGYIRYYN EGSKRPIMYVNYIFSKAEAKFTQTEKLLTTMHKGLIKAMDLAMGQEILVYSPIVSMTKIQRTPLPERKALPVRWITWMTYLEDPRIQFHYDKSLPELQQIPNVTEDVIAKTK HPSEFAMVFYTDGSAIKHPDVNKSHSAGMGIAQVQFIPEYKIVHQWSIPLGDHTAQLAEIAAVEFACKKALKISGPVLIVTDSFYVAESANKELPYWKSNGFLNNKKKPLRH VSKWKSIAECLQLKPDIIIMHEKGHQQPMTTLHTEGNNLADKLATQGSYVVHAGKRTADGSEFEKRTADGSEFESPKKKAKVE
550	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAAKEAAAKEAAAKGGIPWLMKKPLQLTTLVPLQEYEERLLKQTMLTGSYKEKLQSLFL KYDALWQHWENQVGHRRIKPHHIATGTVNPRPQKQYPINPKAKASIQTVINDLLKQGVLIQQNSIMNTPVYPVPKPDGKWRMVLDYREVNKTIPLIAAQNQHSAGILSSIFR GKYKTTLDLSNGFWAHSITPESYWLTAFTWLGQQYCWTRLPQGFLNSPALFNADVVDLLKEVPNVQVYVDDIYISHDDPREHLEQLEKVFSLLLNAGYVVSLKKSEIAQHEV

	EFLGFNITKEGRGLTETFKQKLLNITPPRDLKQLQSILGKLNFARNFIPNFSELVKPLYNIIATAPGKYITWTTDNSQQLQNIISMLNSAENLEERNPEVRLIMKVNTSPSA GYIRFYNEFAKRPIMYLNYVYTKAEVKFTNTEKLLTTIHKGLIKALDLGMGQEILVYSPIVSMTKIQKTPLPERKALPIRWITWMSYLEDPRIQFHYDKTLPELQQVPTVTD DIIAKIKHPSEFSMVFYTDGSAIKHPNVNKSHNAGMGIAQVQFKPEFTVINTWSIPLGDHTAQLAEVAAVEFACKKALKIDGPVLIVTDSFYVAESVNKELPYWQSNGFFNN KKKPLKHVSKWKSIADCIQLKPDIIIIHEKGHQPTASTFHTEGNNLADKLATQGSYVVNAGKRTADGSEFEKRTADGSEFESPKKKAKVE
590	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAAKEAAAKEAAAKGGMDPLQLLQPLEAEIKGTKLKAHWNSGATITCVPQAFLEEEVPI KNIWIKTIHGEKEQPVYYLTFKIQGRKVEAEVISSPYDYILVSPSDIPWLMKKPLQLTTLVPLQEYEERLLKQTMLTGSYKEKLQSLFLKYDALWQHWENQVGHRRIKPHHI ATGTVNPRPQKQYPINPKAKASIQTVINDLLKQGVLIQQNSIMNTPVYPVPKPDGKWRMVLDYREVNKTIPLIAAQNQHSAGILSSIFRGKYKTTLDLSNGFWAHSITPESY WLTAFTWLGQQYCWTRLPQGFLNSPALFNADVVDLLKEVPNVQVYVDDIYISHDDPREHLEQLEKVFSLLLNAGYVVSLKKSEIAQHEVEFLGFNITKEGRGLTETFKQKLL NITPPRDLKQLQSILGLLNFARNFIPNFSELVKPLYNIIATAPGKYITWTTDNSQQLQNIISMLNSAENLEERNPEVRLIMKVNTSPSAGYIRFYNEFAKRPIMYLNYVYTK AEVKFTNTEKLLTTIHKGLIKALDLGMGQEILVYSPIVSMTKIQKTPLPERKALPIRWITWMSYLEDPRIQFHYDKTLPELQQVPTVTDDIIAKIKHPSEFSMVFYTDGSAI KHPNVNKSHNAGMGIAQVQFKPEFTVINTWSIPLGDHTAQLAEVAAVEFACKKALKIDGPVLIVTDSFYVAESVNKELPYWQSNGFFNNKKKPLKHVSKWKSIADCIQLKPD IIIIHEKGHQPTASTFHTEGNNLADKLATQGSYVVNAGKRTADGSEFEKRTADGSEFESPKKKAKVE
591	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKAGGMDPLQLLQPLEAEIKGTKLKAHWNSGA TITCVPQAFLEEEVPIKNIWIKTIHGEKEQPVYYLTFKIQGRKVEAEVISSPYDYILVSPSDIPWLMKKPLQLTTLVPLQEYEERLLKQTMLTGSYKEKLQSLFLKYDALWQ HWENQVGHRRIKPHHIATGTVNPRPQKQYPINPKAKASIQTVINDLLKQGVLIQQNSIMNTPVYPVPKPDGKWRMVLDYREVNKTIPLIAAQNQHSAGILSSIFRGKYKTTL DLSNGFWAHSITPESYWLTAFTWLGQQYCWTRLPQGFLNSPALFNADVVDLLKEVPNVQVYVDDIYISHDDPREHLEQLEKVFSLLLNAGYVVSLKKSEIAQHEVEFLGFNI TKEGRGLTETFKQKLLNITPPRDLKQLQSILGLLNFARNFIPNFSELVKPLYNIIATAPGKYITWTTDNSQQLQNIISMLNSAENLEERNPEVRLIMKVNTSPSAGYIRFYN EFAKRPIMYLNYVYTKAEVKFTNTEKLLTTIHKGLIKALDLGMGQEILVYSPIVSMTKIQKTPLPERKALPIRWITWMSYLEDPRIQFHYDKTLPELQQVPTVTDDIIAKIK

	HPSEFSMVFYTDGSAIKHPNVNKSHNAGMGIAQVQFKPEFTVINTWSIPLGDHTAQLAEVAAVEFACKKALKIDGPVLIVTDSFYVAESVNKELPYWQSNGFFNNKKKPLKH VSKWKSIADCIQLKPDIIIIHEKGHQPTASTFHTEGNNLADKLATQGSYVVNAGKRTADGSEFEKRTADGSEFESPKKKAKVE
647	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKEAAAKAGGMDPLQLLQPLEAEIKGTKLKAHWNSGA TITCVPQAFLEEEVPIKNIWIKTIHGEKEQPVYYLTFKIQGRKVEAEVISSPYDYILVSPSDIPWLMKKPLQLTTLVPLQEYEERLLKQTMLTGSYKEKLQSLFLKYDALWQ HWENQVGHRRIKPHHIATGTVNPRPQKQYPINPKAKASIQTVINDLLKQGVLIQQNSIMNTPVYPVPKPDGKWRMVLDYREVNKTIPLIAAQNQHSAGILSSIFRGKYKTTL DLSNGFWAHSITPESYWLTAFTWLGQQYCWTRLPQGFLNSPALFNADVVDLLKEVPNVQVYVDDIYISHDDPREHLEQLEKVFSLLLNAGYVVSLKKSEIAQHEVEFLGFNI TKEGRGLTETFKQKLLNITPPRDLKQLQSILGKLNFARNFIPNFSELVKPLYNIIATAPGKYITWTTDNSQQLQNIISMLNSAENLEERNPEVRLIMKVNTSPSAGYIRFYN EFAKRPIMYLNYVYTKAEVKFTNTEKLLTTIHKGLIKALDLGMGQEILVYSPIVSMTKIQKTPLPERKALPIRWITWMSYLEDPRIQFHYDKTLPELQQVPTVTDDIIAKIK HPSEFSMVFYTDGSAIKHPNVNKSHNAGMGIAQVQFKPEFTVINTWSIPLGDHTAQLAEVAAVEFACKKALKIDGPVLIVTDSFYVAESVNKELPYWQSNGFFNNKKKPLKH VSKWKSIADCIQLKPDIIIIHEKGHQPTASTFHTEGNNLADKLATQGSYVVNAGKRTADGSEFEKRTADGSEFESPKKKAKVE
715	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKEAAAKAGGMDLLKPLTVERKGVKIKGYWNSQADIT CVPKDLLQGEEPVRQQNVTTIHGTQEGDVYYVNLKIDGRRINTEVIGTTLDYAIITPGDVPWILKKPLELTIKLDLEEQQGTLLNNSILSKKGKEELKQLFEKYSALWQSWE NQVGHRRIRPHKIATGTVKPTPQKQYHINPKAKPDIQIVINDLLKQGVLIQKESTMNTPVYPVPKPNGRWRMVLDYRAVNKVTPLIAVQNQHSYGILGSLFKGRYKTTIDLS NGFWAHPIVPEDYWITAFTWQGKQYCWTVLPQGFLNSPGLFTGDVVDLLQGIPNVEVYVDDVYISHDSEKEHLEYLDILFNRLKEAGYIISLKKSNIANSIVDFLGFQITNE GRGLTDTFKEKLENITAPTTLKQLQSILGLLNFARNFIPDFTELIAPLYALIPKSTKNYVPWQIEHSTTLETLITKLNGAEYLQGRKGDKTLIMKVNASYTTGYIRYYNEGE KKPISYVSIVFSKTELKFTELEKLLTTVHKGLLKALDLSMGQNIHVYSPIVSMQNIQKTPQTAKKALASRWLSWLSYLEDPRIRFFYDPQMPALKDLPAVDTGKDNKKHPSN FQHIFYTDGSAITSPTKEGHLNAGMGIVYFINKDGNLQKQQEWSISLGNHTAQFAEIAAFEFALKKCLPLGGNILVVTDSNYVAKAYNEELDVWASNGFVNNRKKPLKHISK WKSVADLKRLRPDVVVTHEPGHQKLDSSPHAYGNNLADQLATQASFKVHAGKRTADGSEFEKRTADGSEFESPKKKAKVE

800	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGGSEAAAKGGVLNLEEEYRLHEKPVPSSIDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQY PMSKEAREGIRPHIQRFLDLGVLVPCQSPWNTPLLPVKKPGTNDYRPVQDLREINKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPE KGNTGQLTWTRLPQGFKNSPTLFNEALHRDLAPFRALNPQVVLLQYVDDLLVAAPTYRDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLLKEGKRWLTPARKATV MKIPPPTTPRQVREFLGTAGFCRLWIPGFASLAAPLYPLTKPSIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVAYLSKKLD PVASGWPTCLKAVAAVALLLKDADKLTLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVHRCSEILAEETGTRRDLKDQ PLPGVPAWYTDGSSFIAEGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDINIYTDSRYAFATAHIHGAIYKQRGWLTSAGKDIKNKEEILALLEAIH LPKRVAIIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
801	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKAGGVLNLEEEYRLHEKPVPSSIDPSWLQLF PTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMSKEAREGIRPHIQRFLDLGVLVPCQSPWNTPLLPVKKPGTNDYRPVQDLREINKRVQDIHPTVPNPYNLLSSLPP SHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLAPFRALNPQVVLLQYVDDLLVAAPTYRDCKEGTQKLLQELSKLGYR VSAKKAQLCQKEVTYLGYLLKEGKRWLTPARKATVMKIPPPTTPRQVREFLGTAGFCRLWIPGFASLAAPLYPLTKPSIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKP FTLYVDERAGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAVAAVALLLKDADKLTLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVL NPATLLPVESEATPVHRCSEILAEETGTRRDLKDQPLPGVPAWYTDGSSFIAEGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDINIYTDSRYAFAT AHIHGAIYKQRGWLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKPAGKRTADGSEFEKRTADGSEFESPKKKAKV E
804	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR

	EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSSGGSGGVLNLEEEYRLHEKPVPSSIDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPM SKEAREGIRPHIQRFLDLGVLVPCQSPWNTPLLPVKKPGTNDYRPVQDLREINKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKG NTGQLTWTRLPQGFKNSPTLFNEALHRDLAPFRALNPQVVLLQYVDDLLVAAPTYRDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLLKEGKRWLTPARKATVMK IPPPTTPRQVREFLGTAGFCRLWIPGFASLAAPLYPLTKPSIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVAYLSKKLDPV ASGWPTCLKAVAAVALLLKDADKLTLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVHRCSEILAEETGTRRDLKDQPL PGVPAWYTDGSSFIAEGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDINIYTDSRYAFATAHIHGAIYKQRGWLTSAGKDIKNKEEILALLEAIHLP KRVAIIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
805	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGGGGGVLNLEEEYRLHEKPVPSSIDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMSKE AREGIRPHIQRFLDLGVLVPCQSPWNTPLLPVKKPGTNDYRPVQDLREINKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTG QLTWTRLPQGFKNSPTLFNEALHRDLAPFRALNPQVVLLQYVDDLLVAAPTYRDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLLKEGKRWLTPARKATVMKIPP PTTPRQVREFLGTAGFCRLWIPGFASLAAPLYPLTKPSIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVAYLSKKLDPVASG WPTCLKAVAAVALLLKDADKLTLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVHRCSEILAEETGTRRDLKDQPLPGV PAWYTDGSSFIAEGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDINIYTDSRYAFATAHIHGAIYKQRGWLTSAGKDIKNKEEILALLEAIHLPKRV AIIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
806	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL

	IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGSGSETPGTSESATPESGGVLNLEEEYRLHEKPVPSSIDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPV AVRQYPMSKEAREGIRPHIQRFLDLGVLVPCQSPWNTPLLPVKKPGTNDYRPVQDLREINKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFE WRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLAPFRALNPQVVLLQYVDDLLVAAPTYRDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLLKEGKRWLTPA RKATVMKIPPPTTPRQVREFLGTAGFCRLWIPGFASLAAPLYPLTKPSIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVAYL SKKLDPVASGWPTCLKAVAAVALLLKDADKLTLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVHRCSEILAEETGTRR DLKDQPLPGVPAWYTDGSSFIAEGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDINIYTDSRYAFATAHIHGAIYKQRGWLTSAGKDIKNKEEILAL LEAIHLPKRVAIIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
818	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGSSGSSGSSGSSGSSGSSGGVLNLEEEYRLHEKPVPSSIDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGAS PVAVRQYPMSKEAREGIRPHIQRFLDLGVLVPCQSPWNTPLLPVKKPGTNDYRPVQDLREINKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFA FEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLAPFRALNPQVVLLQYVDDLLVAAPTYRDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLLKEGKRWLT PARKATVMKIPPPTTPRQVREFLGTAGFCRLWIPGFASLAAPLYPLTKPSIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVA YLSKKLDPVASGWPTCLKAVAAVALLLKDADKLTLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVHRCSEILAEETGT RRDLKDQPLPGVPAWYTDGSSFIAEGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDINIYTDSRYAFATAHIHGAIYKQRGWLTSAGKDIKNKEEIL ALLEAIHLPKRVAIIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
819	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPEAAAKGGVLNLEEEYRLHEKPVPSSIDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMS KEAREGIRPHIQRFLDLGVLVPCQSPWNTPLLPVKKPGTNDYRPVQDLREINKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGN

	TGQLTWTRLPQGFKNSPTLFNEALHRDLAPFRALNPQVVLLQYVDDLLVAAPTYRDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLLKEGKRWLTPARKATVMKI PPPTTPRQVREFLGTAGFCRLWIPGFASLAAPLYPLTKPSIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVAYLSKKLDPVA SGWPTCLKAVAAVALLLKDADKLTLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVHRCSEILAEETGTRRDLKDQPLP GVPAWYTDGSSFIAEGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDINIYTDSRYAFATAHIHGAIYKQRGWLTSAGKDIKNKEEILALLEAIHLPK RVAIIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
871	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKAGGVLNLEEEYRLHEKPVPSSIDPSWLQLF PTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMSKEAREGIRPHIQRFLDLGVLVPCQSPWNTPLLPVKKPGTNDYRPVQDLREINKRVQDIHPTVPNPYNLLSSLPP SHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLAPFRALNPQVVLLQYVDDLLVAAPTYRDCKEGTQKLLQELSKLGYR VSAKKAQLCQKEVTYLGYLLKEGKRWLTPARKATVMKIPPPTTPRQVREFLGKAGFCRLFIPGFASLAAPLYPLTKPSIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKP FTLYVDERAGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAVAAVALLLKDADKLTLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVL NPATLLPVESEATPVHRCSEILAEETGTRRDLKDQPLPGVPAWYTDGSSFIAEGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDINIYTDSRYAFAT AHIHGAIYKQRGWLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKPAGKRTADGSEFEKRTADGSEFESPKKKAKV E
872	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGGGSSGGVLNLEEEYRLHEKPVPSSIDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPM SKEAREGIRPHIQRFLDLGVLVPCQSPWNTPLLPVKKPGTNDYRPVQDLREINKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKG NTGQLTWTRLPQGFKNSPTLFNEALHRDLAPFRALNPQVVLLQYVDDLLVAAPTYRDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLLKEGKRWLTPARKATVMK IPPPTTPRQVREFLGKAGFCRLFIPGFASLAAPLYPLTKPSIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVAYLSKKLDPV ASGWPTCLKAVAAVALLLKDADKLTLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVHRCSEILAEETGTRRDLKDQPL

	PGVPAWYTDGSSFIAEGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDINIYTDSRYAFATAHIHGAIYKQRGWLTSAGKDIKNKEEILALLEAIHLP KRVAIIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
873	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSGGGGSGGGGSGGGGSGGGGSGGVLNLEEEYRLHEKPVPSSIDPSWLQLFPTVWAERAGMGLANQVPPVVV ELRSGASPVAVRQYPMSKEAREGIRPHIQRFLDLGVLVPCQSPWNTPLLPVKKPGTNDYRPVQDLREINKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHP NSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLAPFRALNPQVVLLQYVDDLLVAAPTYRDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLLK EGKRWLTPARKATVMKIPPPTTPRQVREFLGKAGFCRLFIPGFASLAAPLYPLTKPSIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKPFTLYVDERAGVARGVLTQTLG PWRRPVAYLSKKLDPVASGWPTCLKAVAAVALLLKDADKLTLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVHRCSEI LAEETGTRRDLKDQPLPGVPAWYTDGSSFIAEGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDINIYTDSRYAFATAHIHGAIYKQRGWLTSAGKDI KNKEEILALLEAIHLPKRVAIIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
874	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKPAPGSSGGVLNLEEEYRLHEKPVPSSIDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQY PMSKEAREGIRPHIQRFLDLGVLVPCQSPWNTPLLPVKKPGTNDYRPVQDLREINKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPE KGNTGQLTWTRLPQGFKNSPTLFNEALHRDLAPFRALNPQVVLLQYVDDLLVAAPTYRDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLLKEGKRWLTPARKATV MKIPPPTTPRQVREFLGKAGFCRLFIPGFASLAAPLYPLTKPSIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVAYLSKKLD PVASGWPTCLKAVAAVALLLKDADKLTLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVHRCSEILAEETGTRRDLKDQ PLPGVPAWYTDGSSFIAEGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDINIYTDSRYAFATAHIHGAIYKQRGWLTSAGKDIKNKEEILALLEAIH LPKRVAIIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
876	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY

	DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGVLNLEEEYRLHEKPVPSSIDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMSKEARE GIRPHIQRFLDLGVLVPCQSPWNTPLLPVKKPGTNDYRPVQDLREINKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLT WTRLPQGFKNSPTLFNEALHRDLAPFRALNPQVVLLQYVDDLLVAAPTYRDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLLKEGKRWLTPARKATVMKIPPPTT PRQVREFLGKAGFCRLFIPGFASLAAPLYPLTKPSIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPT CLKAVAAVALLLKDADKLTLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVHRCSEILAEETGTRRDLKDQPLPGVPAW YTDGSSFIAEGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDINIYTDSRYAFATAHIHGAIYKQRGWLTSAGKDIKNKEEILALLEAIHLPKRVAII HCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
878	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGPAPGGSGGVLNLEEEYRLHEKPVPSSIDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPM SKEAREGIRPHIQRFLDLGVLVPCQSPWNTPLLPVKKPGTNDYRPVQDLREINKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKG NTGQLTWTRLPQGFKNSPTLFNEALHRDLAPFRALNPQVVLLQYVDDLLVAAPTYRDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLLKEGKRWLTPARKATVMK IPPPTTPRQVREFLGKAGFCRLFIPGFASLAAPLYPLTKPSIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVAYLSKKLDPV ASGWPTCLKAVAAVALLLKDADKLTLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVHRCSEILAEETGTRRDLKDQPL PGVPAWYTDGSSFIAEGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDINIYTDSRYAFATAHIHGAIYKQRGWLTSAGKDIKNKEEILALLEAIHLP KRVAIIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
880	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ

	LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGSGSSGGVLNLEEEYRLHEKPVPSSIDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPM SKEAREGIRPHIQRFLDLGVLVPCQSPWNTPLLPVKKPGTNDYRPVQDLREINKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKG NTGQLTWTRLPQGFKNSPTLFNEALHRDLAPFRALNPQVVLLQYVDDLLVAAPTYRDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLLKEGKRWLTPARKATVMK IPPPTTPRQVREFLGKAGFCRLFIPGFASLAAPLYPLTKPSIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVAYLSKKLDPV ASGWPTCLKAVAAVALLLKDADKLTLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVHRCSEILAEETGTRRDLKDQPL PGVPAWYTDGSSFIAEGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDINIYTDSRYAFATAHIHGAIYKQRGWLTSAGKDIKNKEEILALLEAIHLP KRVAIIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
882	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGGGGGVLNLEEEYRLHEKPVPSSIDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMSKE AREGIRPHIQRFLDLGVLVPCQSPWNTPLLPVKKPGTNDYRPVQDLREINKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTG QLTWTRLPQGFKNSPTLFNEALHRDLAPFRALNPQVVLLQYVDDLLVAAPTYRDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLLKEGKRWLTPARKATVMKIPP PTTPRQVREFLGKAGFCRLFIPGFASLAAPLYPLTKPSIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVAYLSKKLDPVASG WPTCLKAVAAVALLLKDADKLTLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVHRCSEILAEETGTRRDLKDQPLPGV PAWYTDGSSFIAEGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDINIYTDSRYAFATAHIHGAIYKQRGWLTSAGKDIKNKEEILALLEAIHLPKRV AIIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
883	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSEAAAKGGVLNLEEEYRLHEKPVPSSIDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMS

	KEAREGIRPHIQRFLDLGVLVPCQSPWNTPLLPVKKPGTNDYRPVQDLREINKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGN TGQLTWTRLPQGFKNSPTLFNEALHRDLAPFRALNPQVVLLQYVDDLLVAAPTYRDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLLKEGKRWLTPARKATVMKI PPPTTPRQVREFLGKAGFCRLFIPGFASLAAPLYPLTKPSIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVAYLSKKLDPVA SGWPTCLKAVAAVALLLKDADKLTLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVHRCSEILAEETGTRRDLKDQPLP GVPAWYTDGSSFIAEGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDINIYTDSRYAFATAHIHGAIYKQRGWLTSAGKDIKNKEEILALLEAIHLPK RVAIIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
884	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSPAPGGVLNLEEEYRLHEKPVPSSIDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMSKE AREGIRPHIQRFLDLGVLVPCQSPWNTPLLPVKKPGTNDYRPVQDLREINKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTG QLTWTRLPQGFKNSPTLFNEALHRDLAPFRALNPQVVLLQYVDDLLVAAPTYRDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLLKEGKRWLTPARKATVMKIPP PTTPRQVREFLGKAGFCRLFIPGFASLAAPLYPLTKPSIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVAYLSKKLDPVASG WPTCLKAVAAVALLLKDADKLTLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVHRCSEILAEETGTRRDLKDQPLPGV PAWYTDGSSFIAEGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDINIYTDSRYAFATAHIHGAIYKQRGWLTSAGKDIKNKEEILALLEAIHLPKRV AIIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
890	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPAPAPGGVLNLEEEYRLHEKPVPSSIDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVR QYPMSKEAREGIRPHIQRFLDLGVLVPCQSPWNTPLLPVKKPGTNDYRPVQDLREINKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRD PEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLAPFRALNPQVVLLQYVDDLLVAAPTYRDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLLKEGKRWLTPARKA TVMKIPPPTTPRQVREFLGKAGFCRLFIPGFASLAAPLYPLTKPSIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVAYLSKK LDPVASGWPTCLKAVAAVALLLKDADKLTLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVHRCSEILAEETGTRRDLK

	DQPLPGVPAWYTDGSSFIAEGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDINIYTDSRYAFATAHIHGAIYKQRGWLTSAGKDIKNKEEILALLEA IHLPKRVAIIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
898	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSPAPEAAAKGGVLNLEEEYRLHEKPVPSSIDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQY PMSKEAREGIRPHIQRFLDLGVLVPCQSPWNTPLLPVKKPGTNDYRPVQDLREINKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPE KGNTGQLTWTRLPQGFKNSPTLFNEALHRDLAPFRALNPQVVLLQYVDDLLVAAPTYRDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLLKEGKRWLTPARKATV MKIPPPTTPRQVREFLGKAGFCRLFIPGFASLAAPLYPLTKPSIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVAYLSKKLD PVASGWPTCLKAVAAVALLLKDADKLTLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVHRCSEILAEETGTRRDLKDQ PLPGVPAWYTDGSSFIAEGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDINIYTDSRYAFATAHIHGAIYKQRGWLTSAGKDIKNKEEILALLEAIH LPKRVAIIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
900	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGSEAAAKGGVLNLEEEYRLHEKPVPSSIDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVA VRQYPMSKEAREGIRPHIQRFLDLGVLVPCQSPWNTPLLPVKKPGTNDYRPVQDLREINKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEW RDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLAPFRALNPQVVLLQYVDDLLVAAPTYRDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLLKEGKRWLTPAR KATVMKIPPPTTPRQVREFLGKAGFCRLFIPGFASLAAPLYPLTKPSIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVAYLS KKLDPVASGWPTCLKAVAAVALLLKDADKLTLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVHRCSEILAEETGTRRD LKDQPLPGVPAWYTDGSSFIAEGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDINIYTDSRYAFATAHIHGAIYKQRGWLTSAGKDIKNKEEILALL EAIHLPKRVAIIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
901	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY

	DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGEAAAKGGSGGVLNLEEEYRLHEKPVPSSIDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQY PMSKEAREGIRPHIQRFLDLGVLVPCQSPWNTPLLPVKKPGTNDYRPVQDLREINKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPE KGNTGQLTWTRLPQGFKNSPTLFNEALHRDLAPFRALNPQVVLLQYVDDLLVAAPTYRDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLLKEGKRWLTPARKATV MKIPPPTTPRQVREFLGKAGFCRLFIPGFASLAAPLYPLTKPSIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVAYLSKKLD PVASGWPTCLKAVAAVALLLKDADKLTLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVHRCSEILAEETGTRRDLKDQ PLPGVPAWYTDGSSFIAEGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDINIYTDSRYAFATAHIHGAIYKQRGWLTSAGKDIKNKEEILALLEAIH LPKRVAIIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
912	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSEAAAKPAPGGVLNLEEEYRLHEKPVPSSIDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQY PMSKEAREGIRPHIQRFLDLGVLVPCQSPWNTPLLPVKKPGTNDYRPVQDLREINKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPE KGNTGQLTWTRLPQGFKNSPTLFNEALHRDLAPFRALNPQVVLLQYVDDLLVAAPTYRDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLLKEGKRWLTPARKATV MKIPPPTTPRQVREFLGKAGFCRLFIPGFASLAAPLYPLTKPSIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVAYLSKKLD PVASGWPTCLKAVAAVALLLKDADKLTLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVHRCSEILAEETGTRRDLKDQ PLPGVPAWYTDGSSFIAEGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDINIYTDSRYAFATAHIHGAIYKQRGWLTSAGKDIKNKEEILALLEAIH LPKRVAIIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
915	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ

	LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGSEAAAKGGVLNLEEEYRLHEKPVPSSIDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQY PMSKEAREGIRPHIQRFLDLGVLVPCQSPWNTPLLPVKKPGTNDYRPVQDLREINKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPE KGNTGQLTWTRLPQGFKNSPTLFNEALHRDLAPFRALNPQVVLLQYVDDLLVAAPTYRDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLLKEGKRWLTPARKATV MKIPPPTTPRQVREFLGKAGFCRLFIPGFASLAAPLYPLTKPSIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVAYLSKKLD PVASGWPTCLKAVAAVALLLKDADKLTLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVHRCSEILAEETGTRRDLKDQ PLPGVPAWYTDGSSFIAEGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDINIYTDSRYAFATAHIHGAIYKQRGWLTSAGKDIKNKEEILALLEAIH LPKRVAIIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
929	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGSSGSSGGVLNLEEEYRLHEKPVPSSIDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPM SKEAREGIRPHIQRFLDLGVLVPCQSPWNTPLLPVKKPGTNDYRPVQDLREINKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKG NTGQLTWTRLPQGFKNSPTLFNEALHRDLAPFRALNPQVVLLQYVDDLLVAAPTYRDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLLKEGKRWLTPARKATVMK IPPPTTPRQVREFLGKAGFCRLFIPGFASLAAPLYPLTKPSIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVAYLSKKLDPV ASGWPTCLKAVAAVALLLKDADKLTLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVHRCSEILAEETGTRRDLKDQPL PGVPAWYTDGSSFIAEGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDINIYTDSRYAFATAHIHGAIYKQRGWLTSAGKDIKNKEEILALLEAIHLP KRVAIIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
933	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKGGVLNLEEEYRLHEKPVPSSIDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVA

	VRQYPMSKEAREGIRPHIQRFLDLGVLVPCQSPWNTPLLPVKKPGTNDYRPVQDLREINKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEW RDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLAPFRALNPQVVLLQYVDDLLVAAPTYRDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLLKEGKRWLTPAR KATVMKIPPPTTPRQVREFLGKAGFCRLFIPGFASLAAPLYPLTKPSIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVAYLS KKLDPVASGWPTCLKAVAAVALLLKDADKLTLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVHRCSEILAEETGTRRD LKDQPLPGVPAWYTDGSSFIAEGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDINIYTDSRYAFATAHIHGAIYKQRGWLTSAGKDIKNKEEILALL EAIHLPKRVAIIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
958	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGGSGGSGGSGGSGGSGGTLNIEDEYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKAT STPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPL FAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRW LTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRP VAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETH GTRPDLTDQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIKNKN EILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
960	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGSSPAPGGTLNIEDEYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDLT

	DQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIKNKNEILALLK ALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
961	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKPAPGGSGGTLNIEDEYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDLT DQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIKNKNEILALLK ALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
963	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGPAPGGTLNIEDEYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDLT DQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIKNKNEILALLK ALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
964	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY

	DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGSSGSSGSSGSSGGTLNIEDEYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTP VSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAF EWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTE ARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAY LSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTR PDLTDQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIKNKNEIL ALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
966	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSEAAAKGGTLNIEDEYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYP MSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEM GISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVM GQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDP VAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDLTDQP IPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIKNKNEILALLKALF LPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
967	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ

	LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGSSEAAAKGGTLNIEDEYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDLT DQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIKNKNEILALLK ALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAARAAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
978	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPGGTLNIEDEYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQY PMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPE MGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDLTDQ PIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIKNKNEILALLKAL FLPKRLSIIHCPGHQKGNSAEARGNRMADQAARAAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
987	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSPAPGGSGGTLNIEDEYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQY

	PMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPE MGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDLTDQ PIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIKNKNEILALLKAL FLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1006	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKEAAAKAGGTLNIEDEYRLHETSKEPDVPLGSTWLS DFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGL PPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLG YRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLT KPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPV VALNPATLLPLPEKEAPHDCLEILAETHGTRPDLTDQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYA FATAHVHGEIYRRRGWLTSEGREIKNKNEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKA KVE
1007	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPEAAAKGSSGGTLNIEDEYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDLT

	DQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIKNKNEILALLK ALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1008	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAAKGGTLNIEDEYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLK ATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQ PLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQ RWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWR RPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAE THGTRPDLTDQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIKN KNEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1009	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGTLNIEDEYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQ EARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGIS GQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQP TPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAA GWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDLTDQPIPD ADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIKNKNEILALLKALFLPK RLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1011	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY

	DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGTLNIEDEYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEA RLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQ LTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTP KTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDLTDQPIPDAD YTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIKNKNEILALLKALFLPKRL SIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1012	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGSSGGGGGTLNIEDEYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDLT DQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIKNKNEILALLK ALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1015	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ

	LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSPAPGGTLNIEDEYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQY PMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPE MGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDLTDQ PIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIKNKNEILALLKAL FLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1016	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGSSGGTLNIEDEYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMS QEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGI SGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQ PTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVA AGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDLTDQPIP DADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIKNKNEILALLKALFLP KRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1017	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSPAPGGTLNIEDEYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMS

	QEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGI SGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQ PTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVA AGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDLTDQPIP DADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIKNKNEILALLKALFLP KRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1018	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGEAAAKGGSGGTLNIEDEYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDLT DQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIKNKNEILALLK ALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1019	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGSGGSGGSGGTLNIEDEYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSI KQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWR DPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARK ETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSK KLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDL

	TDQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIKNKNEILALL KALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1020	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPAPAPGGTLNIEDEYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVS IKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEW RDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEAR KETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLS KKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPD LTDQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIKNKNEILAL LKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1021	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGTLNIEDEYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAV RQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAF FCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVK YLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKG VLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEA PHDCLEILAETHGTRPDLTDQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGW LTSEGREIKNKNEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1022	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY

	DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGSSGGGGGTLNIEDEYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQY PMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPE MGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDLTDQ PIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIKNKNEILALLKAL FLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1023	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSGGTLNIEDEYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYP MSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEM GISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVM GQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDP VAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDLTDQP IPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIKNKNEILALLKALF LPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1025	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ

	LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGSSGGGGGTLNIEDEYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQY PMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPE MGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDLTDQ PIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIKNKNEILALLKAL FLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1029	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAAKEAAAKGGTLNIEDEYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPL IIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRL HPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYL LKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQK LGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCL EILAETHGTRPDLTDQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEG REIKNKNEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1033	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGSSGGGGGTLNIEDEYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQY

	PMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPE MGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDLTDQ PIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIKNKNEILALLKAL FLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1034	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGSEAAAKGGTLNIEDEYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDLT DQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIKNKNEILALLK ALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1037	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGSEAAAKGGTLNIEDEYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTP VSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAF EWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTE ARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAY LSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTR

	PDLTDQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIKNKNEIL ALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1038	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSPAPGGGGGTLNIEDEYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQY PMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPE MGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDLTDQ PIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIKNKNEILALLKAL FLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1039	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGSSPAPGGTLNIEDEYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDLT DQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIKNKNEILALLK ALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1043	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY

	DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGSSGGSGGTLNIEDEYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQY PMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPE MGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDLTDQ PIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIKNKNEILALLKAL FLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1044	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGEAAAKGGTLNIEDEYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYP MSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEM GISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVM GQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDP VAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDLTDQP IPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIKNKNEILALLKALF LPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1046	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ

	LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGGSGGTLNIEDEYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDLT DQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIKNKNEILALLK ALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1047	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGSSGGTLNIEDEYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMS QEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGI SGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQ PTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVA AGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDLTDQPIP DADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIKNKNEILALLKALFLP KRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1049	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSGGGGSGGGGSGGGGSGGTLNIEDEYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLK

	ATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQ PLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQ RWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWR RPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAE THGTRPDLTDQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIKN KNEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1052	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAAKEAAAKEAAAKEAAAKGGTLNIEDEYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAV RQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAF FCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVK YLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKG VLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEA PHDCLEILAETHGTRPDLTDQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGW LTSEGREIKNKNEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1056	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGSSGGTLNIEDEYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDLT

	DQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIKNKNEILALLK ALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1059	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGSSEAAAKGGTLNIEDEYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDLT DQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIKNKNEILALLK ALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1060	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGSEAAAKGGTLNIEDEYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDLT DQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIKNKNEILALLK ALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1061	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY

	DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGSPAPGGTLNIEDEYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQY PMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPE MGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDLTDQ PIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIKNKNEILALLKAL FLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1076	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGPAPEAAAKGGTLNIEDEYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDLT DQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIKNKNEILALLK ALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1083	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ

	LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSEAAAKGGTLNIEDEYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYP MSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEM GISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVM GQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDP VAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDLTDQP IPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIKNKNEILALLKALF LPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1093	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKAGGVPWILKKPLELTIKLDLEEQQGTLLNN SILSKKGKEELKQLFEKYSALWQSWENQVGHRRIRPHKIATGTVKPTPQKQYHINPKAKPDIQIVINDLLKQGVLIQKESTMNTPVYPVPKPNGRWRMVLDYRAVNKVTPLI AVQNQHSYGILGSLFKGRYKTTIDLSNGFWAHPIVPEDYWITAFTWQGKQYCWTVLPQGFLNSPGLFNGDVVDLLQGIPNVEVYVDDVYISHDSEKEHLEYLDILFNRLKEA GYIISLKKSNIANSIVDFLGFQITNEGRGLTDTFKEKLENITAPTTLKQLQSILGLLNFARNFIPDFTELIAPLYALIPKSPKNYVPWQIEHSTTLETLITKLNGAEYLQGR KGDKTLIMKVNASYTTGYIRYYNEGEKKPISYVSIVFSKTELKFTELEKLLTTVHKGLLKALDLSMGQNIHVYSPIVSMQNIQKTPQTAKKALASRWLSWLSYLEDPRIRFF YDPQMPALKDLPAVDTGKDNKKHPSNFQHIFYTDGSAITSPTKEGHLNAGMGIVYFINKDGNLQKQQEWSISLGNHTAQFAEIAAFEFALKKCLPLGGNILVVTDSNYVAKA YNEELDVWASNGFVNNRKKPLKHISKWKSVADLKRLRPDVVVTHEPGHQKLDSSPHAYGNNLADQLATQASFKVHAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1115	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKAGGMDLLKPLTVERKGVKIKGYWNSQADIT

	CVPKDLLQGEEPVRQQNVTTIHGTQEGDVYYVNLKIDGRRINTEVIGTTLDYAIITPGDVPWILKKPLELTIKLDLEEQQGTLLNNSILSKKGKEELKQLFEKYSALWQSWE NQVGHRRIRPHKIATGTVKPTPQKQYHINPKAKPDIQIVINDLLKQGVLIQKESTMNTPVYPVPKPNGRWRMVLDYRAVNKVTPLIAVQNQHSYGILGSLFKGRYKTTIDLS NGFWAHPIVPEDYWITAFTWQGKQYCWTVLPQGFLNSPGLFNGDVVDLLQGIPNVEVYVDDVYISHDSEKEHLEYLDILFNRLKEAGYIISLKKSNIANSIVDFLGFQITNE GRGLTDTFKEKLENITAPTTLKQLQSILGLLNFARNFIPDFTELIAPLYALIPKSPKNYVPWQIEHSTTLETLITKLNGAEYLQGRKGDKTLIMKVNASYTTGYIRYYNEGE KKPISYVSIVFSKTELKFTELEKLLTTVHKGLLKALDLSMGQNIHVYSPIVSMQNIQKTPQTAKKALASRWLSWLSYLEDPRIRFFYDPQMPALKDLPAVDTGKDNKKHPSN FQHIFYTDGSAITSPTKEGHLNAGMGIVYFINKDGNLQKQQEWSISLGNHTAQFAEIAAFEFALKKCLPLGGNILVVTDSNYVAKAYNEELDVWASNGFVNNRKKPLKHISK WKSVADLKRLRPDVVVTHEPGHQKLDSSPHAYGNNLADQLATQASFKVHAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1137	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAAKGGTAPLEEEYRLFLEAPIQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLL STALPVRVRQYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGTSEYRMVQDLREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQ LIFAFEWADAEEGESGQLTWTRLPQGFKNSPTLFNEALNRDLQGFRLDHPSVSLLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGS RSLSNSRTQAILQIPVPKTKRQVREFLGTIGYCRLWIPGFAELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPW KRPVAYLSKRLDPVAAGWPRCLRAIAAAALLTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTL DSLTSTRPDLTDQPLAQAEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWLTAGGKAI KNAPEILALLTAVWLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1168	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGGSPAPGGTLQLEEEYRLFEPESTQKQEMDIWLKNFPQAWAETGGMGTAHCQAPVLIQLKATATPISIRQYP MPHEAYQGIKPHIRRMLDQGILKPCQSPWNTPLLPVKKPGTEDYRPVQDLREVNKRVEDIHPTVPNPYNLLSTLPPSHPWYTVLDLKDAFFCLRLHSESQLLFAFEWRDPEI GLSGQLTWTRLPQGFKNSPTLFNEALHSDLADFRVRYPALVLLQYVDDLLLAAATRTECLEGTKALLETLGNKGYRASAKKAQICLQEVTYLGYSLKDGQRWLTKARKEAIL SIPVPKNSRQVREFLGTAGYCRLWIPGFAELAAPLYPLTRPGTLFQWGTEQQLAFEDIKKALLSSPALGLPDITKPFELFIDENSGFAKGVLVQKLGPWKRPVAYLSKKLDT VASGWPPCLRMVAAIAILVKDAGKLTLGQPLTILTSHPVEALVRQPPNKWLSNARMTHYQAMLLDAERVHFGPTVSLNPATLLPLPSGGNHHDCLQILAETHGTRPDLTDQP

	LPDADLTWYTDGSSFIRNGEREAGAAVTTESEVIWAAPLPPGTSAQRAELIALTQALKMAEGKKLTVYTDSRYAFATTHVHGEIYRRRGWLTSEGKEIKNKNEILALLEALF LPKRLSIIHCPGHQKGDSPQAKGNRLADDTAKKAATETHSSLTVLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1171	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAAKEAAAKEAAAKGGTLQLEEEYRLFEPESTQKQEMDIWLKNFPQAWAETGGMGTAHC QAPVLIQLKATATPISIRQYPMPHEAYQGIKPHIRRMLDQGILKPCQSPWNTPLLPVKKPGTEDYRPVQDLREVNKRVEDIHPTVPNPYNLLSTLPPSHPWYTVLDLKDAFF CLRLHSESQLLFAFEWRDPEIGLSGQLTWTRLPQGFKNSPTLFNEALHSDLADFRVRYPALVLLQYVDDLLLAAATRTECLEGTKALLETLGNKGYRASAKKAQICLQEVTY LGYSLKDGQRWLTKARKEAILSIPVPKNSRQVREFLGTAGYCRLWIPGFAELAAPLYPLTRPGTLFQWGTEQQLAFEDIKKALLSSPALGLPDITKPFELFIDENSGFAKGV LVQKLGPWKRPVAYLSKKLDTVASGWPPCLRMVAAIAILVKDAGKLTLGQPLTILTSHPVEALVRQPPNKWLSNARMTHYQAMLLDAERVHFGPTVSLNPATLLPLPSGGNH HDCLQILAETHGTRPDLTDQPLPDADLTWYTDGSSFIRNGEREAGAAVTTESEVIWAAPLPPGTSAQRAELIALTQALKMAEGKKLTVYTDSRYAFATTHVHGEIYRRRGWL TSEGKEIKNKNEILALLEALFLPKRLSIIHCPGHQKGDSPQAKGNRLADDTAKKAATETHSSLTVLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1197	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKEAAAKAGGTLQLEEEYRLFEPESTQKQEMDIWLKN FPQAWAETGGMGTAHCQAPVLIQLKATATPISIRQYPMPHEAYQGIKPHIRRMLDQGILKPCQSPWNTPLLPVKKPGTEDYRPVQDLREVNKRVEDIHPTVPNPYNLLSTLP PSHPWYTVLDLKDAFFCLRLHSESQLLFAFEWRDPEIGLSGQLTWTRLPQGFKNSPTLFNEALHSDLADFRVRYPALVLLQYVDDLLLAAATRTECLEGTKALLETLGNKGY RASAKKAQICLQEVTYLGYSLKDGQRWLTKARKEAILSIPVPKNSRQVREFLGKAGYCRLFIPGFAELAAPLYPLTRPGTLFQWGTEQQLAFEDIKKALLSSPALGLPDITK PFELFIDENSGFAKGVLVQKLGPWKRPVAYLSKKLDTVASGWPPCLRMVAAIAILVKDAGKLTLGQPLTILTSHPVEALVRQPPNKWLSNARMTHYQAMLLDAERVHFGPTV SLNPATLLPLPSGGNHHDCLQILAETHGTRPDLTDQPLPDADLTWYTDGSSFIRNGEREAGAAVTTESEVIWAAPLPPGTSAQRAELIALTQALKMAEGKKLTVYTDSRYAF ATTHVHGEIYRRRGWLTSEGKEIKNKNEILALLEALFLPKRLSIIHCPGHQKGDSPQAKGNRLADDTAKKAATETHSSLTVLPAGKRTADGSEFEKRTADGSEFESPKKKAK VE
1198	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS

	ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAAKGGTLQLEEEYRLFEPESTQKQEMDIWLKNFPQAWAETGGMGTAHCQAPVLIQLKA TATPISIRQYPMPHEAYQGIKPHIRRMLDQGILKPCQSPWNTPLLPVKKPGTEDYRPVQDLREVNKRVEDIHPTVPNPYNLLSTLPPSHPWYTVLDLKDAFFCLRLHSESQL LFAFEWRDPEIGLSGQLTWTRLPQGFKNSPTLFNEALHSDLADFRVRYPALVLLQYVDDLLLAAATRTECLEGTKALLETLGNKGYRASAKKAQICLQEVTYLGYSLKDGQR WLTKARKEAILSIPVPKNSRQVREFLGKAGYCRLFIPGFAELAAPLYPLTRPGTLFQWGTEQQLAFEDIKKALLSSPALGLPDITKPFELFIDENSGFAKGVLVQKLGPWKR PVAYLSKKLDTVASGWPPCLRMVAAIAILVKDAGKLTLGQPLTILTSHPVEALVRQPPNKWLSNARMTHYQAMLLDAERVHFGPTVSLNPATLLPLPSGGNHHDCLQILAET HGTRPDLTDQPLPDADLTWYTDGSSFIRNGEREAGAAVTTESEVIWAAPLPPGTSAQRAELIALTQALKMAEGKKLTVYTDSRYAFATTHVHGEIYRRRGWLTSEGKEIKNK NEILALLEALFLPKRLSIIHCPGHQKGDSPQAKGNRLADDTAKKAATETHSSLTVLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1202	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSGGGGSGGGGSGGGGSGGGGSGGTLQLEEEYRLFEPESTQKQEMDIWLKNFPQAWAETGGMGTAHCQAPVL IQLKATATPISIRQYPMPHEAYQGIKPHIRRMLDQGILKPCQSPWNTPLLPVKKPGTEDYRPVQDLREVNKRVEDIHPTVPNPYNLLSTLPPSHPWYTVLDLKDAFFCLRLH SESQLLFAFEWRDPEIGLSGQLTWTRLPQGFKNSPTLFNEALHSDLADFRVRYPALVLLQYVDDLLLAAATRTECLEGTKALLETLGNKGYRASAKKAQICLQEVTYLGYSL KDGQRWLTKARKEAILSIPVPKNSRQVREFLGKAGYCRLFIPGFAELAAPLYPLTRPGTLFQWGTEQQLAFEDIKKALLSSPALGLPDITKPFELFIDENSGFAKGVLVQKL GPWKRPVAYLSKKLDTVASGWPPCLRMVAAIAILVKDAGKLTLGQPLTILTSHPVEALVRQPPNKWLSNARMTHYQAMLLDAERVHFGPTVSLNPATLLPLPSGGNHHDCLQ ILAETHGTRPDLTDQPLPDADLTWYTDGSSFIRNGEREAGAAVTTESEVIWAAPLPPGTSAQRAELIALTQALKMAEGKKLTVYTDSRYAFATTHVHGEIYRRRGWLTSEGK EIKNKNEILALLEALFLPKRLSIIHCPGHQKGDSPQAKGNRLADDTAKKAATETHSSLTVLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1203	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG

	QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSEAAAKGGGGSGGTLQLEEEYRLFEPESTQKQEMDIWLKNFPQAWAETGGMGTAHCQAPVLIQLKATATPI SIRQYPMPHEAYQGIKPHIRRMLDQGILKPCQSPWNTPLLPVKKPGTEDYRPVQDLREVNKRVEDIHPTVPNPYNLLSTLPPSHPWYTVLDLKDAFFCLRLHSESQLLFAFE WRDPEIGLSGQLTWTRLPQGFKNSPTLFNEALHSDLADFRVRYPALVLLQYVDDLLLAAATRTECLEGTKALLETLGNKGYRASAKKAQICLQEVTYLGYSLKDGQRWLTKA RKEAILSIPVPKNSRQVREFLGKAGYCRLFIPGFAELAAPLYPLTRPGTLFQWGTEQQLAFEDIKKALLSSPALGLPDITKPFELFIDENSGFAKGVLVQKLGPWKRPVAYL SKKLDTVASGWPPCLRMVAAIAILVKDAGKLTLGQPLTILTSHPVEALVRQPPNKWLSNARMTHYQAMLLDAERVHFGPTVSLNPATLLPLPSGGNHHDCLQILAETHGTRP DLTDQPLPDADLTWYTDGSSFIRNGEREAGAAVTTESEVIWAAPLPPGTSAQRAELIALTQALKMAEGKKLTVYTDSRYAFATTHVHGEIYRRRGWLTSEGKEIKNKNEILA LLEALFLPKRLSIIHCPGHQKGDSPQAKGNRLADDTAKKAATETHSSLTVLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1210	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGSSGGGGGTLQLEEEYRLFEPESTQKQEMDIWLKNFPQAWAETGGMGTAHCQAPVLIQLKATATPISIRQ YPMPHEAYQGIKPHIRRMLDQGILKPCQSPWNTPLLPVKKPGTEDYRPVQDLREVNKRVEDIHPTVPNPYNLLSTLPPSHPWYTVLDLKDAFFCLRLHSESQLLFAFEWRDP EIGLSGQLTWTRLPQGFKNSPTLFNEALHSDLADFRVRYPALVLLQYVDDLLLAAATRTECLEGTKALLETLGNKGYRASAKKAQICLQEVTYLGYSLKDGQRWLTKARKEA ILSIPVPKNSRQVREFLGKAGYCRLFIPGFAELAAPLYPLTRPGTLFQWGTEQQLAFEDIKKALLSSPALGLPDITKPFELFIDENSGFAKGVLVQKLGPWKRPVAYLSKKL DTVASGWPPCLRMVAAIAILVKDAGKLTLGQPLTILTSHPVEALVRQPPNKWLSNARMTHYQAMLLDAERVHFGPTVSLNPATLLPLPSGGNHHDCLQILAETHGTRPDLTD QPLPDADLTWYTDGSSFIRNGEREAGAAVTTESEVIWAAPLPPGTSAQRAELIALTQALKMAEGKKLTVYTDSRYAFATTHVHGEIYRRRGWLTSEGKEIKNKNEILALLEA LFLPKRLSIIHCPGHQKGDSPQAKGNRLADDTAKKAATETHSSLTVLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1216	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR

	KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPGGTLQLEEEYRLFEPESTQKQEMDIWLKNFPQAWAETGGMGTAHCQAPVLIQLKATATPISIRQYP MPHEAYQGIKPHIRRMLDQGILKPCQSPWNTPLLPVKKPGTEDYRPVQDLREVNKRVEDIHPTVPNPYNLLSTLPPSHPWYTVLDLKDAFFCLRLHSESQLLFAFEWRDPEI GLSGQLTWTRLPQGFKNSPTLFNEALHSDLADFRVRYPALVLLQYVDDLLLAAATRTECLEGTKALLETLGNKGYRASAKKAQICLQEVTYLGYSLKDGQRWLTKARKEAIL SIPVPKNSRQVREFLGKAGYCRLFIPGFAELAAPLYPLTRPGTLFQWGTEQQLAFEDIKKALLSSPALGLPDITKPFELFIDENSGFAKGVLVQKLGPWKRPVAYLSKKLDT VASGWPPCLRMVAAIAILVKDAGKLTLGQPLTILTSHPVEALVRQPPNKWLSNARMTHYQAMLLDAERVHFGPTVSLNPATLLPLPSGGNHHDCLQILAETHGTRPDLTDQP LPDADLTWYTDGSSFIRNGEREAGAAVTTESEVIWAAPLPPGTSAQRAELIALTQALKMAEGKKLTVYTDSRYAFATTHVHGEIYRRRGWLTSEGKEIKNKNEILALLEALF LPKRLSIIHCPGHQKGDSPQAKGNRLADDTAKKAATETHSSLTVLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1219	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPAPGGTLQLEEEYRLFEPESTQKQEMDIWLKNFPQAWAETGGMGTAHCQAPVLIQLKATATPISI RQYPMPHEAYQGIKPHIRRMLDQGILKPCQSPWNTPLLPVKKPGTEDYRPVQDLREVNKRVEDIHPTVPNPYNLLSTLPPSHPWYTVLDLKDAFFCLRLHSESQLLFAFEWR DPEIGLSGQLTWTRLPQGFKNSPTLFNEALHSDLADFRVRYPALVLLQYVDDLLLAAATRTECLEGTKALLETLGNKGYRASAKKAQICLQEVTYLGYSLKDGQRWLTKARK EAILSIPVPKNSRQVREFLGKAGYCRLFIPGFAELAAPLYPLTRPGTLFQWGTEQQLAFEDIKKALLSSPALGLPDITKPFELFIDENSGFAKGVLVQKLGPWKRPVAYLSK KLDTVASGWPPCLRMVAAIAILVKDAGKLTLGQPLTILTSHPVEALVRQPPNKWLSNARMTHYQAMLLDAERVHFGPTVSLNPATLLPLPSGGNHHDCLQILAETHGTRPDL TDQPLPDADLTWYTDGSSFIRNGEREAGAAVTTESEVIWAAPLPPGTSAQRAELIALTQALKMAEGKKLTVYTDSRYAFATTHVHGEIYRRRGWLTSEGKEIKNKNEILALL EALFLPKRLSIIHCPGHQKGDSPQAKGNRLADDTAKKAATETHSSLTVLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1225	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSPAPEAAAKGGTLQLEEEYRLFEPESTQKQEMDIWLKNFPQAWAETGGMGTAHCQAPVLIQLKATATPISIRQ YPMPHEAYQGIKPHIRRMLDQGILKPCQSPWNTPLLPVKKPGTEDYRPVQDLREVNKRVEDIHPTVPNPYNLLSTLPPSHPWYTVLDLKDAFFCLRLHSESQLLFAFEWRDP EIGLSGQLTWTRLPQGFKNSPTLFNEALHSDLADFRVRYPALVLLQYVDDLLLAAATRTECLEGTKALLETLGNKGYRASAKKAQICLQEVTYLGYSLKDGQRWLTKARKEA ILSIPVPKNSRQVREFLGKAGYCRLFIPGFAELAAPLYPLTRPGTLFQWGTEQQLAFEDIKKALLSSPALGLPDITKPFELFIDENSGFAKGVLVQKLGPWKRPVAYLSKKL DTVASGWPPCLRMVAAIAILVKDAGKLTLGQPLTILTSHPVEALVRQPPNKWLSNARMTHYQAMLLDAERVHFGPTVSLNPATLLPLPSGGNHHDCLQILAETHGTRPDLTD

	QPLPDADLTWYTDGSSFIRNGEREAGAAVTTESEVIWAAPLPPGTSAQRAELIALTQALKMAEGKKLTVYTDSRYAFATTHVHGEIYRRRGWLTSEGKEIKNKNEILALLEA LFLPKRLSIIHCPGHQKGDSPQAKGNRLADDTAKKAATETHSSLTVLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1235	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGGSGGTLQLEEEYRLFEPESTQKQEMDIWLKNFPQAWAETGGMGTAHCQAPVLIQLKATATPISIRQ YPMPHEAYQGIKPHIRRMLDQGILKPCQSPWNTPLLPVKKPGTEDYRPVQDLREVNKRVEDIHPTVPNPYNLLSTLPPSHPWYTVLDLKDAFFCLRLHSESQLLFAFEWRDP EIGLSGQLTWTRLPQGFKNSPTLFNEALHSDLADFRVRYPALVLLQYVDDLLLAAATRTECLEGTKALLETLGNKGYRASAKKAQICLQEVTYLGYSLKDGQRWLTKARKEA ILSIPVPKNSRQVREFLGKAGYCRLFIPGFAELAAPLYPLTRPGTLFQWGTEQQLAFEDIKKALLSSPALGLPDITKPFELFIDENSGFAKGVLVQKLGPWKRPVAYLSKKL DTVASGWPPCLRMVAAIAILVKDAGKLTLGQPLTILTSHPVEALVRQPPNKWLSNARMTHYQAMLLDAERVHFGPTVSLNPATLLPLPSGGNHHDCLQILAETHGTRPDLTD QPLPDADLTWYTDGSSFIRNGEREAGAAVTTESEVIWAAPLPPGTSAQRAELIALTQALKMAEGKKLTVYTDSRYAFATTHVHGEIYRRRGWLTSEGKEIKNKNEILALLEA LFLPKRLSIIHCPGHQKGDSPQAKGNRLADDTAKKAATETHSSLTVLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1242	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGSEAAAKGGTLQLEEEYRLFEPESTQKQEMDIWLKNFPQAWAETGGMGTAHCQAPVLIQLKATATPISIRQ YPMPHEAYQGIKPHIRRMLDQGILKPCQSPWNTPLLPVKKPGTEDYRPVQDLREVNKRVEDIHPTVPNPYNLLSTLPPSHPWYTVLDLKDAFFCLRLHSESQLLFAFEWRDP EIGLSGQLTWTRLPQGFKNSPTLFNEALHSDLADFRVRYPALVLLQYVDDLLLAAATRTECLEGTKALLETLGNKGYRASAKKAQICLQEVTYLGYSLKDGQRWLTKARKEA ILSIPVPKNSRQVREFLGKAGYCRLFIPGFAELAAPLYPLTRPGTLFQWGTEQQLAFEDIKKALLSSPALGLPDITKPFELFIDENSGFAKGVLVQKLGPWKRPVAYLSKKL DTVASGWPPCLRMVAAIAILVKDAGKLTLGQPLTILTSHPVEALVRQPPNKWLSNARMTHYQAMLLDAERVHFGPTVSLNPATLLPLPSGGNHHDCLQILAETHGTRPDLTD QPLPDADLTWYTDGSSFIRNGEREAGAAVTTESEVIWAAPLPPGTSAQRAELIALTQALKMAEGKKLTVYTDSRYAFATTHVHGEIYRRRGWLTSEGKEIKNKNEILALLEA LFLPKRLSIIHCPGHQKGDSPQAKGNRLADDTAKKAATETHSSLTVLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1262	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY

	DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGEAAAKPAPGGTLQLEEEYRLFEPESTQKQEMDIWLKNFPQAWAETGGMGTAHCQAPVLIQLKATATPISIRQ YPMPHEAYQGIKPHIRRMLDQGILKPCQSPWNTPLLPVKKPGTEDYRPVQDLREVNKRVEDIHPTVPNPYNLLSTLPPSHPWYTVLDLKDAFFCLRLHSESQLLFAFEWRDP EIGLSGQLTWTRLPQGFKNSPTLFNEALHSDLADFRVRYPALVLLQYVDDLLLAAATRTECLEGTKALLETLGNKGYRASAKKAQICLQEVTYLGYSLKDGQRWLTKARKEA ILSIPVPKNSRQVREFLGKAGYCRLFIPGFAELAAPLYPLTRPGTLFQWGTEQQLAFEDIKKALLSSPALGLPDITKPFELFIDENSGFAKGVLVQKLGPWKRPVAYLSKKL DTVASGWPPCLRMVAAIAILVKDAGKLTLGQPLTILTSHPVEALVRQPPNKWLSNARMTHYQAMLLDAERVHFGPTVSLNPATLLPLPSGGNHHDCLQILAETHGTRPDLTD QPLPDADLTWYTDGSSFIRNGEREAGAAVTTESEVIWAAPLPPGTSAQRAELIALTQALKMAEGKKLTVYTDSRYAFATTHVHGEIYRRRGWLTSEGKEIKNKNEILALLEA LFLPKRLSIIHCPGHQKGDSPQAKGNRLADDTAKKAATETHSSLTVLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1371	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGSEAAAKGGTAPLEEEYRLFLEAPIQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVR QYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGTSEYRMVQDLREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWAD AEEGESGQLTWTRLPQGFKNSPTLFNEALNRDLQGFRLDHPSVSLLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQ AILQIPVPKTKRQVREFLGKIGYCRLFIPGFAELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSK RLDPVAAGWPRCLRAIAAAALLTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTSTRPD LTDQPLAQAEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWLTAGGKAIKNAPEILAL LTAVWLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1372	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ

	LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKEAAAKAGGTAPLEEEYRLFLEAPIQNVTLLEQWKR EIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGTSEYRMVQDLREVNKRVETIHPTVPNPYTLLSLL PPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEEGESGQLTWTRLPQGFKNSPTLFNEALNRDLQGFRLDHPSVSLLQYVDDLLIAADTQAACLSATRDLLMTLAELG YRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAILQIPVPKTKRQVREFLGKIGYCRLFIPGFAELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSL DKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSKRLDPVAAGWPRCLRAIAAAALLTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQ TAALNPATLLPETDDTLPIHHCLDTLDSLTSTRPDLTDQPLAQAEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSR YAFATLHVHGMIYRERGWLTAGGKAIKNAPEILALLTAVWLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFEKRTADGSEFESPKK KAKVE
1373	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGTAPLEEEYRLFLEAPIQNVTLLEQWKREIPKVWAEINPPGLAS TQAPIHVQLLSTALPVRVRQYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGTSEYRMVQDLREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAF FCIPLAPESQLIFAFEWADAEEGESGQLTWTRLPQGFKNSPTLFNEALNRDLQGFRLDHPSVSLLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVT YLGFKIHKGSRSLSNSRTQAILQIPVPKTKRQVREFLGKIGYCRLFIPGFAELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAK GVLTQALGPWKRPVAYLSKRLDPVAAGWPRCLRAIAAAALLTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDT LPIHHCLDTLDSLTSTRPDLTDQPLAQAEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRER GWLTAGGKAIKNAPEILALLTAVWLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1374	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR

	KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSGGGGSGGGGSGGGGSGGTAPLEEEYRLFLEAPIQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLL STALPVRVRQYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGTSEYRMVQDLREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQ LIFAFEWADAEEGESGQLTWTRLPQGFKNSPTLFNEALNRDLQGFRLDHPSVSLLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGS RSLSNSRTQAILQIPVPKTKRQVREFLGKIGYCRLFIPGFAELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPW KRPVAYLSKRLDPVAAGWPRCLRAIAAAALLTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTL DSLTSTRPDLTDQPLAQAEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWLTAGGKAI KNAPEILALLTAVWLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1375	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSPAPGGTAPLEEEYRLFLEAPIQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYPIT LEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGTSEYRMVQDLREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEEGE SGQLTWTRLPQGFKNSPTLFNEALNRDLQGFRLDHPSVSLLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAILQI PVPKTKRQVREFLGKIGYCRLFIPGFAELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSKRLDPV AAGWPRCLRAIAAAALLTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTSTRPDLTDQP LAQAEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWLTAGGKAIKNAPEILALLTAVW LPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1376	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGSGSETPGTSESATPESGGTAPLEEEYRLFLEAPIQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTAL PVRVRQYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGTSEYRMVQDLREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFA FEWADAEEGESGQLTWTRLPQGFKNSPTLFNEALNRDLQGFRLDHPSVSLLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLS NSRTQAILQIPVPKTKRQVREFLGKIGYCRLFIPGFAELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPV AYLSKRLDPVAAGWPRCLRAIAAAALLTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLT

	STRPDLTDQPLAQAEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWLTAGGKAIKNAP EILALLTAVWLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1377	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPEAAAKGGSGGTAPLEEEYRLFLEAPIQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVR QYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGTSEYRMVQDLREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWAD AEEGESGQLTWTRLPQGFKNSPTLFNEALNRDLQGFRLDHPSVSLLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQ AILQIPVPKTKRQVREFLGKIGYCRLFIPGFAELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSK RLDPVAAGWPRCLRAIAAAALLTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTSTRPD LTDQPLAQAEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWLTAGGKAIKNAPEILAL LTAVWLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1380	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGTAPLEEEYRLFLEAPIQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYPITL EAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGTSEYRMVQDLREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEEGES GQLTWTRLPQGFKNSPTLFNEALNRDLQGFRLDHPSVSLLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAILQIP VPKTKRQVREFLGKIGYCRLFIPGFAELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSKRLDPVA AGWPRCLRAIAAAALLTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTSTRPDLTDQPL AQAEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWLTAGGKAIKNAPEILALLTAVWL PKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1381	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY

	DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSEAAAKPAPGGTAPLEEEYRLFLEAPIQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVR QYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGTSEYRMVQDLREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWAD AEEGESGQLTWTRLPQGFKNSPTLFNEALNRDLQGFRLDHPSVSLLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQ AILQIPVPKTKRQVREFLGKIGYCRLFIPGFAELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSK RLDPVAAGWPRCLRAIAAAALLTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTSTRPD LTDQPLAQAEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWLTAGGKAIKNAPEILAL LTAVWLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1382	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGSSGSSGSSGSSGSSGGTAPLEEEYRLFLEAPIQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLLST ALPVRVRQYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGTSEYRMVQDLREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLI FAFEWADAEEGESGQLTWTRLPQGFKNSPTLFNEALNRDLQGFRLDHPSVSLLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRS LSNSRTQAILQIPVPKTKRQVREFLGKIGYCRLFIPGFAELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKR PVAYLSKRLDPVAAGWPRCLRAIAAAALLTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDS LTSTRPDLTDQPLAQAEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWLTAGGKAIKN APEILALLTAVWLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1383	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ

	LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSPAPGGGGGTAPLEEEYRLFLEAPIQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQY PITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGTSEYRMVQDLREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAE EGESGQLTWTRLPQGFKNSPTLFNEALNRDLQGFRLDHPSVSLLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAI LQIPVPKTKRQVREFLGKIGYCRLFIPGFAELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSKRL DPVAAGWPRCLRAIAAAALLTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTSTRPDLT DQPLAQAEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWLTAGGKAIKNAPEILALLT AVWLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1384	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGEAAAKPAPGGTAPLEEEYRLFLEAPIQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVR QYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGTSEYRMVQDLREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWAD AEEGESGQLTWTRLPQGFKNSPTLFNEALNRDLQGFRLDHPSVSLLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQ AILQIPVPKTKRQVREFLGKIGYCRLFIPGFAELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSK RLDPVAAGWPRCLRAIAAAALLTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTSTRPD LTDQPLAQAEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWLTAGGKAIKNAPEILAL LTAVWLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1385	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGSGSSGGTAPLEEEYRLFLEAPIQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQY

	PITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGTSEYRMVQDLREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAE EGESGQLTWTRLPQGFKNSPTLFNEALNRDLQGFRLDHPSVSLLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAI LQIPVPKTKRQVREFLGKIGYCRLFIPGFAELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSKRL DPVAAGWPRCLRAIAAAALLTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTSTRPDLT DQPLAQAEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWLTAGGKAIKNAPEILALLT AVWLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1389	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGGTAPLEEEYRLFLEAPIQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYPITLEA KRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGTSEYRMVQDLREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEEGESGQ LTWTRLPQGFKNSPTLFNEALNRDLQGFRLDHPSVSLLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAILQIPVP KTKRQVREFLGKIGYCRLFIPGFAELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSKRLDPVAAG WPRCLRAIAAAALLTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTSTRPDLTDQPLAQ AEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWLTAGGKAIKNAPEILALLTAVWLPK RVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1390	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGGSGGTAPLEEEYRLFLEAPIQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVR QYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGTSEYRMVQDLREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWAD AEEGESGQLTWTRLPQGFKNSPTLFNEALNRDLQGFRLDHPSVSLLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQ AILQIPVPKTKRQVREFLGKIGYCRLFIPGFAELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSK RLDPVAAGWPRCLRAIAAAALLTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTSTRPD

	LTDQPLAQAEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWLTAGGKAIKNAPEILAL LTAVWLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1394	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSEAAAKGGGGGTAPLEEEYRLFLEAPIQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVR QYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGTSEYRMVQDLREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWAD AEEGESGQLTWTRLPQGFKNSPTLFNEALNRDLQGFRLDHPSVSLLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQ AILQIPVPKTKRQVREFLGKIGYCRLFIPGFAELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSK RLDPVAAGWPRCLRAIAAAALLTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTSTRPD LTDQPLAQAEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWLTAGGKAIKNAPEILAL LTAVWLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1397	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGPAPGGTAPLEEEYRLFLEAPIQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYPIT LEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGTSEYRMVQDLREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEEGE SGQLTWTRLPQGFKNSPTLFNEALNRDLQGFRLDHPSVSLLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAILQI PVPKTKRQVREFLGKIGYCRLFIPGFAELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSKRLDPV AAGWPRCLRAIAAAALLTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTSTRPDLTDQP LAQAEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWLTAGGKAIKNAPEILALLTAVW LPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1399	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY

	DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGSEAAAKGGTAPLEEEYRLFLEAPIQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALP VRVRQYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGTSEYRMVQDLREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAF EWADAEEGESGQLTWTRLPQGFKNSPTLFNEALNRDLQGFRLDHPSVSLLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSN SRTQAILQIPVPKTKRQVREFLGKIGYCRLFIPGFAELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVA YLSKRLDPVAAGWPRCLRAIAAAALLTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTS TRPDLTDQPLAQAEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWLTAGGKAIKNAPE ILALLTAVWLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1400	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAAKEAAAKGGTAPLEEEYRLFLEAPIQNVTLLEQWKREIPKVWAEINPPGLASTQAPI HVQLLSTALPVRVRQYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGTSEYRMVQDLREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPL APESQLIFAFEWADAEEGESGQLTWTRLPQGFKNSPTLFNEALNRDLQGFRLDHPSVSLLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFK IHKGSRSLSNSRTQAILQIPVPKTKRQVREFLGKIGYCRLFIPGFAELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQ ALGPWKRPVAYLSKRLDPVAAGWPRCLRAIAAAALLTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHH CLDTLDSLTSTRPDLTDQPLAQAEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWLTA GGKAIKNAPEILALLTAVWLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1401	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ

	LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGSSGGSGGTAPLEEEYRLFLEAPIQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQY PITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGTSEYRMVQDLREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAE EGESGQLTWTRLPQGFKNSPTLFNEALNRDLQGFRLDHPSVSLLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAI LQIPVPKTKRQVREFLGKIGYCRLFIPGFAELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSKRL DPVAAGWPRCLRAIAAAALLTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTSTRPDLT DQPLAQAEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWLTAGGKAIKNAPEILALLT AVWLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1402	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGPAPGGSGGTAPLEEEYRLFLEAPIQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQY PITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGTSEYRMVQDLREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAE EGESGQLTWTRLPQGFKNSPTLFNEALNRDLQGFRLDHPSVSLLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAI LQIPVPKTKRQVREFLGKIGYCRLFIPGFAELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSKRL DPVAAGWPRCLRAIAAAALLTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTSTRPDLT DQPLAQAEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWLTAGGKAIKNAPEILALLT AVWLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1404	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSSEAAAKGGTAPLEEEYRLFLEAPIQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVR

	QYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGTSEYRMVQDLREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWAD AEEGESGQLTWTRLPQGFKNSPTLFNEALNRDLQGFRLDHPSVSLLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQ AILQIPVPKTKRQVREFLGKIGYCRLFIPGFAELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSK RLDPVAAGWPRCLRAIAAAALLTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTSTRPD LTDQPLAQAEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWLTAGGKAIKNAPEILAL LTAVWLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1405	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSEAAAKGGTAPLEEEYRLFLEAPIQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYP ITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGTSEYRMVQDLREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEE GESGQLTWTRLPQGFKNSPTLFNEALNRDLQGFRLDHPSVSLLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAIL QIPVPKTKRQVREFLGKIGYCRLFIPGFAELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSKRLD PVAAGWPRCLRAIAAAALLTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTSTRPDLTD QPLAQAEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWLTAGGKAIKNAPEILALLTA VWLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1406	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSGSSGGTAPLEEEYRLFLEAPIQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVR QYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGTSEYRMVQDLREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWAD AEEGESGQLTWTRLPQGFKNSPTLFNEALNRDLQGFRLDHPSVSLLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQ AILQIPVPKTKRQVREFLGKIGYCRLFIPGFAELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSK RLDPVAAGWPRCLRAIAAAALLTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTSTRPD

	LTDQPLAQAEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWLTAGGKAIKNAPEILAL LTAVWLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1410	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGGGGTAPLEEEYRLFLEAPIQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYPIT LEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGTSEYRMVQDLREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEEGE SGQLTWTRLPQGFKNSPTLFNEALNRDLQGFRLDHPSVSLLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAILQI PVPKTKRQVREFLGKIGYCRLFIPGFAELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSKRLDPV AAGWPRCLRAIAAAALLTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTSTRPDLTDQP LAQAEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWLTAGGKAIKNAPEILALLTAVW LPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1415	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGPAPEAAAKGGTAPLEEEYRLFLEAPIQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVR QYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGTSEYRMVQDLREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWAD AEEGESGQLTWTRLPQGFKNSPTLFNEALNRDLQGFRLDHPSVSLLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQ AILQIPVPKTKRQVREFLGKIGYCRLFIPGFAELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSK RLDPVAAGWPRCLRAIAAAALLTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTSTRPD LTDQPLAQAEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWLTAGGKAIKNAPEILAL LTAVWLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1419	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY

	DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGSSGGGGGTAPLEEEYRLFLEAPIQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVR QYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGTSEYRMVQDLREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWAD AEEGESGQLTWTRLPQGFKNSPTLFNEALNRDLQGFRLDHPSVSLLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQ AILQIPVPKTKRQVREFLGKIGYCRLFIPGFAELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSK RLDPVAAGWPRCLRAIAAAALLTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTSTRPD LTDQPLAQAEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWLTAGGKAIKNAPEILAL LTAVWLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1422	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGGTAPLEEEYRLFLEAPIQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYP ITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGTSEYRMVQDLREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEE GESGQLTWTRLPQGFKNSPTLFNEALNRDLQGFRLDHPSVSLLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAIL QIPVPKTKRQVREFLGKIGYCRLFIPGFAELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSKRLD PVAAGWPRCLRAIAAAALLTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTSTRPDLTD QPLAQAEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWLTAGGKAIKNAPEILALLTA VWLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1423	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ

	LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGGGSGGTAPLEEEYRLFLEAPIQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQ YPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGTSEYRMVQDLREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADA EEGESGQLTWTRLPQGFKNSPTLFNEALNRDLQGFRLDHPSVSLLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQA ILQIPVPKTKRQVREFLGKIGYCRLFIPGFAELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSKR LDPVAAGWPRCLRAIAAAALLTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTSTRPDL TDQPLAQAEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWLTAGGKAIKNAPEILALL TAVWLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1424	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGGEAAAKGGTAPLEEEYRLFLEAPIQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVR QYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGTSEYRMVQDLREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWAD AEEGESGQLTWTRLPQGFKNSPTLFNEALNRDLQGFRLDHPSVSLLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQ AILQIPVPKTKRQVREFLGKIGYCRLFIPGFAELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSK RLDPVAAGWPRCLRAIAAAALLTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTSTRPD LTDQPLAQAEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWLTAGGKAIKNAPEILAL LTAVWLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1441	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSGGGGGTAPLEEEYRLFLEAPIQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVR

	QYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGTSEYRMVQDLREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWAD AEEGESGQLTWTRLPQGFKNSPTLFNEALNRDLQGFRLDHPSVSLLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQ AILQIPVPKTKRQVREFLGKIGYCRLFIPGFAELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSK RLDPVAAGWPRCLRAIAAAALLTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTSTRPD LTDQPLAQAEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWLTAGGKAIKNAPEILAL LTAVWLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1540	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSSEAAAKGGTVSLQDEHRLFDIPVTTSLPDVWLQDFPQAWAETGGLGRAKCQAPIIIDLKPTAVPVSIKQY PMSLEAHMGIRQHIIKFLELGVLRPCRSPWNTPLLPVKKPGTQDYRPVQDLREINKRTVDIHPTVPNPYNLLSTLKPDYSWYTVLDLKDAFFCLPLAPQSQELFAFEWKDPE RGISGQLTWTRLPQGFKNSPTLFNEALHRDLTDFRTQHPEVTLLQYVDDLLLAAPTKKACTQGTRHLLQELGEKGYRASAKKAQICQTKVTYLGYILSEGKRWLTPGRIETV ARIPPPRNPREVREFLGTAGFCRLWIPGFAELAAPLYALTKPSTPFTWQTEHQLAFEALKKALLSAPALGLPDTSKPFTLFLDERQGIAKGVLTQKLGPWKRPVAYLSKKLD PVAAGWPPCLRIMAATAMLVKDSAKLTLGQPLTVITPHTLEAIVRQPPDRWITNARLTHYQALLLDTDRVQFGPPVTLNPATLLPVPENQPSPHDCRQVLAETHGTREDLKD QELPDADHTWYTDGSSYLDSGTRRAGAAVVDGHNTIWAQSLPPGTSAQKAELIALTKALELSKGKKANIYTDSRYAFATAHTHGSIYERRGWLTSEGKEIKNKAEIIALLKA LFLPQEVAIIHCPGHQKGQDPVAVGNRQADRVARQAAMAEVLTLATEPDNTSHITAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1543	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSGGGGSGGGGSGGGGSGGGGSGGTVSLQDEHRLFDIPVTTSLPDVWLQDFPQAWAETGGLGRAKCQAPIII DLKPTAVPVSIKQYPMSLEAHMGIRQHIIKFLELGVLRPCRSPWNTPLLPVKKPGTQDYRPVQDLREINKRTVDIHPTVPNPYNLLSTLKPDYSWYTVLDLKDAFFCLPLAP QSQELFAFEWKDPERGISGQLTWTRLPQGFKNSPTLFNEALHRDLTDFRTQHPEVTLLQYVDDLLLAAPTKKACTQGTRHLLQELGEKGYRASAKKAQICQTKVTYLGYILS EGKRWLTPGRIETVARIPPPRNPREVREFLGTAGFCRLWIPGFAELAAPLYALTKPSTPFTWQTEHQLAFEALKKALLSAPALGLPDTSKPFTLFLDERQGIAKGVLTQKLG PWKRPVAYLSKKLDPVAAGWPPCLRIMAATAMLVKDSAKLTLGQPLTVITPHTLEAIVRQPPDRWITNARLTHYQALLLDTDRVQFGPPVTLNPATLLPVPENQPSPHDCRQ

	VLAETHGTREDLKDQELPDADHTWYTDGSSYLDSGTRRAGAAVVDGHNTIWAQSLPPGTSAQKAELIALTKALELSKGKKANIYTDSRYAFATAHTHGSIYERRGWLTSEGK EIKNKAEIIALLKALFLPQEVAIIHCPGHQKGQDPVAVGNRQADRVARQAAMAEVLTLATEPDNTSHITAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1550	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGSSGGGGGTVSLQDEHRLFDIPVTTSLPDVWLQDFPQAWAETGGLGRAKCQAPIIIDLKPTAVPVSIKQYPM SLEAHMGIRQHIIKFLELGVLRPCRSPWNTPLLPVKKPGTQDYRPVQDLREINKRTVDIHPTVPNPYNLLSTLKPDYSWYTVLDLKDAFFCLPLAPQSQELFAFEWKDPERG ISGQLTWTRLPQGFKNSPTLFNEALHRDLTDFRTQHPEVTLLQYVDDLLLAAPTKKACTQGTRHLLQELGEKGYRASAKKAQICQTKVTYLGYILSEGKRWLTPGRIETVAR IPPPRNPREVREFLGTAGFCRLWIPGFAELAAPLYALTKPSTPFTWQTEHQLAFEALKKALLSAPALGLPDTSKPFTLFLDERQGIAKGVLTQKLGPWKRPVAYLSKKLDPV AAGWPPCLRIMAATAMLVKDSAKLTLGQPLTVITPHTLEAIVRQPPDRWITNARLTHYQALLLDTDRVQFGPPVTLNPATLLPVPENQPSPHDCRQVLAETHGTREDLKDQE LPDADHTWYTDGSSYLDSGTRRAGAAVVDGHNTIWAQSLPPGTSAQKAELIALTKALELSKGKKANIYTDSRYAFATAHTHGSIYERRGWLTSEGKEIKNKAEIIALLKALF LPQEVAIIHCPGHQKGQDPVAVGNRQADRVARQAAMAEVLTLATEPDNTSHITAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1553	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGSSGSSGSSGSSGGTVSLQDEHRLFDIPVTTSLPDVWLQDFPQAWAETGGLGRAKCQAPIIIDLKPTAVPVS IKQYPMSLEAHMGIRQHIIKFLELGVLRPCRSPWNTPLLPVKKPGTQDYRPVQDLREINKRTVDIHPTVPNPYNLLSTLKPDYSWYTVLDLKDAFFCLPLAPQSQELFAFEW KDPERGISGQLTWTRLPQGFKNSPTLFNEALHRDLTDFRTQHPEVTLLQYVDDLLLAAPTKKACTQGTRHLLQELGEKGYRASAKKAQICQTKVTYLGYILSEGKRWLTPGR IETVARIPPPRNPREVREFLGTAGFCRLWIPGFAELAAPLYALTKPSTPFTWQTEHQLAFEALKKALLSAPALGLPDTSKPFTLFLDERQGIAKGVLTQKLGPWKRPVAYLS KKLDPVAAGWPPCLRIMAATAMLVKDSAKLTLGQPLTVITPHTLEAIVRQPPDRWITNARLTHYQALLLDTDRVQFGPPVTLNPATLLPVPENQPSPHDCRQVLAETHGTRE DLKDQELPDADHTWYTDGSSYLDSGTRRAGAAVVDGHNTIWAQSLPPGTSAQKAELIALTKALELSKGKKANIYTDSRYAFATAHTHGSIYERRGWLTSEGKEIKNKAEIIA LLKALFLPQEVAIIHCPGHQKGQDPVAVGNRQADRVARQAAMAEVLTLATEPDNTSHITAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1616	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY

	DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPGGLLGRDLLTKLKAQIQFSTEGPQVTWEDRPAMCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPMVWAE KAGMGLANQVPPVVVELKSDASPVAVRQYPMSKEAREGIRPHIQRFLDLGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPSHTWYS VLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLASFRALNPQVVMLQYVDDLLVAAPTYRDCKEGTRRLLQELSKLGYRVSAKKA QLCREEVTYLGYLLKGGKRWLTPARKATVMKIPTPTTPRQVREFLGTAGFCRLWIPGFASLAAPLYPLTRPKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFALYVD EKEGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAILNPATLL PVESDDTPIHICSEILAEETGTRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALTQALRLAEGKSINIYTDSRYAFATAHVHGA IYKQRGWLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTETTKNAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1618	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKPAPGSSGGLLGRDLLTKLKAQIQFSTEGPQVTWEDRPAMCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPM VWAEKAGMGLANQVPPVVVELKSDASPVAVRQYPMSKEAREGIRPHIQRFLDLGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPSH TWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLASFRALNPQVVMLQYVDDLLVAAPTYRDCKEGTRRLLQELSKLGYRVS AKKAQLCREEVTYLGYLLKGGKRWLTPARKATVMKIPTPTTPRQVREFLGTAGFCRLWIPGFASLAAPLYPLTRPKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFA LYVDEKEGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAILNP ATLLPVESDDTPIHICSEILAEETGTRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALTQALRLAEGKSINIYTDSRYAFATAH VHGAIYKQRGWLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTETTKNAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1619	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ

	LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPAPGGLLGRDLLTKLKAQIQFSTEGPQVTWEDRPAMCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPM VWAEKAGMGLANQVPPVVVELKSDASPVAVRQYPMSKEAREGIRPHIQRFLDLGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPSH TWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLASFRALNPQVVMLQYVDDLLVAAPTYRDCKEGTRRLLQELSKLGYRVS AKKAQLCREEVTYLGYLLKGGKRWLTPARKATVMKIPTPTTPRQVREFLGTAGFCRLWIPGFASLAAPLYPLTRPKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFA LYVDEKEGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAILNP ATLLPVESDDTPIHICSEILAEETGTRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALTQALRLAEGKSINIYTDSRYAFATAH VHGAIYKQRGWLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTETTKNAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1666	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSPAPEAAAKGGLLGRDLLTKLKAQIQFSTEGPQVTWEDRPAMCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPM VWAEKAGMGLANQVPPVVVELKSDASPVAVRQYPMSKEAREGIRPHIQRFLDLGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPSH TWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLASFRALNPQVVMLQYVDDLLVAAPTYRDCKEGTRRLLQELSKLGYRVS AKKAQLCREEVTYLGYLLKGGKRWLTPARKATVMKIPTPTTPRQVREFLGKAGFCRLFIPGFASLAAPLYPLTRPKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFA LYVDEKEGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAILNP ATLLPVESDDTPIHICSEILAEETGTRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALTQALRLAEGKSINIYTDSRYAFATAH VHGAIYKQRGWLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTETTKNAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1668	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGGGGLLGRDLLTKLKAQIQFSTEGPQVTWEDRPAMCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPMVWAEK

	AGMGLANQVPPVVVELKSDASPVAVRQYPMSKEAREGIRPHIQRFLDLGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPSHTWYSV LDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLASFRALNPQVVMLQYVDDLLVAAPTYRDCKEGTRRLLQELSKLGYRVSAKKAQ LCREEVTYLGYLLKGGKRWLTPARKATVMKIPTPTTPRQVREFLGKAGFCRLFIPGFASLAAPLYPLTRPKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFALYVDE KEGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAILNPATLLP VESDDTPIHICSEILAEETGTRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALTQALRLAEGKSINIYTDSRYAFATAHVHGAI YKQRGWLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTETTKNAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1672	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGEAAAKPAPGGLLGRDLLTKLKAQIQFSTEGPQVTWEDRPAMCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPM VWAEKAGMGLANQVPPVVVELKSDASPVAVRQYPMSKEAREGIRPHIQRFLDLGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPSH TWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLASFRALNPQVVMLQYVDDLLVAAPTYRDCKEGTRRLLQELSKLGYRVS AKKAQLCREEVTYLGYLLKGGKRWLTPARKATVMKIPTPTTPRQVREFLGKAGFCRLFIPGFASLAAPLYPLTRPKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFA LYVDEKEGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAILNP ATLLPVESDDTPIHICSEILAEETGTRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALTQALRLAEGKSINIYTDSRYAFATAH VHGAIYKQRGWLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTETTKNAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1677	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGSSGGLLGRDLLTKLKAQIQFSTEGPQVTWEDRPAMCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPM VWAEKAGMGLANQVPPVVVELKSDASPVAVRQYPMSKEAREGIRPHIQRFLDLGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPSH TWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLASFRALNPQVVMLQYVDDLLVAAPTYRDCKEGTRRLLQELSKLGYRVS AKKAQLCREEVTYLGYLLKGGKRWLTPARKATVMKIPTPTTPRQVREFLGKAGFCRLFIPGFASLAAPLYPLTRPKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFA LYVDEKEGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAILNP

	ATLLPVESDDTPIHICSEILAEETGTRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALTQALRLAEGKSINIYTDSRYAFATAH VHGAIYKQRGWLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTETTKNAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1679	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSGGLLGRDLLTKLKAQIQFSTEGPQVTWEDRPAMCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPMVWA EKAGMGLANQVPPVVVELKSDASPVAVRQYPMSKEAREGIRPHIQRFLDLGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPSHTWY SVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLASFRALNPQVVMLQYVDDLLVAAPTYRDCKEGTRRLLQELSKLGYRVSAKK AQLCREEVTYLGYLLKGGKRWLTPARKATVMKIPTPTTPRQVREFLGKAGFCRLFIPGFASLAAPLYPLTRPKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFALYV DEKEGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAILNPATL LPVESDDTPIHICSEILAEETGTRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALTQALRLAEGKSINIYTDSRYAFATAHVHG AIYKQRGWLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTETTKNAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1682	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGGSEAAAKGGLLGRDLLTKLKAQIQFSTEGPQVTWEDRPAMCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPM VWAEKAGMGLANQVPPVVVELKSDASPVAVRQYPMSKEAREGIRPHIQRFLDLGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPSH TWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLASFRALNPQVVMLQYVDDLLVAAPTYRDCKEGTRRLLQELSKLGYRVS AKKAQLCREEVTYLGYLLKGGKRWLTPARKATVMKIPTPTTPRQVREFLGKAGFCRLFIPGFASLAAPLYPLTRPKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFA LYVDEKEGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAILNP ATLLPVESDDTPIHICSEILAEETGTRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALTQALRLAEGKSINIYTDSRYAFATAH VHGAIYKQRGWLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTETTKNAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1686	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY

	DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGSGGSGGLLGRDLLTKLKAQIQFSTEGPQVTWEDRPAMCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPMVW AEKAGMGLANQVPPVVVELKSDASPVAVRQYPMSKEAREGIRPHIQRFLDLGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPSHTW YSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLASFRALNPQVVMLQYVDDLLVAAPTYRDCKEGTRRLLQELSKLGYRVSAK KAQLCREEVTYLGYLLKGGKRWLTPARKATVMKIPTPTTPRQVREFLGKAGFCRLFIPGFASLAAPLYPLTRPKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFALY VDEKEGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAILNPAT LLPVESDDTPIHICSEILAEETGTRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALTQALRLAEGKSINIYTDSRYAFATAHVH GAIYKQRGWLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTETTKNAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1690	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGSSGGSGGLLGRDLLTKLKAQIQFSTEGPQVTWEDRPAMCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPM VWAEKAGMGLANQVPPVVVELKSDASPVAVRQYPMSKEAREGIRPHIQRFLDLGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPSH TWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLASFRALNPQVVMLQYVDDLLVAAPTYRDCKEGTRRLLQELSKLGYRVS AKKAQLCREEVTYLGYLLKGGKRWLTPARKATVMKIPTPTTPRQVREFLGKAGFCRLFIPGFASLAAPLYPLTRPKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFA LYVDEKEGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAILNP ATLLPVESDDTPIHICSEILAEETGTRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALTQALRLAEGKSINIYTDSRYAFATAH VHGAIYKQRGWLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTETTKNAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1691	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ

	LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGGGSSGGLLGRDLLTKLKAQIQFSTEGPQVTWEDRPAMCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPMVW AEKAGMGLANQVPPVVVELKSDASPVAVRQYPMSKEAREGIRPHIQRFLDLGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPSHTW YSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLASFRALNPQVVMLQYVDDLLVAAPTYRDCKEGTRRLLQELSKLGYRVSAK KAQLCREEVTYLGYLLKGGKRWLTPARKATVMKIPTPTTPRQVREFLGKAGFCRLFIPGFASLAAPLYPLTRPKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFALY VDEKEGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAILNPAT LLPVESDDTPIHICSEILAEETGTRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALTQALRLAEGKSINIYTDSRYAFATAHVH GAIYKQRGWLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTETTKNAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1695	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGSSGGLLGRDLLTKLKAQIQFSTEGPQVTWEDRPAMCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPMVWAEK AGMGLANQVPPVVVELKSDASPVAVRQYPMSKEAREGIRPHIQRFLDLGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPSHTWYSV LDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLASFRALNPQVVMLQYVDDLLVAAPTYRDCKEGTRRLLQELSKLGYRVSAKKAQ LCREEVTYLGYLLKGGKRWLTPARKATVMKIPTPTTPRQVREFLGKAGFCRLFIPGFASLAAPLYPLTRPKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFALYVDE KEGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAILNPATLLP VESDDTPIHICSEILAEETGTRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALTQALRLAEGKSINIYTDSRYAFATAHVHGAI YKQRGWLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTETTKNAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1698	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGGGGLLGRDLLTKLKAQIQFSTEGPQVTWEDRPAMCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPMVWAEK

	AGMGLANQVPPVVVELKSDASPVAVRQYPMSKEAREGIRPHIQRFLDLGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPSHTWYSV LDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLASFRALNPQVVMLQYVDDLLVAAPTYRDCKEGTRRLLQELSKLGYRVSAKKAQ LCREEVTYLGYLLKGGKRWLTPARKATVMKIPTPTTPRQVREFLGKAGFCRLFIPGFASLAAPLYPLTRPKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFALYVDE KEGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAILNPATLLP VESDDTPIHICSEILAEETGTRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALTQALRLAEGKSINIYTDSRYAFATAHVHGAI YKQRGWLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTETTKNAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1721	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSPAPEAAAKGGLLGRDLLTKLKAQIQFSTEGPQVTWEDRPAMCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPM VWAEKAGMGLANQVPPVVVELKSDASPVAVRQYPMSKEAREGIRPHIQRFLDLGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPSH TWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLASFRALNPQVVMLQYVDDLLVAAPTYRDCKEGTRRLLQELSKLGYRVS AKKAQLCREEVTYLGYLLKGGKRWLTPARKATVMKIPTPTTPRQVREFLGKAGFCRLFIPGFASLAAPLYPLTRPKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFA LYVDEKEGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAILNP ATLLPVESDDTPIHICSEILAEETGTRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALTQALRLAEGKSINIYTDSRYAFATAH VHGAIYKQRGWLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTETTKNAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1754	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGSEAAAKGGTLGDQGSRGSDPLPEPRVTLTVEGIPTEFLVNTGAEHSVLTKPMGKMGSKRTVVAGATGSKV YPWTTKRLLKIGQKQVTHSFLVIPECPAPLLGRDLLTKLKAQIQFSTEGPQVTWEDRPAMCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPMVWAEKAGMGLANQVPPVVVEL KSDASPVAVRQYPMSKEAREGIRPHIQRFLDLGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNS QPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLASFRALNPQVVMLQYVDDLLVAAPTYRDCKEGTRRLLQELSKLGYRVSAKKAQLCREEVTYLGYLLKGG KRWLTPARKATVMKIPTPTTPRQVREFLGTAGFCRLWIPGFASLAAPLYPLTRPKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFALYVDEKEGVARGVLTQTLGPW RRPVAYLSKKLDPVASGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAILNPATLLPVESDDTPIHICSEILA

	EETGTRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGKDIKN KEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTETTKNAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1759	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGGEAAAKGGTLGDQGSRGSDPLPEPRVTLTVEGIPTEFLVNTGAEHSVLTKPMGKMGSKRTVVAGATGSKV YPWTTKRLLKIGQKQVTHSFLVIPECPAPLLGRDLLTKLKAQIQFSTEGPQVTWEDRPAMCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPMVWAEKAGMGLANQVPPVVVEL KSDASPVAVRQYPMSKEAREGIRPHIQRFLDLGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNS QPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLASFRALNPQVVMLQYVDDLLVAAPTYRDCKEGTRRLLQELSKLGYRVSAKKAQLCREEVTYLGYLLKGG KRWLTPARKATVMKIPTPTTPRQVREFLGTAGFCRLWIPGFASLAAPLYPLTRPKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFALYVDEKEGVARGVLTQTLGPW RRPVAYLSKKLDPVASGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAILNPATLLPVESDDTPIHICSEILA EETGTRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGKDIKN KEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTETTKNAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1769	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSEAAAKGSSGGTLGDQGSRGSDPLPEPRVTLTVEGIPTEFLVNTGAEHSVLTKPMGKMGSKRTVVAGATGSKV YPWTTKRLLKIGQKQVTHSFLVIPECPAPLLGRDLLTKLKAQIQFSTEGPQVTWEDRPAMCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPMVWAEKAGMGLANQVPPVVVEL KSDASPVAVRQYPMSKEAREGIRPHIQRFLDLGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNS QPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLASFRALNPQVVMLQYVDDLLVAAPTYRDCKEGTRRLLQELSKLGYRVSAKKAQLCREEVTYLGYLLKGG KRWLTPARKATVMKIPTPTTPRQVREFLGKAGFCRLFIPGFASLAAPLYPLTRPKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFALYVDEKEGVARGVLTQTLGPW RRPVAYLSKKLDPVASGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAILNPATLLPVESDDTPIHICSEILA EETGTRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGKDIKN KEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTETTKNAGKRTADGSEFEKRTADGSEFESPKKKAKVE

1770	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGPAPGGTLGDQGSRGSDPLPEPRVTLTVEGIPTEFLVNTGAEHSVLTKPMGKMGSKRTVVAGATGSKV YPWTTKRLLKIGQKQVTHSFLVIPECPAPLLGRDLLTKLKAQIQFSTEGPQVTWEDRPAMCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPMVWAEKAGMGLANQVPPVVVEL KSDASPVAVRQYPMSKEAREGIRPHIQRFLDLGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNS QPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLASFRALNPQVVMLQYVDDLLVAAPTYRDCKEGTRRLLQELSKLGYRVSAKKAQLCREEVTYLGYLLKGG KRWLTPARKATVMKIPTPTTPRQVREFLGKAGFCRLFIPGFASLAAPLYPLTRPKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFALYVDEKEGVARGVLTQTLGPW RRPVAYLSKKLDPVASGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAILNPATLLPVESDDTPIHICSEILA EETGTRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGKDIKN KEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTETTKNAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1772	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSSGGTLGDQGSRGSDPLPEPRVTLTVEGIPTEFLVNTGAEHSVLTKPMGKMGSKRTVVAGATGSKVYPWTT KRLLKIGQKQVTHSFLVIPECPAPLLGRDLLTKLKAQIQFSTEGPQVTWEDRPAMCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPMVWAEKAGMGLANQVPPVVVELKSDAS PVAVRQYPMSKEAREGIRPHIQRFLDLGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFA FEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLASFRALNPQVVMLQYVDDLLVAAPTYRDCKEGTRRLLQELSKLGYRVSAKKAQLCREEVTYLGYLLKGGKRWLT PARKATVMKIPTPTTPRQVREFLGKAGFCRLFIPGFASLAAPLYPLTRPKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFALYVDEKEGVARGVLTQTLGPWRRPVA YLSKKLDPVASGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAILNPATLLPVESDDTPIHICSEILAEETGT RPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGKDIKNKEEIL ALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTETTKNAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1773	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY

	DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKGGTLGDQGSRGSDPLPEPRVTLTVEGIPTEFLVNTGAEHSVLTKPMGKMGSKRTVVAGATGSKVY PWTTKRLLKIGQKQVTHSFLVIPECPAPLLGRDLLTKLKAQIQFSTEGPQVTWEDRPAMCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPMVWAEKAGMGLANQVPPVVVELK SDASPVAVRQYPMSKEAREGIRPHIQRFLDLGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQ PLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLASFRALNPQVVMLQYVDDLLVAAPTYRDCKEGTRRLLQELSKLGYRVSAKKAQLCREEVTYLGYLLKGGK RWLTPARKATVMKIPTPTTPRQVREFLGKAGFCRLFIPGFASLAAPLYPLTRPKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFALYVDEKEGVARGVLTQTLGPWR RPVAYLSKKLDPVASGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAILNPATLLPVESDDTPIHICSEILAE ETGTRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGKDIKNK EEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTETTKNAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1856	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGGEAAAKGGTLNLEDEYRLYETSAEPEVSPGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEAKLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHRWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLLTLGNLGYRASAKKAQLCQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLRKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLT DQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLK ALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1857	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG

	QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGPAPGSSGGTLNLEDEYRLYETSAEPEVSPGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQY PMSQEAKLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHRWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPG MGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLLTLGNLGYRASAKKAQLCQKQVKYLGYLLKEGQRWLTEARKETV MGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLRKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQ PIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKAL FLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1860	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGSEAAAKGGTLNLEDEYRLYETSAEPEVSPGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTP VSIKQYPMSQEAKLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHRWYTVLDLKDAFFCLRLHPTSQPLFAF EWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLLTLGNLGYRASAKKAQLCQKQVKYLGYLLKEGQRWLTE ARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAY LSKKLDPVAAGWPPCLRMVAAIAVLRKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTR PDLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEIL ALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1861	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR

	KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSEAAAKGGGGGTLNLEDEYRLYETSAEPEVSPGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEAKLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHRWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLLTLGNLGYRASAKKAQLCQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLRKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLT DQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLK ALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1863	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPAPAPGGTLNLEDEYRLYETSAEPEVSPGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVS IKQYPMSQEAKLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHRWYTVLDLKDAFFCLRLHPTSQPLFAFEW RDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLLTLGNLGYRASAKKAQLCQKQVKYLGYLLKEGQRWLTEAR KETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLS KKLDPVAAGWPPCLRMVAAIAVLRKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPD LTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILAL LKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1864	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPEAAAKGGGGGTLNLEDEYRLYETSAEPEVSPGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEAKLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHRWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLLTLGNLGYRASAKKAQLCQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLRKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLT

	DQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLK ALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1865	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAAKGGTLNLEDEYRLYETSAEPEVSPGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLK ATSTPVSIKQYPMSQEAKLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHRWYTVLDLKDAFFCLRLHPTSQ PLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLLTLGNLGYRASAKKAQLCQKQVKYLGYLLKEGQ RWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWR RPVAYLSKKLDPVAAGWPPCLRMVAAIAVLRKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAE THGTRPDLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKN KSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1867	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGPAPGGTLNLEDEYRLYETSAEPEVSPGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEAKLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHRWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLLTLGNLGYRASAKKAQLCQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLRKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLT DQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLK ALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1868	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY

	DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGTLNLEDEYRLYETSAEPEVSPGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQ EAKLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHRWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGIS GQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLLTLGNLGYRASAKKAQLCQKQVKYLGYLLKEGQRWLTEARKETVMGQP TPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAA GWPPCLRMVAAIAVLRKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQPIPD ADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALFLPK RLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1870	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSAGSAAGSGEFGGTLNLEDEYRLYETSAEPEVSPGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSI KQYPMSQEAKLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHRWYTVLDLKDAFFCLRLHPTSQPLFAFEWR DPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLLTLGNLGYRASAKKAQLCQKQVKYLGYLLKEGQRWLTEARK ETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSK KLDPVAAGWPPCLRMVAAIAVLRKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDL TDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALL KALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1871	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ

	LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKPAPGGSGGTLNLEDEYRLYETSAEPEVSPGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEAKLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHRWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLLTLGNLGYRASAKKAQLCQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLRKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLT DQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLK ALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1874	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSPAPGGGGGTLNLEDEYRLYETSAEPEVSPGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQY PMSQEAKLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHRWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPG MGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLLTLGNLGYRASAKKAQLCQKQVKYLGYLLKEGQRWLTEARKETV MGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLRKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQ PIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKAL FLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1875	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGGEAAAKGGTLNLEDEYRLYETSAEPEVSPGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK

	QYPMSQEAKLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHRWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLLTLGNLGYRASAKKAQLCQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLRKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLT DQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLK ALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1876	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSGGGGSGGGGSGGGGSGGTLNLEDEYRLYETSAEPEVSPGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLK ATSTPVSIKQYPMSQEAKLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHRWYTVLDLKDAFFCLRLHPTSQ PLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLLTLGNLGYRASAKKAQLCQKQVKYLGYLLKEGQ RWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWR RPVAYLSKKLDPVAAGWPPCLRMVAAIAVLRKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAE THGTRPDLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKN KSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1877	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGSSGSSGSSGGTLNLEDEYRLYETSAEPEVSPGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSI KQYPMSQEAKLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHRWYTVLDLKDAFFCLRLHPTSQPLFAFEWR DPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLLTLGNLGYRASAKKAQLCQKQVKYLGYLLKEGQRWLTEARK ETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSK KLDPVAAGWPPCLRMVAAIAVLRKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDL

	TDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALL KALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1881	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPGGTLNLEDEYRLYETSAEPEVSPGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQY PMSQEAKLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHRWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPG MGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLLTLGNLGYRASAKKAQLCQKQVKYLGYLLKEGQRWLTEARKETV MGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLRKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQ PIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKAL FLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1883	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGSSGGSGGTLNLEDEYRLYETSAEPEVSPGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQY PMSQEAKLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHRWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPG MGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLLTLGNLGYRASAKKAQLCQKQVKYLGYLLKEGQRWLTEARKETV MGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLRKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQ PIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKAL FLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1889	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY

	DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGSSEAAAKGGTLNLEDEYRLYETSAEPEVSPGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEAKLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHRWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLLTLGNLGYRASAKKAQLCQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLRKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLT DQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLK ALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1899	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSPAPGGGGGTLNLEDEYRLYETSAEPEVSPGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQY PMSQEAKLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHRWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPG MGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLLTLGNLGYRASAKKAQLCQKQVKYLGYLLKEGQRWLTEARKETV MGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLRKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQ PIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKAL FLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1937	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ

	LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSEAAAKGGTVSLQDEHRLFDIPVTTSLPDVWLQDFPQAWAETGGLGRAKCQAPIIIDLKPTAVPVSIKQY PMSLEAHMGIRQHIIKFLELGVLRPCRSPWNTPLLPVKKPGTQDYRPVQDLREINKRTVDIHPTVPNPYNLLSTLKPDYSWYTVLDLKDAFFCLPLAPQSQELFAFEWKDPE RGISGQLTWTRLPQGFKNSPTLFNEALHRDLTDFRTQHPEVTLLQYVDDLLLAAPTKKACTQGTRHLLQELGEKGYRASAKKAQICQTKVTYLGYILSEGKRWLTPGRIETV ARIPPPRNPREVREFLGKAGFCRLFIPGFAELAAPLYALTKPSTPFTWQTEHQLAFEALKKALLSAPALGLPDTSKPFTLFLDERQGIAKGVLTQKLGPWKRPVAYLSKKLD PVAAGWPPCLRIMAATAMLVKDSAKLTLGQPLTVITPHTLEAIVRQPPDRWITNARLTHYQALLLDTDRVQFGPPVTLNPATLLPVPENQPSPHDCRQVLAETHGTREDLKD QELPDADHTWYTDGSSYLDSGTRRAGAAVVDGHNTIWAQSLPPGTSAQKAELIALTKALELSKGKKANIYTDSRYAFATAHTHGSIYERRGWLTSEGKEIKNKAEIIALLKA LFLPQEVAIIHCPGHQKGQDPVAVGNRQADRVARQAAMAEVLTLATEPDNTSHITAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1938	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPEAAAKGGTVSLQDEHRLFDIPVTTSLPDVWLQDFPQAWAETGGLGRAKCQAPIIIDLKPTAVPVSIKQY PMSLEAHMGIRQHIIKFLELGVLRPCRSPWNTPLLPVKKPGTQDYRPVQDLREINKRTVDIHPTVPNPYNLLSTLKPDYSWYTVLDLKDAFFCLPLAPQSQELFAFEWKDPE RGISGQLTWTRLPQGFKNSPTLFNEALHRDLTDFRTQHPEVTLLQYVDDLLLAAPTKKACTQGTRHLLQELGEKGYRASAKKAQICQTKVTYLGYILSEGKRWLTPGRIETV ARIPPPRNPREVREFLGKAGFCRLFIPGFAELAAPLYALTKPSTPFTWQTEHQLAFEALKKALLSAPALGLPDTSKPFTLFLDERQGIAKGVLTQKLGPWKRPVAYLSKKLD PVAAGWPPCLRIMAATAMLVKDSAKLTLGQPLTVITPHTLEAIVRQPPDRWITNARLTHYQALLLDTDRVQFGPPVTLNPATLLPVPENQPSPHDCRQVLAETHGTREDLKD QELPDADHTWYTDGSSYLDSGTRRAGAAVVDGHNTIWAQSLPPGTSAQKAELIALTKALELSKGKKANIYTDSRYAFATAHTHGSIYERRGWLTSEGKEIKNKAEIIALLKA LFLPQEVAIIHCPGHQKGQDPVAVGNRQADRVARQAAMAEVLTLATEPDNTSHITAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1939	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGSEAAAKGGTVSLQDEHRLFDIPVTTSLPDVWLQDFPQAWAETGGLGRAKCQAPIIIDLKPTAVPVSIKQY

	PMSLEAHMGIRQHIIKFLELGVLRPCRSPWNTPLLPVKKPGTQDYRPVQDLREINKRTVDIHPTVPNPYNLLSTLKPDYSWYTVLDLKDAFFCLPLAPQSQELFAFEWKDPE RGISGQLTWTRLPQGFKNSPTLFNEALHRDLTDFRTQHPEVTLLQYVDDLLLAAPTKKACTQGTRHLLQELGEKGYRASAKKAQICQTKVTYLGYILSEGKRWLTPGRIETV ARIPPPRNPREVREFLGKAGFCRLFIPGFAELAAPLYALTKPSTPFTWQTEHQLAFEALKKALLSAPALGLPDTSKPFTLFLDERQGIAKGVLTQKLGPWKRPVAYLSKKLD PVAAGWPPCLRIMAATAMLVKDSAKLTLGQPLTVITPHTLEAIVRQPPDRWITNARLTHYQALLLDTDRVQFGPPVTLNPATLLPVPENQPSPHDCRQVLAETHGTREDLKD QELPDADHTWYTDGSSYLDSGTRRAGAAVVDGHNTIWAQSLPPGTSAQKAELIALTKALELSKGKKANIYTDSRYAFATAHTHGSIYERRGWLTSEGKEIKNKAEIIALLKA LFLPQEVAIIHCPGHQKGQDPVAVGNRQADRVARQAAMAEVLTLATEPDNTSHITAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1940	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGGGGTVSLQDEHRLFDIPVTTSLPDVWLQDFPQAWAETGGLGRAKCQAPIIIDLKPTAVPVSIKQYPMSLE AHMGIRQHIIKFLELGVLRPCRSPWNTPLLPVKKPGTQDYRPVQDLREINKRTVDIHPTVPNPYNLLSTLKPDYSWYTVLDLKDAFFCLPLAPQSQELFAFEWKDPERGISG QLTWTRLPQGFKNSPTLFNEALHRDLTDFRTQHPEVTLLQYVDDLLLAAPTKKACTQGTRHLLQELGEKGYRASAKKAQICQTKVTYLGYILSEGKRWLTPGRIETVARIPP PRNPREVREFLGKAGFCRLFIPGFAELAAPLYALTKPSTPFTWQTEHQLAFEALKKALLSAPALGLPDTSKPFTLFLDERQGIAKGVLTQKLGPWKRPVAYLSKKLDPVAAG WPPCLRIMAATAMLVKDSAKLTLGQPLTVITPHTLEAIVRQPPDRWITNARLTHYQALLLDTDRVQFGPPVTLNPATLLPVPENQPSPHDCRQVLAETHGTREDLKDQELPD ADHTWYTDGSSYLDSGTRRAGAAVVDGHNTIWAQSLPPGTSAQKAELIALTKALELSKGKKANIYTDSRYAFATAHTHGSIYERRGWLTSEGKEIKNKAEIIALLKALFLPQ EVAIIHCPGHQKGQDPVAVGNRQADRVARQAAMAEVLTLATEPDNTSHITAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1942	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGGPAPGGTVSLQDEHRLFDIPVTTSLPDVWLQDFPQAWAETGGLGRAKCQAPIIIDLKPTAVPVSIKQYPM SLEAHMGIRQHIIKFLELGVLRPCRSPWNTPLLPVKKPGTQDYRPVQDLREINKRTVDIHPTVPNPYNLLSTLKPDYSWYTVLDLKDAFFCLPLAPQSQELFAFEWKDPERG ISGQLTWTRLPQGFKNSPTLFNEALHRDLTDFRTQHPEVTLLQYVDDLLLAAPTKKACTQGTRHLLQELGEKGYRASAKKAQICQTKVTYLGYILSEGKRWLTPGRIETVAR IPPPRNPREVREFLGKAGFCRLFIPGFAELAAPLYALTKPSTPFTWQTEHQLAFEALKKALLSAPALGLPDTSKPFTLFLDERQGIAKGVLTQKLGPWKRPVAYLSKKLDPV AAGWPPCLRIMAATAMLVKDSAKLTLGQPLTVITPHTLEAIVRQPPDRWITNARLTHYQALLLDTDRVQFGPPVTLNPATLLPVPENQPSPHDCRQVLAETHGTREDLKDQE

	LPDADHTWYTDGSSYLDSGTRRAGAAVVDGHNTIWAQSLPPGTSAQKAELIALTKALELSKGKKANIYTDSRYAFATAHTHGSIYERRGWLTSEGKEIKNKAEIIALLKALF LPQEVAIIHCPGHQKGQDPVAVGNRQADRVARQAAMAEVLTLATEPDNTSHITAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1943	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGEAAAKGGSGGTVSLQDEHRLFDIPVTTSLPDVWLQDFPQAWAETGGLGRAKCQAPIIIDLKPTAVPVSIKQY PMSLEAHMGIRQHIIKFLELGVLRPCRSPWNTPLLPVKKPGTQDYRPVQDLREINKRTVDIHPTVPNPYNLLSTLKPDYSWYTVLDLKDAFFCLPLAPQSQELFAFEWKDPE RGISGQLTWTRLPQGFKNSPTLFNEALHRDLTDFRTQHPEVTLLQYVDDLLLAAPTKKACTQGTRHLLQELGEKGYRASAKKAQICQTKVTYLGYILSEGKRWLTPGRIETV ARIPPPRNPREVREFLGKAGFCRLFIPGFAELAAPLYALTKPSTPFTWQTEHQLAFEALKKALLSAPALGLPDTSKPFTLFLDERQGIAKGVLTQKLGPWKRPVAYLSKKLD PVAAGWPPCLRIMAATAMLVKDSAKLTLGQPLTVITPHTLEAIVRQPPDRWITNARLTHYQALLLDTDRVQFGPPVTLNPATLLPVPENQPSPHDCRQVLAETHGTREDLKD QELPDADHTWYTDGSSYLDSGTRRAGAAVVDGHNTIWAQSLPPGTSAQKAELIALTKALELSKGKKANIYTDSRYAFATAHTHGSIYERRGWLTSEGKEIKNKAEIIALLKA LFLPQEVAIIHCPGHQKGQDPVAVGNRQADRVARQAAMAEVLTLATEPDNTSHITAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1945	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPGGTVSLQDEHRLFDIPVTTSLPDVWLQDFPQAWAETGGLGRAKCQAPIIIDLKPTAVPVSIKQYPMSLEA HMGIRQHIIKFLELGVLRPCRSPWNTPLLPVKKPGTQDYRPVQDLREINKRTVDIHPTVPNPYNLLSTLKPDYSWYTVLDLKDAFFCLPLAPQSQELFAFEWKDPERGISGQ LTWTRLPQGFKNSPTLFNEALHRDLTDFRTQHPEVTLLQYVDDLLLAAPTKKACTQGTRHLLQELGEKGYRASAKKAQICQTKVTYLGYILSEGKRWLTPGRIETVARIPPP RNPREVREFLGKAGFCRLFIPGFAELAAPLYALTKPSTPFTWQTEHQLAFEALKKALLSAPALGLPDTSKPFTLFLDERQGIAKGVLTQKLGPWKRPVAYLSKKLDPVAAGW PPCLRIMAATAMLVKDSAKLTLGQPLTVITPHTLEAIVRQPPDRWITNARLTHYQALLLDTDRVQFGPPVTLNPATLLPVPENQPSPHDCRQVLAETHGTREDLKDQELPDA DHTWYTDGSSYLDSGTRRAGAAVVDGHNTIWAQSLPPGTSAQKAELIALTKALELSKGKKANIYTDSRYAFATAHTHGSIYERRGWLTSEGKEIKNKAEIIALLKALFLPQE VAIIHCPGHQKGQDPVAVGNRQADRVARQAAMAEVLTLATEPDNTSHITAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1949	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY

	DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSEAAAKGGGGSGGTVSLQDEHRLFDIPVTTSLPDVWLQDFPQAWAETGGLGRAKCQAPIIIDLKPTAVPVS IKQYPMSLEAHMGIRQHIIKFLELGVLRPCRSPWNTPLLPVKKPGTQDYRPVQDLREINKRTVDIHPTVPNPYNLLSTLKPDYSWYTVLDLKDAFFCLPLAPQSQELFAFEW KDPERGISGQLTWTRLPQGFKNSPTLFNEALHRDLTDFRTQHPEVTLLQYVDDLLLAAPTKKACTQGTRHLLQELGEKGYRASAKKAQICQTKVTYLGYILSEGKRWLTPGR IETVARIPPPRNPREVREFLGKAGFCRLFIPGFAELAAPLYALTKPSTPFTWQTEHQLAFEALKKALLSAPALGLPDTSKPFTLFLDERQGIAKGVLTQKLGPWKRPVAYLS KKLDPVAAGWPPCLRIMAATAMLVKDSAKLTLGQPLTVITPHTLEAIVRQPPDRWITNARLTHYQALLLDTDRVQFGPPVTLNPATLLPVPENQPSPHDCRQVLAETHGTRE DLKDQELPDADHTWYTDGSSYLDSGTRRAGAAVVDGHNTIWAQSLPPGTSAQKAELIALTKALELSKGKKANIYTDSRYAFATAHTHGSIYERRGWLTSEGKEIKNKAEIIA LLKALFLPQEVAIIHCPGHQKGQDPVAVGNRQADRVARQAAMAEVLTLATEPDNTSHITAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1951	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGSSEAAAKGGTVSLQDEHRLFDIPVTTSLPDVWLQDFPQAWAETGGLGRAKCQAPIIIDLKPTAVPVSIKQY PMSLEAHMGIRQHIIKFLELGVLRPCRSPWNTPLLPVKKPGTQDYRPVQDLREINKRTVDIHPTVPNPYNLLSTLKPDYSWYTVLDLKDAFFCLPLAPQSQELFAFEWKDPE RGISGQLTWTRLPQGFKNSPTLFNEALHRDLTDFRTQHPEVTLLQYVDDLLLAAPTKKACTQGTRHLLQELGEKGYRASAKKAQICQTKVTYLGYILSEGKRWLTPGRIETV ARIPPPRNPREVREFLGKAGFCRLFIPGFAELAAPLYALTKPSTPFTWQTEHQLAFEALKKALLSAPALGLPDTSKPFTLFLDERQGIAKGVLTQKLGPWKRPVAYLSKKLD PVAAGWPPCLRIMAATAMLVKDSAKLTLGQPLTVITPHTLEAIVRQPPDRWITNARLTHYQALLLDTDRVQFGPPVTLNPATLLPVPENQPSPHDCRQVLAETHGTREDLKD QELPDADHTWYTDGSSYLDSGTRRAGAAVVDGHNTIWAQSLPPGTSAQKAELIALTKALELSKGKKANIYTDSRYAFATAHTHGSIYERRGWLTSEGKEIKNKAEIIALLKA LFLPQEVAIIHCPGHQKGQDPVAVGNRQADRVARQAAMAEVLTLATEPDNTSHITAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1953	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ

	LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPGGTVSLQDEHRLFDIPVTTSLPDVWLQDFPQAWAETGGLGRAKCQAPIIIDLKPTAVPVSIKQYPMSL EAHMGIRQHIIKFLELGVLRPCRSPWNTPLLPVKKPGTQDYRPVQDLREINKRTVDIHPTVPNPYNLLSTLKPDYSWYTVLDLKDAFFCLPLAPQSQELFAFEWKDPERGIS GQLTWTRLPQGFKNSPTLFNEALHRDLTDFRTQHPEVTLLQYVDDLLLAAPTKKACTQGTRHLLQELGEKGYRASAKKAQICQTKVTYLGYILSEGKRWLTPGRIETVARIP PPRNPREVREFLGKAGFCRLFIPGFAELAAPLYALTKPSTPFTWQTEHQLAFEALKKALLSAPALGLPDTSKPFTLFLDERQGIAKGVLTQKLGPWKRPVAYLSKKLDPVAA GWPPCLRIMAATAMLVKDSAKLTLGQPLTVITPHTLEAIVRQPPDRWITNARLTHYQALLLDTDRVQFGPPVTLNPATLLPVPENQPSPHDCRQVLAETHGTREDLKDQELP DADHTWYTDGSSYLDSGTRRAGAAVVDGHNTIWAQSLPPGTSAQKAELIALTKALELSKGKKANIYTDSRYAFATAHTHGSIYERRGWLTSEGKEIKNKAEIIALLKALFLP QEVAIIHCPGHQKGQDPVAVGNRQADRVARQAAMAEVLTLATEPDNTSHITAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1961	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGSSGGSGGTVSLQDEHRLFDIPVTTSLPDVWLQDFPQAWAETGGLGRAKCQAPIIIDLKPTAVPVSIKQYPM SLEAHMGIRQHIIKFLELGVLRPCRSPWNTPLLPVKKPGTQDYRPVQDLREINKRTVDIHPTVPNPYNLLSTLKPDYSWYTVLDLKDAFFCLPLAPQSQELFAFEWKDPERG ISGQLTWTRLPQGFKNSPTLFNEALHRDLTDFRTQHPEVTLLQYVDDLLLAAPTKKACTQGTRHLLQELGEKGYRASAKKAQICQTKVTYLGYILSEGKRWLTPGRIETVAR IPPPRNPREVREFLGKAGFCRLFIPGFAELAAPLYALTKPSTPFTWQTEHQLAFEALKKALLSAPALGLPDTSKPFTLFLDERQGIAKGVLTQKLGPWKRPVAYLSKKLDPV AAGWPPCLRIMAATAMLVKDSAKLTLGQPLTVITPHTLEAIVRQPPDRWITNARLTHYQALLLDTDRVQFGPPVTLNPATLLPVPENQPSPHDCRQVLAETHGTREDLKDQE LPDADHTWYTDGSSYLDSGTRRAGAAVVDGHNTIWAQSLPPGTSAQKAELIALTKALELSKGKKANIYTDSRYAFATAHTHGSIYERRGWLTSEGKEIKNKAEIIALLKALF LPQEVAIIHCPGHQKGQDPVAVGNRQADRVARQAAMAEVLTLATEPDNTSHITAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1967	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKAGGTVSLQDEHRLFDIPVTTSLPDVWLQDF

	PQAWAETGGLGRAKCQAPIIIDLKPTAVPVSIKQYPMSLEAHMGIRQHIIKFLELGVLRPCRSPWNTPLLPVKKPGTQDYRPVQDLREINKRTVDIHPTVPNPYNLLSTLKP DYSWYTVLDLKDAFFCLPLAPQSQELFAFEWKDPERGISGQLTWTRLPQGFKNSPTLFNEALHRDLTDFRTQHPEVTLLQYVDDLLLAAPTKKACTQGTRHLLQELGEKGYR ASAKKAQICQTKVTYLGYILSEGKRWLTPGRIETVARIPPPRNPREVREFLGKAGFCRLFIPGFAELAAPLYALTKPSTPFTWQTEHQLAFEALKKALLSAPALGLPDTSKP FTLFLDERQGIAKGVLTQKLGPWKRPVAYLSKKLDPVAAGWPPCLRIMAATAMLVKDSAKLTLGQPLTVITPHTLEAIVRQPPDRWITNARLTHYQALLLDTDRVQFGPPVT LNPATLLPVPENQPSPHDCRQVLAETHGTREDLKDQELPDADHTWYTDGSSYLDSGTRRAGAAVVDGHNTIWAQSLPPGTSAQKAELIALTKALELSKGKKANIYTDSRYAF ATAHTHGSIYERRGWLTSEGKEIKNKAEIIALLKALFLPQEVAIIHCPGHQKGQDPVAVGNRQADRVARQAAMAEVLTLATEPDNTSHITAGKRTADGSEFEKRTADGSEFE SPKKKAKVE
1968	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGSSEAAAKGGTVSLQDEHRLFDIPVTTSLPDVWLQDFPQAWAETGGLGRAKCQAPIIIDLKPTAVPVSIKQY PMSLEAHMGIRQHIIKFLELGVLRPCRSPWNTPLLPVKKPGTQDYRPVQDLREINKRTVDIHPTVPNPYNLLSTLKPDYSWYTVLDLKDAFFCLPLAPQSQELFAFEWKDPE RGISGQLTWTRLPQGFKNSPTLFNEALHRDLTDFRTQHPEVTLLQYVDDLLLAAPTKKACTQGTRHLLQELGEKGYRASAKKAQICQTKVTYLGYILSEGKRWLTPGRIETV ARIPPPRNPREVREFLGKAGFCRLFIPGFAELAAPLYALTKPSTPFTWQTEHQLAFEALKKALLSAPALGLPDTSKPFTLFLDERQGIAKGVLTQKLGPWKRPVAYLSKKLD PVAAGWPPCLRIMAATAMLVKDSAKLTLGQPLTVITPHTLEAIVRQPPDRWITNARLTHYQALLLDTDRVQFGPPVTLNPATLLPVPENQPSPHDCRQVLAETHGTREDLKD QELPDADHTWYTDGSSYLDSGTRRAGAAVVDGHNTIWAQSLPPGTSAQKAELIALTKALELSKGKKANIYTDSRYAFATAHTHGSIYERRGWLTSEGKEIKNKAEIIALLKA LFLPQEVAIIHCPGHQKGQDPVAVGNRQADRVARQAAMAEVLTLATEPDNTSHITAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1970	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGSSGGTVSLQDEHRLFDIPVTTSLPDVWLQDFPQAWAETGGLGRAKCQAPIIIDLKPTAVPVSIKQYPMSLE AHMGIRQHIIKFLELGVLRPCRSPWNTPLLPVKKPGTQDYRPVQDLREINKRTVDIHPTVPNPYNLLSTLKPDYSWYTVLDLKDAFFCLPLAPQSQELFAFEWKDPERGISG QLTWTRLPQGFKNSPTLFNEALHRDLTDFRTQHPEVTLLQYVDDLLLAAPTKKACTQGTRHLLQELGEKGYRASAKKAQICQTKVTYLGYILSEGKRWLTPGRIETVARIPP PRNPREVREFLGKAGFCRLFIPGFAELAAPLYALTKPSTPFTWQTEHQLAFEALKKALLSAPALGLPDTSKPFTLFLDERQGIAKGVLTQKLGPWKRPVAYLSKKLDPVAAG WPPCLRIMAATAMLVKDSAKLTLGQPLTVITPHTLEAIVRQPPDRWITNARLTHYQALLLDTDRVQFGPPVTLNPATLLPVPENQPSPHDCRQVLAETHGTREDLKDQELPD

	ADHTWYTDGSSYLDSGTRRAGAAVVDGHNTIWAQSLPPGTSAQKAELIALTKALELSKGKKANIYTDSRYAFATAHTHGSIYERRGWLTSEGKEIKNKAEIIALLKALFLPQ EVAIIHCPGHQKGQDPVAVGNRQADRVARQAAMAEVLTLATEPDNTSHITAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1976	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSPAPGGGGGTVSLQDEHRLFDIPVTTSLPDVWLQDFPQAWAETGGLGRAKCQAPIIIDLKPTAVPVSIKQYPM SLEAHMGIRQHIIKFLELGVLRPCRSPWNTPLLPVKKPGTQDYRPVQDLREINKRTVDIHPTVPNPYNLLSTLKPDYSWYTVLDLKDAFFCLPLAPQSQELFAFEWKDPERG ISGQLTWTRLPQGFKNSPTLFNEALHRDLTDFRTQHPEVTLLQYVDDLLLAAPTKKACTQGTRHLLQELGEKGYRASAKKAQICQTKVTYLGYILSEGKRWLTPGRIETVAR IPPPRNPREVREFLGKAGFCRLFIPGFAELAAPLYALTKPSTPFTWQTEHQLAFEALKKALLSAPALGLPDTSKPFTLFLDERQGIAKGVLTQKLGPWKRPVAYLSKKLDPV AAGWPPCLRIMAATAMLVKDSAKLTLGQPLTVITPHTLEAIVRQPPDRWITNARLTHYQALLLDTDRVQFGPPVTLNPATLLPVPENQPSPHDCRQVLAETHGTREDLKDQE LPDADHTWYTDGSSYLDSGTRRAGAAVVDGHNTIWAQSLPPGTSAQKAELIALTKALELSKGKKANIYTDSRYAFATAHTHGSIYERRGWLTSEGKEIKNKAEIIALLKALF LPQEVAIIHCPGHQKGQDPVAVGNRQADRVARQAAMAEVLTLATEPDNTSHITAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1978	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPGGTVSLQDEHRLFDIPVTTSLPDVWLQDFPQAWAETGGLGRAKCQAPIIIDLKPTAVPVSIKQYPM SLEAHMGIRQHIIKFLELGVLRPCRSPWNTPLLPVKKPGTQDYRPVQDLREINKRTVDIHPTVPNPYNLLSTLKPDYSWYTVLDLKDAFFCLPLAPQSQELFAFEWKDPERG ISGQLTWTRLPQGFKNSPTLFNEALHRDLTDFRTQHPEVTLLQYVDDLLLAAPTKKACTQGTRHLLQELGEKGYRASAKKAQICQTKVTYLGYILSEGKRWLTPGRIETVAR IPPPRNPREVREFLGKAGFCRLFIPGFAELAAPLYALTKPSTPFTWQTEHQLAFEALKKALLSAPALGLPDTSKPFTLFLDERQGIAKGVLTQKLGPWKRPVAYLSKKLDPV AAGWPPCLRIMAATAMLVKDSAKLTLGQPLTVITPHTLEAIVRQPPDRWITNARLTHYQALLLDTDRVQFGPPVTLNPATLLPVPENQPSPHDCRQVLAETHGTREDLKDQE LPDADHTWYTDGSSYLDSGTRRAGAAVVDGHNTIWAQSLPPGTSAQKAELIALTKALELSKGKKANIYTDSRYAFATAHTHGSIYERRGWLTSEGKEIKNKAEIIALLKALF LPQEVAIIHCPGHQKGQDPVAVGNRQADRVARQAAMAEVLTLATEPDNTSHITAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1991	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY

	DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSSGGSGGTVSLQDEHRLFDIPVTTSLPDVWLQDFPQAWAETGGLGRAKCQAPIIIDLKPTAVPVSIKQYPM SLEAHMGIRQHIIKFLELGVLRPCRSPWNTPLLPVKKPGTQDYRPVQDLREINKRTVDIHPTVPNPYNLLSTLKPDYSWYTVLDLKDAFFCLPLAPQSQELFAFEWKDPERG ISGQLTWTRLPQGFKNSPTLFNEALHRDLTDFRTQHPEVTLLQYVDDLLLAAPTKKACTQGTRHLLQELGEKGYRASAKKAQICQTKVTYLGYILSEGKRWLTPGRIETVAR IPPPRNPREVREFLGKAGFCRLFIPGFAELAAPLYALTKPSTPFTWQTEHQLAFEALKKALLSAPALGLPDTSKPFTLFLDERQGIAKGVLTQKLGPWKRPVAYLSKKLDPV AAGWPPCLRIMAATAMLVKDSAKLTLGQPLTVITPHTLEAIVRQPPDRWITNARLTHYQALLLDTDRVQFGPPVTLNPATLLPVPENQPSPHDCRQVLAETHGTREDLKDQE LPDADHTWYTDGSSYLDSGTRRAGAAVVDGHNTIWAQSLPPGTSAQKAELIALTKALELSKGKKANIYTDSRYAFATAHTHGSIYERRGWLTSEGKEIKNKAEIIALLKALF LPQEVAIIHCPGHQKGQDPVAVGNRQADRVARQAAMAEVLTLATEPDNTSHITAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1992	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGSGGSGGSGGTVSLQDEHRLFDIPVTTSLPDVWLQDFPQAWAETGGLGRAKCQAPIIIDLKPTAVPVS IKQYPMSLEAHMGIRQHIIKFLELGVLRPCRSPWNTPLLPVKKPGTQDYRPVQDLREINKRTVDIHPTVPNPYNLLSTLKPDYSWYTVLDLKDAFFCLPLAPQSQELFAFEW KDPERGISGQLTWTRLPQGFKNSPTLFNEALHRDLTDFRTQHPEVTLLQYVDDLLLAAPTKKACTQGTRHLLQELGEKGYRASAKKAQICQTKVTYLGYILSEGKRWLTPGR IETVARIPPPRNPREVREFLGKAGFCRLFIPGFAELAAPLYALTKPSTPFTWQTEHQLAFEALKKALLSAPALGLPDTSKPFTLFLDERQGIAKGVLTQKLGPWKRPVAYLS KKLDPVAAGWPPCLRIMAATAMLVKDSAKLTLGQPLTVITPHTLEAIVRQPPDRWITNARLTHYQALLLDTDRVQFGPPVTLNPATLLPVPENQPSPHDCRQVLAETHGTRE DLKDQELPDADHTWYTDGSSYLDSGTRRAGAAVVDGHNTIWAQSLPPGTSAQKAELIALTKALELSKGKKANIYTDSRYAFATAHTHGSIYERRGWLTSEGKEIKNKAEIIA LLKALFLPQEVAIIHCPGHQKGQDPVAVGNRQADRVARQAAMAEVLTLATEPDNTSHITAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2048	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ

	LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGSEAAAKGGLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQ YPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDP GMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKET VMGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKL DPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTD QPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKA LFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2048	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGSEAAAKGGLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQ YPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDP GMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKET VMGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKL DPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTD QPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKA LFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2049	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGSEAAAKGGLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPV

	SIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFE WRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEA RKETVMGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYL SKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRP DLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILA LLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2050	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGSSEAAAKGGLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQ YPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDP GMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKET VMGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKL DPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTD QPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKA LFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2054	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGPAPGGLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQ YPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDP GMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKET VMGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKL DPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTD

	QPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKA LFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2055	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSGSSGGLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQ YPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDP GMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKET VMGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKL DPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTD QPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKA LFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2058	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSPAPGGGGGLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYP MSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGM GISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVM GQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDP VAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQP IPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALF LPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2060	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY

	DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSPAPGGGGGLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYP MSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGM GISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVM GQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDP VAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQP IPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALF LPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2085	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSGGGGSGGGGSGGGGSGGLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKA TSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQP LFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQR WLTEARKETVMGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRR PVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAET HGTRPDLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNK SEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2086	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ

	LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAAKEAAAKGGLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLI IPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLH PTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLL REGQRWLTEARKETVMGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKL GPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLE ILAETHGTRPDLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGR EIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2087	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGPAPAPAPAPAPAPGGLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSI QQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWR DPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARK ETVMGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSK KLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDL TDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALL KALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2089	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGSSEAAAKGGLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQ

	YPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDP GMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKET VMGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKL DPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTD QPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKA LFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2090	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGSEAAAKGGLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPV SIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFE WRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEA RKETVMGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYL SKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRP DLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILA LLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2091	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGSSGGGGGLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYP MSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGM GISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVM GQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDP VAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQP

	IPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALF LPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2092	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAAKGGLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKA TSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQP LFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQR WLTEARKETVMGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRR PVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAET HGTRPDLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNK SEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2093	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGSEAAAKGGLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQ YPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDP GMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKET VMGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKL DPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTD QPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKA LFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2093	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY

	DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGSEAAAKGGLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQ YPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDP GMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKET VMGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKL DPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTD QPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKA LFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2094	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVR QAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFF CLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKY LGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGV LTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAP HDCLEILAETHGTRPDLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWL TSEGREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2095	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ

	LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPEAAAKGSSGGLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQ YPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDP GMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKET VMGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKL DPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTD QPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKA LFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2097	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPEAAAKGGSGGLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQ YPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDP GMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKET VMGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKL DPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTD QPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKA LFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2098	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAAKEAAAKEAAAKEAAAKGGLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVR

	QAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFF CLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKY LGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGV LTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAP HDCLEILAETHGTRPDLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWL TSEGREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2099	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKPAPGGSGGLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQ YPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDP GMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKET VMGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKL DPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTD QPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKA LFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2100	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGSSEAAAKGGLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQ YPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDP GMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKET VMGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKL DPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTD

	QPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKA LFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2101	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGGGSSGGLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYP MSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGM GISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVM GQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDP VAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQP IPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALF LPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2102	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSEAAAKGGGGGLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQ YPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDP GMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKET VMGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKL DPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTD QPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKA LFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2104	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY

	DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSGGLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPM SHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMG ISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMG QPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPV AAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQPI PDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALFL PKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2105	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSEAAAKGGLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPM SHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMG ISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMG QPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPV AAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQPI PDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALFL PKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2106	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ

	LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGEAAAKGGGGSGGLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPV SIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFE WRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEA RKETVMGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYL SKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRP DLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILA LLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2109	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSEAAAKPAPGGLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQ YPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDP GMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKET VMGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKL DPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTD QPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKA LFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2110	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGGGGGGLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMS

	HEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGI SGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQ PVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVA AGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQPIP DADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALFLP KRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2112	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSPAPGGLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQ YPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDP GMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKET VMGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKL DPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTD QPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKA LFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2114	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSPAPGGGGGLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYP MSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGM GISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVM GQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDP VAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQP

	IPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALF LPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2115	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSEAAAKGGLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPM SHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMG ISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMG QPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPV AAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQPI PDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALFL PKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2116	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSGGGGSGGGGSGGLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPV SIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFE WRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEA RKETVMGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYL SKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRP DLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILA LLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2117	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY

	DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGSEAAAKGGLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQ YPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDP GMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKET VMGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKL DPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTD QPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKA LFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2120	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPEAAAKGGGGGLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQ YPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDP GMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKET VMGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKL DPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTD QPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKA LFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2122	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ

	LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSPAPGGGGGLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYP MSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGM GISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVM GQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDP VAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQP IPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALF LPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2123	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGPAPGGLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQ YPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDP GMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKET VMGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKL DPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTD QPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKA LFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2131	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGGLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEAR

	LGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQL TWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPK TPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWP PCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQPIPDADH TWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALFLPKRLS IIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2132	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGEAAAKGGSGGLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQ YPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDP GMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKET VMGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKL DPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTD QPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKA LFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2133	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGGSPAPGGLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYP MSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGM GISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVM GQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDP VAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQP

	IPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALF LPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2137	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGSGGSGGSGGLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQ QYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKE TVMGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLT DQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLK ALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2140	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGSSGSSGSSGSSGSSGGLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATS TPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLF AFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWL TEARKETVMGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPV AYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHG TRPDLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSE ILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2142	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY

	DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGSSGSSGGLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYP MSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGM GISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVM GQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDP VAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQP IPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALF LPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2144	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPGGLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHE ARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISG QLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPV PKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAG WPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQPIPDA DHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALFLPKR LSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2145	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ

	LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSSEAAAKGGLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQ YPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDP GMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKET VMGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKL DPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTD QPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKA LFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2146	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSEAAAKPAPGGLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQ YPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDP GMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKET VMGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKL DPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTD QPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKA LFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2148	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGGGGLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSH

	EARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGIS GQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQP VPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAA GWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQPIPD ADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALFLPK RLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2149	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSPAPEAAAKGGLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQ YPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDP GMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKET VMGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKL DPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTD QPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKA LFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2151	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGGGGSGGLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYP MSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGM GISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVM GQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDP VAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQP

	IPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALF LPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2154	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGPAPGGSGGLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYP MSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGM GISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVM GQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDP VAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQP IPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALF LPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2158	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGSSGGLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSH EARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGIS GQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQP VPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAA GWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQPIPD ADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALFLPK RLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2159	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY

	DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSGSSGGLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQ YPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDP GMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKET VMGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKL DPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTD QPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKA LFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2161	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGGSGGLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQ YPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDP GMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKET VMGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKL DPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTD QPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKA LFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2165	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ

	LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGSGGGGGLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYP MSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGM GISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVM GQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDP VAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQP IPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALF LPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2172	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGGGGSSGGLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYP MSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGM GISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVM GQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDP VAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQP IPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALF LPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2174	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGEAAAKGSSGGLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQ

	YPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDP GMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKET VMGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKL DPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTD QPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKA LFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2187	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPAPGGTLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQ QYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKE TVMGQPVPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLT DQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLK ALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2188	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAAKEAAAKGGTLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPL IIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRL HPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYL LREGQRWLTEARKETVMGQPVPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQK LGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCL

	EILAETHGTRPDLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG REIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2190	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGSSGGSGGTLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQ QYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKE TVMGQPVPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLT DQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLK ALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2192	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSPAPEAAAKGGTLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQ QYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKE TVMGQPVPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLT DQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLK ALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2196	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY

	DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSSEAAAKGGTLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQ QYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKE TVMGQPVPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLT DQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLK ALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2225	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGSSEAAAKGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPIPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLM DQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAARREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2226	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ

	LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGSEAAAKGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTP VSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAF EWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTE ARKETVMGQPIPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAY LSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTR SDLMDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEIL ALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2227	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGSSGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMS QEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGI SGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQ PIPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVA AGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMDQPLP DADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLP KRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2231	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSGSSGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQY

	PMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPE MGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPIPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMDQ PLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKAL FLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2235	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGSSPAPGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPIPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLM DQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2236	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQ YPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDP EMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKET VMGQPIPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKL DPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMD

	QPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKA LFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2249	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAAKEAAAKEAAAKGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAV RQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAF FCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVK YLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKG VLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGL QHDCLDILAEAHGTRSDLMDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGW LTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2280	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGSSGSSGSSGSSGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTP VSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAF EWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTE ARKETVMGQPIPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAY LSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTR SDLMDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEIL ALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2299	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY

	DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEA RLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQ LTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIP KTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMDQPLPDAD HTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRL SIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2300	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGGSGGSGGSGGSGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKAT STPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPL FAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRW LTEARKETVMGQPIPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRP VAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAH GTRSDLMDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKD EILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2301	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ

	LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPIPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLM DQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAARE VATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2302	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGPAPGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMS QEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGI SGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQ PIPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVA AGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMDQPLP DADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLP KRLSIIHCPGHQKGNSAEARGNRMADQAARE VATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2303	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAV

	RQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAF FCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVK YLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKG VLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGL QHDCLDILAEAHGTRSDLMDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGW LTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2304	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGSSGSSGSSGSSGSSGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKAT STPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPL FAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRW LTEARKETVMGQPIPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRP VAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAH GTRSDLMDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKD EILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2305	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGSEAAAKGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTP VSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAF EWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTE ARKETVMGQPIPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAY LSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTR

	SDLMDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEIL ALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2308	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGGGSSGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQY PMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPE MGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPIPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMDQ PLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKAL FLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2309	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPAPAPGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVS IKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEW RDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEAR KETVMGQPIPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLS KKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSD LMDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILAL LKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2311	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY

	DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSGGGGSGGGGSGGGGSGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLK ATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQ PLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQ RWLTEARKETVMGQPIPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWR RPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAE AHGTRSDLMDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKN KDEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAARE VATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2312	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSGSSGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQY PMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPE MGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPIPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMDQ PLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKAL FLPKRLSIIHCPGHQKGNSAEARGNRMADQAARE VATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2313	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ

	LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGSAGSAAGSGEFGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSI KQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWR DPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARK ETVMGQPIPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSK KLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDL MDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALL KALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAARE VATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2314	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPEAAAKGGSGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPIPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLM DQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAARE VATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2315	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKPAPGGSGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK

	QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPIPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLM DQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAARE VATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2316	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGEAAAKGSSGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPIPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLM DQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAARE VATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2317	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGGPAPGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQY PMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPE MGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPIPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMDQ

	PLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKAL FLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2319	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGSGGSGGSGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSI KQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWR DPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARK ETVMGQPIPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSK KLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDL MDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALL KALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2320	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGPAPGGSGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQY PMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPE MGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPIPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMDQ PLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKAL FLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2322	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY

	DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAAKEAAAKEAAAKGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAV RQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAF FCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVK YLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKG VLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGL QHDCLDILAEAHGTRSDLMDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGW LTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2323	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEA RLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQ LTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIP KTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMDQPLPDAD HTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRL SIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2324	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ

	LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAAKEAAAKGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPL IIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRL HPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYL LKEGQRWLTEARKETVMGQPIPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQK LGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCL DILAEAHGTRSDLMDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAARE VATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2325	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAAKEAAAKGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLK ATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQ PLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQ RWLTEARKETVMGQPIPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWR RPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAE AHGTRSDLMDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKN KDEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAARE VATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2326	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSEAAAKPAPGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK

	QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPIPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLM DQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAARE VATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2327	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSSEAAAKGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPIPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLM DQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAARE VATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2328	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQ EARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGIS GQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQP IPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAA GWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMDQPLPD

	ADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPK RLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2329	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSPAPGGGGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQY PMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPE MGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPIPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMDQ PLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKAL FLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2331	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGSSGGGGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQY PMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPE MGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPIPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMDQ PLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKAL FLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2332	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY

	DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGSEAAAKGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPIPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLM DQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2333	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSGGGGSGGGGSGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTP VSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAF EWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTE ARKETVMGQPIPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAY LSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTR SDLMDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEIL ALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2335	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ

	LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGGGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMS QEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGI SGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQ PIPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVA AGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMDQPLP DADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLP KRLSIIHCPGHQKGNSAEARGNRMADQAARE VATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2338	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSPAPEAAAKGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPIPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLM DQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAARE VATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2342	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGEAAAKGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYP

	MSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEM GISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVM GQPIPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDP VAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMDQP LPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALF LPKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2343	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKEAAAKAGGTLNIEDEYRLHETSKEPDVSLGSTWLS DFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGL PPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLG YRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLT KPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPV VALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYA FATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKA KVE
2345	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSPAPEAAAKGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPIPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLM

	DQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAARE VATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2346	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSSPAPGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQY PMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPE MGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPIPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMDQ PLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKAL FLPKRLSIIHCPGHQKGNSAEARGNRMADQAARE VATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2347	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPEAAAKGSSGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPIPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLM DQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAARE VATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2353	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY

	DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGSSGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMS QEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGI SGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQ PIPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVA AGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMDQPLP DADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLP KRLSIIHCPGHQKGNSAEARGNRMADQAARE VATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2359	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSEAAAKPAPGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPIPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLM DQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAARE VATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2360	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ

	LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGGSGGSGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQY PMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPE MGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPIPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMDQ PLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKAL FLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2363	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSEAAAKGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYP MSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEM GISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVM GQPIPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDP VAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMDQP LPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALF LPKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2364	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQ

	EARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGIS GQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQP IPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAA GWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMDQPLPD ADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPK RLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2365	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSPAPGGGGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQY PMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPE MGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPIPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMDQ PLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKAL FLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2370	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSGSSGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPIPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLM

	DQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAARE VATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2371	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGGGSSGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQY PMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPE MGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPIPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMDQ PLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKAL FLPKRLSIIHCPGHQKGNSAEARGNRMADQAARE VATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2382	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSEAAAKGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYP MSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEM GISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVM GQPIPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDP VAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMDQP LPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALF LPKRLSIIHCPGHQKGNSAEARGNRMADQAARE VATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2395	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY

	DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGGGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMS QEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGI SGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQ PIPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVA AGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMDQPLP DADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLP KRLSIIHCPGHQKGNSAEARGNRMADQAARE VATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2400	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPEAAAKGGGGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPIPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLM DQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAARE VATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2403	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ

	LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGSGGGGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQY PMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPE MGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPIPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMDQ PLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKAL FLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2405	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGSSGSSGSSGSSGSSGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTP VSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAF EWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTE ARKETVMGQPIPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAY LSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTR SDLMDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEIL ALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2449	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPAPAPGGTLNIEDEYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVS

	IKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEW RDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEAR KETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLS KKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPD LTDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILAL LKALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2503	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSEAAAKGGTLNIEDEYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYP MSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEM GISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVM GQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDP VAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLTDQP LPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALF LPKRLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2504	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSGGTLNIEDEYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQ EARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGIS GQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQP TPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAA GWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLTDQPLPD

	ADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPK RLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2505	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPEAAAKGGTLNIEDEYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYP MSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEM GISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVM GQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDP VAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLTDQP LPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALF LPKRLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2506	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKPAPGGGGGTLNIEDEYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2507	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY

	DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKGGTLNIEDEYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTP VSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAF EWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTE ARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAY LSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEIL ALLKALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2508	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGTLNIEDEYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEA RLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQ LTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTP KTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLTDQPLPDAD HTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRL SIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2510	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ

	LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPAPGGTLNIEDEYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2511	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSGGGGSGGTLNIEDEYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQ YPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDP EMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKET VMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKL DPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLTD QPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKA LFLPKRLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2512	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKPAPGGSGGTLNIEDEYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK

	QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2513	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGGSGGSGGSGGSGGSGGTLNIEDEYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKAT STPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSL FAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRW LTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRP VAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAH GTRPDLTDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKD EILALLKALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2514	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPEAAAKGSSGGTLNIEDEYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLT

	DQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAARE VATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2515	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGGEAAAKGGTLNIEDEYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAARE VATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2518	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGSGSETPGTSESATPESGGTLNIEDEYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATST PVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFA FEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLT EARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVA YLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGT RPDLTDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEI LALLKALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAARE VATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2519	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY

	DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKPAPGSSGGTLNIEDEYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAARREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2521	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGEAAAKGGSGGTLNIEDEYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAARREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2525	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ

	LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPGGTLNIEDEYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQY PMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPE MGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLTDQ PLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKAL FLPKRLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2526	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSEAAAKPAPGGTLNIEDEYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2527	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSPAPEAAAKGGTLNIEDEYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK

	QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2528	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSEAAAKGGGGSGGTLNIEDEYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTP VSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAF EWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTE ARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAY LSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEIL ALLKALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2529	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKAGGTLNIEDEYRLHETSKGPDVPLGSTWLS DFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGL PPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLG YRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLT KPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPI VALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYA

	FATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKA KVE
2530	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSEAAAKPAPGGTLNIEDEYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2531	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGSSGGGGGTLNIEDEYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQY PMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPE MGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLTDQ PLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKAL FLPKRLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2534	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY

	DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPAPAPGGTLNIEDEYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVS IKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEW RDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEAR KETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLS KKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPD LTDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILAL LKALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAARE VATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2535	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSEAAAKPAPGGTLNIEDEYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAARE VATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2536	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ

	LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAAAKEAAAKEAAAKEAAAKEAAAKGGTLNIEDEYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPL IIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRL HPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYL LKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQK LGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCL DILAEAHGTRPDLTDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAARE VATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2539	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGTLNIEDEYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQ EARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGIS GQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQP TPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAA GWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLTDQPLPD ADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPK RLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2542	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGSSEAAAKGGTLNIEDEYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK

	QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2544	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGSGGSGGSGGTLNIEDEYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSI KQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWR DPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARK ETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSK KLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDL TDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALL KALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2547	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGPAPGGTLNIEDEYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMS QEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGI SGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQ PTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVA AGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLTDQPLP

	DADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLP KRLSIIHCPGHQKGNRAEARGNRMADQAARE VATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2548	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSGSSGGTLNIEDEYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAARE VATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2550	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSEAAAKGGGGGTLNIEDEYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAARE VATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2551	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY

	DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSGGGGGTLNIEDEYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAARE VATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2553	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSEAAAKGGSGGTLNIEDEYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAARE VATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2556	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ

	LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGEAAAKGGGPAPGGTLNIEDEYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAARE VATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2559	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGGGGTLNIEDEYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMS QEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGI SGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQ PTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVA AGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLTDQPLP DADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLP KRLSIIHCPGHQKGNRAEARGNRMADQAARE VATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2561	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGSEAAAKGGTLNIEDEYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTP

	VSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAF EWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTE ARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAY LSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEIL ALLKALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2562	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGGGGGTLNIEDEYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMS QEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGI SGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQ PTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVA AGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLTDQPLP DADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLP KRLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2566	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGTLNIEDEYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAV RQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAF FCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVK YLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKG VLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGL

	QHDCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGW LTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2568	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPGGTLNIEDEYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQ EARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGIS GQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQP TPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAA GWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLTDQPLPD ADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPK RLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2573	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSPAPGGGGGTLNIEDEYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQY PMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPE MGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLTDQ PLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKAL FLPKRLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2578	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY

	DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSEAAAKGGGGGTLNIEDEYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2583	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSAGSAAGSGEFGGTLNIEDEYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSI KQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWR DPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARK ETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSK KLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDL TDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALL KALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2585	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ

	LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGSSGGTLNIEDEYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYP MSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEM GISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVM GQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDP VAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLTDQP LPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALF LPKRLSIIHCPGHQKGNRAEARGNRMADQAARELVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2592	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGPAPEAAAKGGTLNIEDEYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAARELVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2599	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSPAPEAAAKGGTLNIEDEYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK

	QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2610	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAAKGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLK ATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQ PLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQ RWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWR RPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAE AHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKN KDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSPGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2611	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKEAAAKAGGTLNIEDEYRLHETSKEPDVSLGSTWLS DFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGL PPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLG YRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLT KPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPV VALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYA

	FATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADG SEFEKRTADGSEFESPKKKAKVE
2612	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGSSGSSGSSGSSGSSGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKAT STPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPL FAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRW LTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRP VAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAH GTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKD EILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2614	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGPAPGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2615	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY

	DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSGGGGSGGGGSGGGGSGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLK ATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQ PLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQ RWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWR RPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAE AHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKN KDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2618	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGPAPGGSGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQY PMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPE MGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQ PLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKAL FLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2619	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ

	LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPAPGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2620	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQ EARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGIS GQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQP TPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAA GWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPD ADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPK RLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2622	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGGPAPGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQY

	PMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPE MGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQ PLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKAL FLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2622	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGGGPAPGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQY PMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPE MGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQ PLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKAL FLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2623	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGSEAAAKGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTP VSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAF EWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTE ARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAY LSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR

	PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEIL ALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2624	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEA RLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQ LTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTP KTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDAD HTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRL SIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2624	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEA RLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQ LTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTP KTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDAD HTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRL SIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2627	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY

	DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTP VSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAF EWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTE ARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAY LSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEIL ALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2629	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSEAAAKGGGGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2631	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ

	LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEA RLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQ LTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTP KTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDAD HTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRL SIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2632	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSSGGSGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQY PMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPE MGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQ PLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKAL FLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2633	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSPAPGGGGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQY

	PMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPE MGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQ PLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKAL FLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2634	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGSSGSSGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQY PMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPE MGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQ PLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKAL FLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2636	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSEAAAKGGGGSGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTP VSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAF EWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTE ARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAY LSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR

	PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEIL ALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2637	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSGGGGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2638	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGEAAAKGGSGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2638	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY

	DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGEAAAKGGSGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2639	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSGGGGSGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQ YPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDP EMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKET VMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKL DPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTD QPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKA LFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2639	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ

	LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGGGSGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQ YPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDP EMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKET VMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKL DPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTD QPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKA LFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2641	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSSEAAAKPAPGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2644	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAV

	RQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAF FCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVK YLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKG VLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGL QHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGW LTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESP KKKAKVE
2647	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQ YPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDP EMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKET VMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKL DPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTD QPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKA LFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2647	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQ YPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDP EMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKET VMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKL DPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTD

	QPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKA LFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2648	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSPAPEAAAKGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2649	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGSGGGGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQY PMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPE MGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQ PLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKAL FLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2649	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY

	DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGSGGGGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQY PMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPE MGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQ PLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKAL FLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2651	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGSSEAAAKGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2653	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ

	LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGGGGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMS QEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGI SGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQ PTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVA AGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLP DADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLP KRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2654	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSPAPGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2655	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEA

	RLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQ LTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTP KTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDAD HTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRL SIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2656	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQY PMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPE MGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQ PLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKAL FLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2657	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYP MSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEM GISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVM GQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDP VAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQP

	LPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALF LPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2660	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGSSEAAAKGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2663	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGSGSETPGTSESATPESGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATST PVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFA FEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLT EARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVA YLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGT RPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEI LALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2665	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY

	DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGSSGSSGSSGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSI KQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWR DPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARK ETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSK KLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDL TDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALL KALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2666	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSGSSGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2667	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ

	LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSPAPGGGGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQY PMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPE MGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQ PLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKAL FLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2669	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGSSGSSGSSGSSGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTP VSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAF EWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTE ARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAY LSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEIL ALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2675	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGSSGGGGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQY

	PMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPE MGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQ PLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKAL FLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2676	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGGGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMS QEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGI SGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQ PTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVA AGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLP DADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLP KRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2676	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGGGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMS QEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGI SGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQ PTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVA AGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLP

	DADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLP KRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2677	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGEAAAKGSSGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2678	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAAKEAAAKGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPL IIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRL HPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYL LKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQK LGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCL DILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAK VE
2681	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS

	ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKPAPGGGGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2684	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSPAPGSSGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQY PMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPE MGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQ PLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKAL FLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2688	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG

	QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSSEAAAKGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2692	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGGEAAAKGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2696	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR

	KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSAGSAAGSGEFGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSI KQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWR DPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARK ETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSK KLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDL TDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALL KALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2700	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSEAAAKGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYP MSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEM GISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVM GQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDP VAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQP LPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALF LPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2701	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSPAPEAAAKGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT

	DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2711	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKEAAAKAGGTLNIEDEHRLHETSKEPDVSLGSTWLS DFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGL PPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLG YRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLT KPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPV VALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYA FATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKA KVE
2712	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGSEAAAKGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTP VSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAF EWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTE ARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAY LSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEIL ALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2712	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS

	ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGSEAAAKGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTP VSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAF EWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTE ARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAY LSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEIL ALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2713	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSEAAAKGGGGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2713	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG

	QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSEAAAKGGGGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2714	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKPAPGGSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2715	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR

	KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGGGGSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQY PMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPE MGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQ PLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKAL FLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2716	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAAKEAAAKGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPL IIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRL HPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYL LKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQK LGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCL DILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2716	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAAKEAAAKGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPL IIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRL HPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYL LKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQK LGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCL

	DILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2718	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSEAAAKGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYP MSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEM GISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVM GQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDP VAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQP LPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALF LPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2719	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGEAAAKPAPGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2721	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY

	DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGEAAAKGGSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2722	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSEAAAKGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2723	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ

	LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGSSPAPGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2723	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGSSPAPGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2724	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKPAPGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYP

	MSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEM GISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVM GQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDP VAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQP LPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALF LPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2726	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYP MSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEM GISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVM GQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDP VAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQP LPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALF LPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2731	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQY PMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPE MGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQ

	PLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKAL FLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2734	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGSGGSSGGSSGSETPGTSESATPESSGGSSGGSSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMG LAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLK DAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQK QVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGY AKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPE EGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRR RGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2737	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGSSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYP MSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEM GISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVM GQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDP VAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQP LPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALF LPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2741	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY

	DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAV RQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAF FCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVK YLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKG VLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGL QHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGW LTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2741	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAV RQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAF FCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVK YLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKG VLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGL QHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGW LTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2744	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ

	LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGEAAAKPAPGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2745	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGGSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2748	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGSSEAAAKGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK

	QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2753	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGSEAAAKGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2760	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGSEAAAKGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT

	DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2764	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSSEAAAKGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2771	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSGGGGSGGGGSGGGGSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLK ATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQ PLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQ RWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWR RPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAE AHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKN KDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2772	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY

	DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTP VSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAF EWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTE ARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAY LSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEIL ALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2776	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSPAPEAAAKGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2780	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ

	LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGGSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMS QEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGI SGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQ PTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVA AGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLP DADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLP KRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2780	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGGSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMS QEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGI SGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQ PTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVA AGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLP DADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLP KRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2781	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKPAPGSSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK

	QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2782	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSPAPGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2782	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSPAPGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT

	DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2783	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYP MSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEM GISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVM GQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDP VAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQP LPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALF LPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2784	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKEAAAKAGGTLNIEDEHRLHETSKEPDVSLGSTWLS DFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGL PPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLG YRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLT KPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPV VALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYA FATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKA KVE
2786	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS

	ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGSEAAAKGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2787	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSEAAAKGGGGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2787	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG

	QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSEAAAKGGGGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2788	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGSEAAAKGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTP VSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAF EWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTE ARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAY LSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEIL ALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2789	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR

	KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGSSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2790	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGGGGGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPM SQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMG ISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMG QPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPV AAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPL PDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2791	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTP VSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAF EWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTE ARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAY LSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR

	PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEIL ALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2792	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGSSPAPGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2793	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGGGSSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQY PMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPE MGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQ PLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKAL FLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2794	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY

	DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSGGGGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2795	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGSGGSGGSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSI KQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWR DPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARK ETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSK KLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDL TDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALL KALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2795	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ

	LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGPGGGPGGGPGGGPGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSI KQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWR DPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARK ETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSK KLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDL TDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALL KALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2797	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPAPAPGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVS IKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEW RDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEAR KETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLS KKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPD LTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILAL LKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2797	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPAPAPGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVS

	IKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEW RDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEAR KETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLS KKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPD LTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILAL LKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2798	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGSSEAAAKGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2798	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGSSEAAAKGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT

	DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2800	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGPAPGGSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQY PMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPE MGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQ PLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKAL FLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2800	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGPAPGGSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQY PMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPE MGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQ PLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKAL FLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2801	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY

	DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSPAPGGGGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQY PMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPE MGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQ PLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKAL FLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2801	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSPAPGGGGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQY PMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPE MGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQ PLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKAL FLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2802	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ

	LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGSSGSSGSSGSSGSSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTP VSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAF EWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTE ARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAY LSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEIL ALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2803	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAAKEAAAKGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPL IIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRL HPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYL LKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQK LGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCL DILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2804	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGGPAPGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQY

	PMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPE MGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQ PLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKAL FLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2804	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGGPAPGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQY PMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPE MGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQ PLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKAL FLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2805	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSPAPEAAAKGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT

	DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2808	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSPAPGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMS QEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGI SGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQ PTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVA AGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLP DADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLP KRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2808	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSPAPGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMS QEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGI SGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQ PTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVA AGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLP DADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLP KRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2809	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY

	DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGSGGSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQY PMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPE MGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQ PLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKAL FLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2810	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGGEAAAKGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2810	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ

	LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGSSGGGEAAAKGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2812	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGPAPGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEA RLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQ LTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTP KTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDAD HTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRL SIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2813	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAAKEAAAKEAAAKEAAAKGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAV

	RQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAF FCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVK YLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKG VLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGL QHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGW LTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2815	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGGSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2815	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGGSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT

	DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2817	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSGSSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2817	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSGSSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2818	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY

	DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGSSGGGGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQY PMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPE MGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQ PLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKAL FLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2818	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGSSGGGGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQY PMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPE MGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQ PLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKAL FLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2819	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ

	LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSGGGGSGGGGSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTP VSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAF EWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTE ARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAY LSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEIL ALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2820	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMS QEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGI SGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQ PTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVA AGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLP DADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLP KRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2822	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGGEAAAKGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK

	QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2823	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQ EARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGIS GQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQP TPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAA GWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPD ADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPK RLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2825	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQ EARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGIS GQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQP TPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAA GWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPD

	ADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPK RLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2826	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSEAAAKGSSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2827	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAV RQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAF FCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVK YLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKG VLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGL QHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGW LTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2828	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY

	DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSEAAAKGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYP MSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEM GISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVM GQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDP VAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQP LPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALF LPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2829	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPEAAAKGGSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2830	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ

	LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGEAAAKPAPGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2830	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGEAAAKPAPGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2831	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSSEAAAKGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK

	QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2833	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGSGGGGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQY PMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPE MGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQ PLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKAL FLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2834	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGGGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQ EARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGIS GQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQP TPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAA GWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPD

	ADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPK RLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2835	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSPAPGGGGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQY PMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPE MGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQ PLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKAL FLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2836	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSEAAAKGGGGSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTP VSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAF EWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTE ARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAY LSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEIL ALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2838	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY

	DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKPAPGGGGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2839	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSPAPEAAAKGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2840	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ

	LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGGSPAPGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQY PMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPE MGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQ PLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKAL FLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2840	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGGSPAPGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQY PMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPE MGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQ PLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKAL FLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2844	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAAKGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLK

	ATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQ PLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQ RWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWR RPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAE AHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKN KDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2845	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQ YPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDP EMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKET VMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKL DPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTD QPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKA LFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2846	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGGSGSSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQY PMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPE MGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQ

	PLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKAL FLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2848	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSSPAPGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQY PMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPE MGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQ PLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKAL FLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2849	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSEAAAKGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYP MSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEM GISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVM GQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDP VAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQP LPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALF LPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2850	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY

	DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKPAPGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYP MSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEM GISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVM GQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDP VAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQP LPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALF LPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2850	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKPAPGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYP MSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEM GISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVM GQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDP VAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQP LPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALF LPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2851	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ

	LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPAPGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2852	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSPAPGSSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQY PMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPE MGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQ PLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKAL FLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2855	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMS

	QEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGI SGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQ PTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVA AGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLP DADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLP KRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2857	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSEAAAKPAPGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2860	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGSEAAAKGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT

	DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2862	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSGGGGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2863	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGGSGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2864	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY

	DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEA RLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQ LTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTP KTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDAD HTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRL SIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2865	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEA RLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQ LTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTP KTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDAD HTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRL SIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2865	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ

	LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEA RLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQ LTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTP KTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDAD HTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRL SIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2866	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGGEAAAKGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2867	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGSSGSSGSSGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSI

	KQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWR DPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARK ETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSK KLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDL TDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALL KALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2868	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPAPAPGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVS IKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEW RDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEAR KETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLS KKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPD LTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILAL LKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2869	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGGGSSGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQY PMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPE MGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQ

	PLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKAL FLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2870	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGEAAAKGSSGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2871	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGGGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMS QEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGI SGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQ PTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVA AGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLP DADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLP KRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2871	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY

	DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGGGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMS QEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGI SGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQ PTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVA AGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLP DADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLP KRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2872	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGGEAAAKGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2873	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ

	LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGSSEAAAKGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2874	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGEAAAKGGSGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2874	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGEAAAKGGSGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK

	QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2877	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTP VSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAF EWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTE ARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAY LSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEIL ALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2878	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGSGGGGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQY PMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPE MGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQ

	PLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKAL FLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2878	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGSGGGGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQY PMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPE MGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQ PLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKAL FLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2879	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGEAAAKPAPGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2880	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY

	DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAAKEAAAKGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPL IIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRL HPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYL LKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQK LGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCL DILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAK VE
2881	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQ EARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGIS GQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQP TPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAA GWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPD ADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPK RLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2883	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG

	QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPEAAAKGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYP MSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEM GISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVM GQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDP VAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQP LPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALF LPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2885	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSSEAAAKGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2886	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR

	KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGGGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMS QEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGI SGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQ PTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVA AGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLP DADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLP KRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2887	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQ YPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDP EMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKET VMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKL DPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTD QPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKA LFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2887	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQ YPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDP EMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKET VMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKL DPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTD

	QPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKA LFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2888	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAAKGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLK ATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQ PLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQ RWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWR RPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAE AHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKN KDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2890	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSPAPGGGGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQY PMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPE MGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQ PLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKAL FLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2891	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY

	DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSEAAAKPAPGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2893	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSPAPEAAAKGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2894	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ

	LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSPAPGSSGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQY PMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPE MGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQ PLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKAL FLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2895	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGGPAPGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQY PMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPE MGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQ PLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKAL FLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2895	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGGPAPGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQY

	PMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPE MGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQ PLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKAL FLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2901	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSEAAAKGGGGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2902	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSAGSAAGSGEFGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSI KQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWR DPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARK ETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSK KLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDL

	TDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALL KALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2903	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGSSGSSGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQY PMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPE MGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQ PLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKAL FLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2904	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGPAPGGSGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQY PMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPE MGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQ PLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKAL FLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2905	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY

	DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGSSGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMS QEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGI SGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQ PTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVA AGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLP DADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLP KRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2907	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGSGSETPGTSESATPESGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATST PVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFA FEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLT EARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVA YLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGT RPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEI LALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2909	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ

	LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSGGGGSGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQ YPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDP EMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKET VMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKL DPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTD QPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKA LFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2909	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGGGSGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQ YPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDP EMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKET VMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKL DPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTD QPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKA LFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2913	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGSSEAAAKGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK

	QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2914	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGSSGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMS QEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGI SGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQ PTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVA AGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLP DADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLP KRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2916	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSEAAAKGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYP MSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEM GISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVM GQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDP VAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQP

	LPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALF LPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2920	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSPAPEAAAKGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2922	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSGSSGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2924	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY

	DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPEAAAKGGSGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2927	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQE ARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISG QLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPT PKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAG WPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDA DHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKR LSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2928	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ

	LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSEAAAKGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2929	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSEAAAKGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYP MSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEM GISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVM GQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDP VAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQP LPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALF LPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2930	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQY

	PMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPE MGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQ PLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKAL FLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2932	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGSEAAAKGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTP VSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAF EWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTE ARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAY LSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEIL ALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2933	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYP MSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEM GISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVM GQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDP VAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQP

	LPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALF LPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2937	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSEAAAKGGGGSGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTP VSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAF EWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTE ARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAY LSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEIL ALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2941	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGSSGSSGSSGSSGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTP VSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAF EWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTE ARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAY LSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEIL ALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2943	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY

	DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGSSGSSGSSGSSGSSGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKAT STPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPL FAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRW LTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRP VAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAH GTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKD EILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2948	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGSSGGGGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQY PMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPE MGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQ PLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKAL FLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2950	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ

	LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSSGGSGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQY PMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPE MGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQ PLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKAL FLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2953	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGEAAAKGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYP MSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEM GISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVM GQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDP VAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQP LPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALF LPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2957	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKAGGTLNIEDEHRLHETSKEPDVSLGSTWLS

	DFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGL PPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFDEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLG YRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKTGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLT KPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPV VALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYA FATAHIHGEIYRRRGLLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKA KVE
2957	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKEAAAKAGGTLNIEDEHRLHETSKEPDVSLGSTWLS DFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGL PPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFDEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLG YRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKTGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLT KPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPV VALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYA FATAHIHGEIYRRRGLLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKA KVE
2965	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGSSGSSGSSGSSGSSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKAT STPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPL FAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRW LTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRP

	VAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAH GTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKD EILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2966	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSEAAAKGGGGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2966	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSEAAAKGGGGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2967	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS

	ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGGGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMS QEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGI SGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQ PTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVA AGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLP DADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLP KRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2968	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSGGGGSGGGGSGGGGSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLK ATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQ PLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQ RWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWR RPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAE AHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKN KDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2969	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG

	QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGSEAAAKGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2971	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKPAPGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYP MSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEM GISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVM GQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDP VAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQP LPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALF LPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2972	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR

	KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKEAAAKAGGTLNIEDEHRLHETSKEPDVSLGSTWLS DFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGL PPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLG YRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLT KPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPV VALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYA FATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKA KVE
2976	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGSSPAPGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2976	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGSSPAPGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK

	LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2979	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGSSGGGGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQY PMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPE MGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQ PLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKAL FLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2982	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYP MSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEM GISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVM GQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDP VAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQP LPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALF LPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2983	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS

	ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAV RQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAF FCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVK YLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKG VLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGL QHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGW LTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2983	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAV RQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAF FCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVK YLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKG VLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGL QHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGW LTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2987	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG

	QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSPAPEAAAKGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2990	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSSEAAAKGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2991	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR

	KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAAKEAAAKGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPL IIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRL HPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYL LKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQK LGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCL DILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2991	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAAKEAAAKGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPL IIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRL HPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYL LKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQK LGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCL DILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2995	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSAGSAAGSGEFGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSI KQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWR DPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARK ETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSK KLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDL

	TDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALL KALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2999	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGEAAAKPAPGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3007	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGSSEAAAKGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3014	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY

	DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKPAPGGSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3015	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSEAAAKGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYP MSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEM GISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVM GQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDP VAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQP LPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALF LPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3018	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ

	LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSEAAAKGGSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3026	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGGGGSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQY PMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPE MGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQ PLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKAL FLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3035	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGSGGSGGSGGSGGSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKAT

	STPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPL FAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRW LTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRP VAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAH GTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKD EILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3036	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAAKGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLK ATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQ PLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQ RWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWR RPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAE AHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKN KDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3037	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEA RLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQ LTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTP KTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDAD

	HTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRL SIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3039	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGSGGSGGSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSI KQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWR DPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARK ETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSK KLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDL TDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALL KALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3039	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGSGGSGGSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSI KQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWR DPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARK ETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSK KLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDL TDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALL KALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3040	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY

	DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSSEAAAKGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3041	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAAKEAAAKGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQ YPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDP EMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKET VMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKL DPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTD QPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKA LFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3042	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ

	LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGSSGGGGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQY PMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPE MGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQ PLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKAL FLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3042	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGSSGGGGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQY PMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPE MGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQ PLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKAL FLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3043	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAAKEAAAKEAAAKGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPL

	IIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRL HPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYL LKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQK LGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCL DILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3044	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGGGGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMS QEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGI SGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQ PTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVA AGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLP DADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLP KRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3044	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGGGGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMS QEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGI SGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQ PTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVA AGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLP

	DADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLP KRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3045	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGEAAAKGGSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3045	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGEAAAKGGSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3046	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY

	DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPEAAAKGGSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3047	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGGGGSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQY PMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPE MGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQ PLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKAL FLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3048	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ

	LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSPAPGSSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQY PMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPE MGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQ PLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKAL FLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3052	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGPAPGGGEAAAKGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3053	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSGSSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK

	QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3053	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSGSSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3054	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPAPGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT

	DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3055	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSPAPGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMS QEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGI SGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQ PTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVA AGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLP DADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLP KRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3056	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGGPAPGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQY PMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPE MGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQ PLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKAL FLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3057	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY

	DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGGEAAAKGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3057	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGGEAAAKGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIK QYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRD PEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE TVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3059	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ

	LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGGPAPGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQY PMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPE MGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQ PLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKAL FLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3059	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRY DEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIV DLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR LSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAL IKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQ KGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGGPAPGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQY PMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPE MGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQ PLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKAL FLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3060	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGPAPGGSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRP VQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDC QQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPD

	LTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPL PEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEI KNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3061	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGPAPEAAAKGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDY RPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSEL DCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGL PDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLL PLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGK EIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3062	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGGSSEAAAKGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDY RPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSEL DCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGL PDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLL PLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGK EIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3063	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA

	SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGGGGGSGGGGSGGGGSGGGGSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTP LLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEI KQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQF GPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEI YRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3063	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGGGGGSGGGGSGGGGSGGGGSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTP LLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEI KQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQF GPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEI YRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3064	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGPAPGGSGSSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSE LDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALG LPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATL LPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3065	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ

	TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGGGGGSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPV QDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQ QGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDL TKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLP EEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIK NKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3067	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGGGSEAAAKGGGGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAAT SELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPA LGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPA TLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3067	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGGGSEAAAKGGGGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAAT SELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPA LGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPA TLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3068	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG

	NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGPAPEAAAKGGGGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAAT SELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPA LGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPA TLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3070	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGGSGGSGGSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSE LDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALG LPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATL LPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3075	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGGSSGGSPAPGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSE LDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALG LPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATL

	LPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3076	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGGGGGGSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRP VQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDC QQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPD LTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPL PEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEI KNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3076	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGGGGGGSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRP VQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDC QQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPD LTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPL PEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEI KNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3079	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ

	LGGDGGEAAAKGGGGSEAAAKGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVK KPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLL LAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALL TAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVA LNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRG WLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3080	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGEAAAKPAPGGSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAAT SELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPA LGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPA TLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3081	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGIL VPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRI QHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWG PDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQA LLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYA FATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3083	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR

	GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGPAPGGSEAAAKGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAAT SELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPA LGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPA TLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3084	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGPAPAPAPAPAPAPGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKP GTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLA ATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTA PALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALN PATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWL TSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3084	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGPAPAPAPAPAPGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKP GTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLA ATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTA PALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALN PATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWL TSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3085	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID

	GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGGGGEAAAKPAPGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAAT SELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPA LGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPA TLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3085	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGGGGEAAAKPAPGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAAT SELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPA LGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPA TLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3086	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGPAPAPAPAPGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSE LDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALG LPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATL

	LPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3087	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGGGSPAPGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRP VQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDC QQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPD LTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPL PEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEI KNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3087	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGGGSPAPGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRP VQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDC QQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPD LTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPL PEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEI KNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3088	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ

	LGGDGGGGSEAAAKPAPGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAAT SELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPA LGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPA TLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3089	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGSSGGSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRP VQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDC QQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPD LTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPL PEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEI KNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3091	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGPAPGSSEAAAKGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAAT SELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPA LGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPA TLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3091	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR

	GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGPAPGSSEAAAKGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAAT SELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPA LGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPA TLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3092	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGGGGSGGGGSGGGGSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVK KPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLL LAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALL TAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVA LNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRG WLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3093	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGGSSPAPGGGGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSE LDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALG LPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATL LPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3094	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID

	GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGGGGGGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQ DLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQ GTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLT KPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPE EGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKN KDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3096	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGGGGGGGGGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYR PVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELD CQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLP DLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLP LPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKE IKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3097	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGGGSEAAAKGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDY RPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSEL DCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGL PDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLL

	PLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGK EIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3098	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATL LPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3099	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGGGGGSEAAAKGGGGSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVK KPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLL LAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALL TAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVA LNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRG WLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3101	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ

	LGGDGGGGGGGSGSSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSE LDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALG LPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATL LPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3103	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGEAAAKGGGGGSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAAT SELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPA LGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPA TLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3103	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGEAAAKGGGGGSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAAT SELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPA LGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPA TLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3107	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR

	GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGGGGGSSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRP VQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDC QQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPD LTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPL PEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEI KNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3108	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGEAAAKGGSPAPGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAAT SELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPA LGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPA TLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3108	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGEAAAKGGSPAPGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAAT SELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPA LGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPA TLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3109	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID

	GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGGSSGGSEAAAKGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAAT SELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPA LGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPA TLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3110	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGGGGSGGGGSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTN DYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATS ELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPAL GLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPAT LLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSE GKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3111	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGGGGPAPGGSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSE LDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALG LPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATL

	LPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3111	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGGGGPAPGGSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSE LDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALG LPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATL LPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3112	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGEAAAKGSSPAPGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAAT SELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPA LGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPA TLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3113	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ

	LGGDGGGGSGSSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRP VQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDC QQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPD LTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPL PEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEI KNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3114	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGGGGGGGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPV QDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQ QGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDL TKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLP EEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIK NKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3116	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGEAAAKGGGGSSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAAT SELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPA LGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPA TLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3117	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR

	GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGGGGGSSPAPGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSE LDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALG LPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATL LPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3118	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGGGSPAPEAAAKGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAAT SELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPA LGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPA TLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3120	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGEAAAKEAAAKEAAAKEAAAKEAAAKEAAAKGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGIL VPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRI QHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWG PDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQA LLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYA FATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3121	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID

	GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGGGSGGGGSSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSE LDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALG LPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATL LPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3121	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGGGSGGGGSSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSE LDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALG LPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATL LPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3123	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGEAAAKGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPV QDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQ QGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDL TKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLP

	EEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIK NKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3124	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGPAPGGSGGGGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSE LDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALG LPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATL LPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3125	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGEAAAKGGSGGGGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAAT SELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPA LGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPA TLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3126	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ

	LGGDGGGSSGSSGSSGSSGSSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVK KPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLL LAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALL TAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVA LNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRG WLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3127	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGGSSPAPEAAAKGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAAT SELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPA LGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPA TLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3130	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGGGSPAPGGGGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSE LDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALG LPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATL LPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3130	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR

	GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGGGSPAPGGGGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSE LDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALG LPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATL LPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3131	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGGSSEAAAKGGSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAAT SELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPA LGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPA TLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3136	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGGGGPAPEAAAKGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAAT SELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPA LGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPA TLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4501	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID

	GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGGGSGGSGGSGGTAPLEEEYRLFLEAPIQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGTSE YRMVQDLREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEEGESGQLTWTRLPQGFKNSPTLFNEALNRDLQGFRLDHPSVSLLQYVDDLLIAADTQ AACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAILQIPVPKTKRQVREFLGKIGYCRLFIPGFAELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPAL ALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSKRLDPVAAGWPRCLRAIAAAALLTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPAT LLPETDDTLPIHHCLDTLDSLTSTRPDLTDQPLAQAEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWLTA GGKAIKNAPEILALLTAVWLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4502	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGGGSGGSGGSGGSGGSGGVLNLEEEYRLHEKPVPSSIDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMSKEAREGIRPHIQRFLDLGVLVPCQSPWNTPLLPVKKP GTNDYRPVQDLREINKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLAPFRALNPQVVLLQYVDDLLVA APTYRDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLLKEGKRWLTPARKATVMKIPPPTTPRQVREFLGTAGFCRLWIPGFASLAAPLYPLTKPSIPFIWTEEHQKAFDRIKEALLSA PALALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAVAAVALLLKDADKLTLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNP ATLLPVESEATPVHRCSEILAEETGTRRDLKDQPLPGVPAWYTDGSSFIAEGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDINIYTDSRYAFATAHIHGAIYKQRGWLT SAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4503	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGGGSGGSGGSGGSGGSGGSGGLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLP VKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDD ILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQA LLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPV

	VALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRR RGWLTSEGREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4504	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGGGGGSGGGGSGGGGSGGGGSGGGGSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQS PWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDL ILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQK AYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDT DRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAH IHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4505	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGGSSGSSGSSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSE LDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALG LPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATL LPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4506	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ

	LGGDGGEAAAKEAAAKEAAAKGGTLNIEDEYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVK KPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLL LAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALL TAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVA LNPATLLPLPEKEAPHDCLEILAETHGTRPDLTDQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRG WLTSEGREIKNKNEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4507	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGEAAAKEAAAKEAAAKEAAAKEAAAKGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQS PWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDL ILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQK AFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDT DRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAH IHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4508	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGPAPAPAPGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYR PVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELD CQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLP DLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLP LPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKE IKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4509	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR

	GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGPAPAPAPAPAPGGVLNLEEEYRLHEKPVPSSIDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMSKEAREGIRPHIQRFLDLGVLVPCQSPWNTPLLPVKKPGT NDYRPVQDLREINKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLAPFRALNPQVVLLQYVDDLLVAAP TYRDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLLKEGKRWLTPARKATVMKIPPPTTPRQVREFLGTAGFCRLWIPGFASLAAPLYPLTKPSIPFIWTEEHQKAFDRIKEALLSAPA LALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAVAAVALLLKDADKLTLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPAT LLPVESEATPVHRCSEILAEETGTRRDLKDQPLPGVPAWYTDGSSFIAEGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDINIYTDSRYAFATAHIHGAIYKQRGWLTSA GKDIKNKEEILALLEAIHLPKRVAIIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4510	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGPAPAPAPAPAPGGTLNIEDEYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKP GTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLA ATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTA PALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALN PATLLPLPEKEAPHDCLEILAETHGTRPDLTDQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWL TSEGREIKNKNEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4511	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGGGGGGSGGLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPV QDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQ QGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDL TKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLP EEGAPHDCLEILAETHGTRPDLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIK NKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4512	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID

	GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGEAAAKGSSGGLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYR PVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELD CQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLP DLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLP LPEEGAPHDCLEILAETHGTRPDLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGRE IKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4513	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGPAPGSSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRP VQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDC QQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPD LTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPL PEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEI KNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4514	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGPAPGSSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRP VQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDC QQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPD LTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPL

	PEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEI KNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4515	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGEAAAKPAPGGVLNLEEEYRLHEKPVPSSIDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMSKEARERGIRPHIQRFLDLGVLVPCQSPWNTPLLPVKKPGTNDYRP VQDLREINKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLAPFRALNPQVVLLQYVDDLLVAAPTYRDC KEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLLKEGKRWLTPARKATVMKIPPPTTPRQVREFLGKAGFCRLFIPGFASLAAPLYPLTKPSIPFIWTEEHQKAFDRIKEALLSAPALALPD LTKPFTLYVDERAGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAVAAVALLLKDADKLTLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVE SEATPVHRCSEILAEETGTRRDLKDQPLPGVPAWYTDGSSFIAEGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDINIYTDSRYAFATAHIHGAIYKQRGWLTSAGKDIK NKEEILALLEAIHLPKRVAIIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4516	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGPAPEAAAKGGLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYR PVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELD CQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLP DLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLP LPEEGAPHDCLEILAETHGTRPDLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGRE IKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4517	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ

	LGGDGGGSSGGGGGSGGLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDY RPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSEL DCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGL PDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLL PLPEEGAPHDCLEILAETHGTRPDLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGR EIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4518	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGGSSGGGGGSGGTLNIEDEYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSE QDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALG LPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATL LPLPEKEAPHDCLEILAETHGTRPDLTDQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEG REIKNKNEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4519	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGGGGGGSEAAAKGGTLNIEDEYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAAT SEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPA LGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPA TLLPLPEKEAPHDCLEILAETHGTRPDLTDQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTS EGREIKNKNEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4520	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR

	GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGGGGGGSPAPGGTLNLEDEYRLYETSAEPEVSPGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEAKLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHRWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSE LDCQQGTRALLLTLGNLGYRASAKKAQLCQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALG LPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLRKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATL LPLPEEGAPHDCLEILAETHGTRPDLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG REIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4521	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGPAPGGGGGSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSE LDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALG LPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATL LPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4522	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGGGSEAAAKGSSGGTLNIEDEYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAAT SEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPA LGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPA TLLPLPEKEAPHDCLEILAETHGTRPDLTDQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTS EGREIKNKNEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4523	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID

	GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGEAAAKGGSGSSGGTLNIEDEYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAAT SEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPA LGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPA TLLPLPEKEAPHDCLEILAETHGTRPDLTDQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTS EGREIKNKNEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4524	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGEAAAKGGSSGGSGGTLNIEDEYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAAT SEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPA LGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPA TLLPLPEKEAPHDCLEILAETHGTRPDLTDQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTS EGREIKNKNEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4525	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGGGSPAPGSSGGTLNIEDEYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSE QDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALG LPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATL

	LPLPEKEAPHDCLEILAETHGTRPDLTDQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEG REIKNKNEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4526	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGGSSPAPGGSGGLLGRDLLTKLKAQIQFSTEGPQVTWEDRPAMCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPMVWAEKAGMGLANQVPPVVVELKSDASPVAVRQYPMSKEAREGIRPH IQRFLDLGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEA LHRDLASFRALNPQVVMLQYVDDLLVAAPTYRDCKEGTRRLLQELSKLGYRVSAKKAQLCREEVTYLGYLLKGGKRWLTPARKATVMKIPTPTTPRQVREFLGTAGFCRLWIPGFASLAAPLYPL TRPKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFALYVDEKEGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWM TNARMTHYQSLLLNERVSFAPPAILNPATLLPVESDDTPIHICSEILAEETGTRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALTQALRLAEGKSI NIYTDSRYAFATAHVHGAIYKQRGWLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTETTKNAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4527	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGEAAAKPAPGGSGGTLNIEDEYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAAT SEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPA LGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPA TLLPLPEKEAPHDCLEILAETHGTRPDLTDQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTS EGREIKNKNEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4528	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ

	LGGDGGPAPEAAAKGGSGGTLNLEDEYRLYETSAEPEVSPGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEAKLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHRWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAAT SELDCQQGTRALLLTLGNLGYRASAKKAQLCQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPA LGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLRKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPA TLLPLPEEGAPHDCLEILAETHGTRPDLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4529	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGPAPEAAAKGGSGGLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYR PVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQD CLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALP DVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPE ETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGRE IKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4530	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGGGGEAAAKGSSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAAT SELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPA LGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPA TLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4531	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR

	GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGEAAAKGGGGSSGGVLNLEEEYRLHEKPVPSSIDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMSKEAREGIRPHIQRFLDLGVLVPCQSPWNTPLLPVKKPGTND YRPVQDLREINKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLAPFRALNPQVVLLQYVDDLLVAAPTY RDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLLKEGKRWLTPARKATVMKIPPPTTPRQVREFLGKAGFCRLFIPGFASLAAPLYPLTKPSIPFIWTEEHQKAFDRIKEALLSAPALA LPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAVAAVALLLKDADKLTLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLL PVESEATPVHRCSEILAEETGTRRDLKDQPLPGVPAWYTDGSSFIAEGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDINIYTDSRYAFATAHIHGAIYKQRGWLTSAGK DIKNKEEILALLEAIHLPKRVAIIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4532	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGGSSGGGPAPGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDY RPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQ DCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALAL PDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLP EETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGR EIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4533	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGPAPGSSGGGGGTLNLEDEYRLYETSAEPEVSPGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEAKLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHRWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSE LDCQQGTRALLLTLGNLGYRASAKKAQLCQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALG LPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLRKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATL LPLPEEGAPHDCLEILAETHGTRPDLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG REIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4534	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID

	GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGGGGPAPEAAAKGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAAT SELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPA LGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPA TLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4535	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGEAAAKGGGPAPGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAAT SELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPA LGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPA TLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4536	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGEAAAKPAPGGGGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVDDLLLAAT SELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPA LGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPA

	TLLPLPEEGLQHDCLDILAEAHGTRSDLMDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4537	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGPAPEAAAKGGGGGLLGRDLLTKLKAQIQFSTEGPQVTWEDRPAMCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPMVWAEKAGMGLANQVPPVVVELKSDASPVAVRQYPMSKEAREGIR PHIQRFLDLGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFN EALHRDLASFRALNPQVVMLQYVDDLLVAAPTYRDCKEGTRRLLQELSKLGYRVSAKKAQLCREEVTYLGYLLKGGKRWLTPARKATVMKIPTPTTPRQVREFLGTAGFCRLWIPGFASLAAPLY PLTRPKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFALYVDEKEGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDR WMTNARMTHYQSLLLNERVSFAPPAILNPATLLPVESDDTPIHICSEILAEETGTRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALTQALRLAEGK SINIYTDSRYAFATAHVHGAIYKQRGWLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTETTKNAGKRTADGSEFEKRTADGSEFESPKKKAK VE
4538	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGGSSEAAAKPAPGGTLNIEDEYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAAT SEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPA LGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPA TLLPLPEKEAPHDCLEILAETHGTRPDLTDQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTS EGREIKNKNEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4539	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA

	SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGGSSPAPEAAAKGGTAPLEEEYRLFLEAPIQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGT SEYRMVQDLREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEEGESGQLTWTRLPQGFKNSPTLFNEALNRDLQGFRLDHPSVSLLQYVDDLLIAAD TQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAILQIPVPKTKRQVREFLGKIGYCRLFIPGFAELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQPP ALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSKRLDPVAAGWPRCLRAIAAAALLTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNP ATLLPETDDTLPIHHCLDTLDSLTSTRPDLTDQPLAQAEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWL TAGGKAIKNAPEILALLTAVWLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4540	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGAEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKAGGTLNIEDEYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEAR LGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSP TLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMA APLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQ PPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALK MAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPK KKAKVE
4541	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHE RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYID GGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENED ILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQ TVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKAR GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKR NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLA SHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQ LGGDGGAEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKAGGIPWLMKKPLQLTTLVPLQEYEERLLKQTMLTGSYKEKLQSLFLKYDALWQHWENQVGHRRIKPHHIATGTV NPRPQKQYPINPKAKASIQTVINDLLKQGVLIQQNSIMNTPVYPVPKPDGKWRMVLDYREVNKTIPLIAAQNQHSAGILSSIFRGKYKTTLDLSNGFWAHSITPESYWLTAFTWLGQQYCWTRLP QGFLNSPALFNADVVDLLKEVPNVQVYVDDIYISHDDPREHLEQLEKVFSLLLNAGYVVSLKKSEIAQHEVEFLGFNITKEGRGLTETFKQKLLNITPPRDLKQLQSILGKLNFARNFIPNFSEL VKPLYNIIATAPGKYITWTTDNSQQLQNIISMLNSAENLEERNPEVRLIMKVNTSPSAGYIRFYNEFAKRPIMYLNYVYTKAEVKFTNTEKLLTTIHKGLIKALDLGMGQEILVYSPIVSMTKIQ KTPLPERKALPIRWITWMSYLEDPRIQFHYDKTLPELQQVPTVTDDIIAKIKHPSEFSMVFYTDGSAIKHPNVNKSHNAGMGIAQVQFKPEFTVINTWSIPLGDHTAQLAEVAAVEFACKKALKI DGPVLIVTDSFYVAESVNKELPYWQSNGFFNNKKKPLKHVSKWKSIADCIQLKPDIIIIHEKGHQPTASTFHTEGNNLADKLATQGSYVVNAGKRTADGSEFEKRTADGSEFESPKKKAKVE

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: 4651), AGKRTADGSEFEKRTADGSEFESPKKKAKVE (SEQ ID NO: 4001) 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.
AHFKISGEKRPSTDPGKKAKNPKKKKKKDP	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
EVLKVIRTGKRKKKAWKRMVTKVC	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

Sequence	Sequence References	SEQ ID No.
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
KRRRRRRREKRKR	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

Sequence	Sequence References	SEQ ID No.
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

Sequence	Sequence References	SEQ ID No.
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
RRTIRLKLVYDKCDRSCKIQKKNRNKCQYCRF HKCLSVGMSHNAIRFGRMPRSEKAKLKAE	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

Sequence	Sequence References	SEQ ID No.
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:
TGCCTGTCATACGAAACCGAGATACTGACAGTAGAATATGGCCTTCTGCCAATCGGGAAGATTGTGGAGAAACGG
ATAGAATGCACAGTTTACTCTGTCGATAACAATGGTAACATTTATACTCAGCCAGTTGCCCAGTGGCACGACCGGG
GAGAGCAGGAAGTATTCGAATACTGTCTGGAGGATGGAAGTCTCATTAGGGCCACTAAGGACCACAAATTTATGA

CAGTCGATGGCCAGATGCTGCCTATAGACGAAATCTTTGAGCGAGAGTTGGACCTCATGCGAGTTGACAACCTTCC
TAAT (SEQ ID NO: 5029)

DnaE Intein-N Protein:
CLSYETEILTVEYGLLPIGKIVEKRIECTVYSVDNNGNIYTQPVAQWHDRGEQEVFEYCLEDGSLIRATKDHKFMTVDGQ
MLPIDEIFERELDLMRVDNLPN (SEQ ID NO: 5030)

DnaE Intein-C DNA:
ATGATCAAGATAGCTACAAGGAAGTATCTTGGCAAACAAAACGTTTATGATATTGGAGTCGAAAGAGATCACAAC
TTTGCTCTGAAGAACGGATTCATAGCTTCTAAT (SEQ ID NO: 5031)

DnaE Intein-C Protein:
MIKIATRKYLGKQNVYDIGVERDHNFALKNGFIASN (SEQ ID NO: 5032)

Cfa-N DNA:
TGCCTGTCTTATGATACCGAGATACTTACCGTTGAATATGGCTTCTTGCCTATTGGAAAGATTGTCGAAGAGAGAA
TTGAATGCACAGTATATACTGTAGACAAGAATGGTTTCGTTTACACACAGCCCATTGCTCAATGGCACAATCGCGG
CGAACAAGAAGTATTTGAGTACTGTCTCGAGGATGGAAGCATCATACGAGCAACTAAAGATCATAAATTCATGAC
CACTGACGGGCAGATGTTGCCAATAGATGAGATATTCGAGCGGGGCTTGGATCTCAAACAAGTGGATGGATTG
CCA (SEQ ID NO: 5033)

Cfa-N Protein:
CLSYDTEILTVEYGFLPIGKIVEERIECTVYTVDKNGFVYTQPIAQWHNRGEQEVFEYCLEDGSIIRATKDHKFMTTDGQ
MLPIDEIFERGLDLKQVDGLP (SEQ ID NO: 5034)

Cfa-C DNA:
ATGAAGAGGACTGCCGATGGATCAGAGTTTGAATCTCCCAAGAAGAAGAGGAAAGTAAAGATAATATCTCGAAA
AAGTCTTGGTACCCAAAATGTCTATGATATTGGAGTGGAGAAAGATCACAACTTCCTTCTCAAGAACGGTCTCGTA
GCCAGCAAC (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, a template RNA may be customized to correct a given mutation in the genomic DNA of a target cell (e.g., *ex vivo* or *in vivo*, e.g., in a target tissue or organ, e.g., in a subject). For example, the mutation may be a disease-associated mutation relative to the wild-type sequence. Without wishing to be bound by theory, any given target site and edit will have a large number of possible template RNA molecules for use in a gene modifying system that will result in a range of editing efficiencies and fidelities. To partially reduce this screening burden, sets of empirical parameters help ensure optimal initial *in silico* designs of template RNAs or portions thereof. As a non-limiting illustrative example, for a selected mutation, the following design parameters may be employed. In some embodiments, design is initiated by acquiring approximately 500 bp (e.g., up to 50, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, or 700 bp, and optionally at least 20, 30, 40, 50, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, or 650 bp) flanking sequence on either side of the mutation to serve as the target region. In some embodiments, a template nucleic acid comprises a gRNA. In some embodiments, a gRNA comprises a sequence (e.g., a CRISPR spacer) that binds a target site. In some embodiments, the sequence (e.g., a CRISPR spacer) that binds a target site for use in targeting a template nucleic acid to a target region is selected by considering the particular gene modifying polypeptide (e.g., endonuclease domain or writing domain, e.g., comprising a CRISPR/Cas domain) being used (e.g., for Cas9, a protospacer-adjacent motif (PAM) of NGG immediately 3′ of a 20 nucleotide gRNA binding region). In some embodiments, the CRISPR spacer is selected by ranking first by whether the PAM will be disrupted by the gene modifying system induced edit. In some embodiments, disruption of the PAM may increase edit efficiency. In some embodiments, the PAM can be disrupted by also introducing (e.g., as part of or in addition to another modification to a target site in genomic DNA) a silent mutation (e.g., a mutation that does not alter an amino acid residue encoded by the target nucleic acid sequence, if any) in the target site during gene modification. In some embodiments, the CRISPR spacer is selected by ranking sequences by the proximity of their corresponding genomic site to the desired edit location. In some embodiments, the gRNA comprises a gRNA scaffold. In some embodiments, the gRNA scaffold used may be a standard scaffold (e.g., for Cas9, 5′-GTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC-3′; SEQ ID NO: 11,003), or may contain one or more nucleotide substitutions. In some embodiments, the heterologous object sequence has at least 90% identity, e.g., at least 90%, 95%, 98%, 99%, or 100% identity, or comprises no more than 1, 2, 3, 4, or 5 positions of non-identity to the target site 3′ of the first strand nick (e.g., immediately 3′ of the first strand nick or up to 1, 2, 3, 4, or 5 nucleotides 3′ of the first strand nick), with the exception of any insertion, substitution, or deletion that may be written into the target site by the gene modifying. In some embodiments, the 3′ target homology domain contains at least 90% identity, e.g., at least 90%, 95%, 98%, 99%, or 100% identity, or comprises no more than 1, 2, 3, 4, or 5 positions of non-identity to the target site 5′ of the first strand nick (e.g., immediately 5′ of the first strand nick or up to 1, 2, 3, 4, or 5 nucleotides 3′ of the first strand nick).

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).

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)	SEQ ID NO:	Cut	Tier	Spacer (min)	Spacer (max)	crRNA	SEQ ID NO:	Tetraloop	SEQ ID NO:	tracrRNA	SEQ ID NO:
Nme2Cas9	NNNNCC		-3	1	22	24	GTTGTAGCTCCCTTTCTCATTTCG	10,051	GAAA		CGAAATGAGAACCGTTGCTACAATAAGGCCGTCTGAAAAGATGTGCCGCAACGCTCTGCCCCTTAAAGCTTCTGCTTTAAGGGGCATCGTTTA	10,151
PpnCas9	NNNNRTT			1	21	24	GTTGTAGCTCCCTTTTTCATTTCGC	10,052	GAAA		GCGAAATGAAAAACGTTGTTACAATAAGAGATGAATTTCTCGCAAAGCTCTGCCTCTTGAAATTTCGGTTTCAAGAGGCATC	10,152
SauCas9	NNGRR; NNGRRT		-3	1	21	23	GTTTTAGTACTCTG	10,053	GAAA		CAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	10,153
SauCas9-KKH	NNNRR; NNNRRT		-3	1	21	21	GTTTTAGTACTCTG	10,054	GAAA		CAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	10,154
SauriCas9	NNGG		-3	1	21	21	GTTTTAGTACTCTG	10,055	GAAA		CAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	10,155
SauriCas9-KKH	NNRG		-3	1	21	21	GTTTTAGTACTCTG	10,056	GAAA		CAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	10,156
ScaCas9-Sc++	NNG		-3	1	20	20	GTTTTAGAGCTA	10,057	GAAA		TAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	10,157
SpyCas9	NGG		-3	1	20	20	GTTTTAGAGCTA	10,058	GAAA		TAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	10,158

SpyCas9_i_v1	NGG		-3	1	20	20	GTTTTAGAGCTA	10057	GAAA		TAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGGACTTCGGTCCAAGTGGCACCGAGTCGGTGC	10,193
SpyCas9_i_v2	NGG		-3	1	20	20	GTTTTAGAGCTA	10057	GAAA		TAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGGAGCTTGCTCCAAGTGGCACCGAGTCGGTGC	10,194
SpyCas9_i_v3	NGG		-3	1	20	20	GTTTTAGAGCTA	10057	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	GTCTTAG TACTCTG	10,064	GAAA		CAGAATCTACTAAGACAAGGCAAAAT GCCGTGTTTATCTCGTCAACTTGTTGG CGAGA	10,164
cCas9-v21	NNVACT; NNVATG M;NNVA TT;NNVG CT;NNVG TG;NNV GTT		-3	2	21	21	GTCTTAG TACTCTG	10,065	GAAA		CAGAATCTACTAAGACAAGGCAAAAT GCCGTGTTTATCTCGTCAACTTGTTGG CGAGA	10,165
cCas9-v42	NNVRRN		-3	2	21	21	GTCTTAG TACTCTG	10,066	GAAA		CAGAATCTACTAAGACAAGGCAAAAT GCCGTGTTTATCTCGTCAACTTGTTGG CGAGA	10,166
CdiCas9	NNRHHH Y;NNRAA AY			2	22	22	ACTGGGG TTCAG	10,067	GAAA		CTGAACCTCAGTAAGCATTGGCTCGT TTCCAATGTTGATTGCTCCGCCGGTG CTCCTTATTTTTAAGGGCGCCGGC	10,167
CjeCas9	NNNNRY AC		-3	2	21	23	GTTTTAGT CCCT	10,068	GAAA		AGGGACTAAAATAAAGAGTTTGCGG GACTCTGCGGGGTTACAATCCCCTAA AACCGC	10,168
GeoCas9	NNNNCR AA			2	21	23	GTCATAG TTCCCCTG A	10,069	GAAA		TCAGGGTTACTATGATAAGGGCTTTC TGCCTAAGGCAGACTGACCCGCGGC GTTGGGGATCGCCTGTCGCCCGCTTT TGGCGGGCATTCCCCATCCTT	10,169
iSpyMacCas 9	NAAN		-3	2	19	21	GTTTTAG AGCTA	10,070	GAAA		TAGCAAGTTAAAATAAGGCTAGTCCG TTATCAACTTGAAAAAGTGGCACCGA GTCGGTGC	10,170
NmeCas9	NNNNGA YT;NNN NGYTT;N NNNGAY A;NNNN GTCT		-3	2	20	24	GTTGTAG CTCCCTTT CTCATTTC G	10,071	GAAA		CGAAATGAGAACCGTTGCTACAATAA GGCCGTCTGAAAAGATGTGCCGCAA CGCTCTGCCCCTTAAAGCTTCTGCTTT AAGGGGCATCGTTTA	10,171

ScaCas9	NNG		-3	2	20	20	GTTTTAG AGCTA	10,072	GAAA		TAGCAAGTTAAAATAAGGCTAGTCCG TTATCAACTTGAAAAAGTGGCACCGA GTCGGTGC	10,172
ScaCas9-HiFi-Sc++	NNG		-3	2	20	20	GTTTTAG AGCTA	10,073	GAAA		TAGCAAGTTAAAATAAGGCTAGTCCG TTATCAACTTGAAAAAGTGGCACCGA GTCGGTGC	10,173
SpyCas9-3var-NRRH	NRRH		-3	2	20	20	GTTTAAG AGCTATG CTG	10,074	GAAA		CAGCATAGCAAGTTTAAATAAGGCTA GTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGC	10,174
SpyCas9-3var-NRTH	NRTH		-3	2	20	20	GTTTAAG AGCTATG CTG	10,075	GAAA		CAGCATAGCAAGTTTAAATAAGGCTA GTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGC	10,175
SpyCas9-3var-NRCH	NRCH		-3	2	20	20	GTTTAAG AGCTATG CTG	10,076	GAAA		CAGCATAGCAAGTTTAAATAAGGCTA GTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGC	10,176
SpyCas9-HF1	NGG		-3	2	20	20	GTTTTAG AGCTA	10,077	GAAA		TAGCAAGTTAAAATAAGGCTAGTCCG TTATCAACTTGAAAAAGTGGCACCGA GTCGGTGC	10,177
SpyCas9-QQR1	NAAG		-3	2	20	20	GTTTTAG AGCTA	10,078	GAAA		TAGCAAGTTAAAATAAGGCTAGTCCG TTATCAACTTGAAAAAGTGGCACCGA GTCGGTGC	10,178
SpyCas9-SpG	NGN		-3	2	20	20	GTTTTAG AGCTA	10,079	GAAA		TAGCAAGTTAAAATAAGGCTAGTCCG TTATCAACTTGAAAAAGTGGCACCGA GTCGGTGC	10,179
SpyCas9-VQR	NGAN		-3	2	20	20	GTTTTAG AGCTA	10,080	GAAA		TAGCAAGTTAAAATAAGGCTAGTCCG TTATCAACTTGAAAAAGTGGCACCGA GTCGGTGC	10,180
SpyCas9-VRER	NGCG		-3	2	20	20	GTTTTAG AGCTA	10,081	GAAA		TAGCAAGTTAAAATAAGGCTAGTCCG TTATCAACTTGAAAAAGTGGCACCGA GTCGGTGC	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.

In some embodiments, the heterologous object sequence of the template nucleic acid (e.g., template RNA) is inserted into the target genome in a genomic safe harbor site, such as AAVS1, CCR5, ROSA26, or albumin locus. In some embodiments, a gene modifying is used to integrate a CAR into the T-cell receptor α constant (*TRAC*) locus (Eyquem et al Nature 543, 113-117 (2017)). In some embodiments, a gene modifying system is used to integrate a CAR into a T-cell receptor β constant (*TRBC*) locus. Many other safe harbors have been identified by computational approaches (Pellenz et al Hum Gen Ther 30, 814-828 (2019)) and could be used for gene modifying system-mediated integration. In some embodiments, the heterologous object sequence of the template nucleic acid (e.g., template RNA) is added to the genome in an intergenic or intragenic region. In some embodiments, the heterologous object sequence of the template nucleic acid (e.g., template RNA) is added to the genome 5′ or 3′ within 0.1 kb, 0.25 kb, 0.5 kb, 0.75, kb, 1 kb, 2 kb, 3 kb, 4 kb, 5 kb, 7.5 kb, 10 kb, 15 kb, 20 kb, 25 kb, 50, 75 kb, or 100 kb of an endogenous active gene. In some embodiments, the heterologous object sequence of the template nucleic acid (e.g., template RNA) is added to the genome 5′ or 3′ within 0.1 kb, 0.25 kb, 0.5 kb, 0.75, kb, 1 kb, 2 kb, 3 kb, 4 kb, 5 kb, 7.5 kb, 10 kb, 15 kb, 20 kb, 25 kb, 50, 75 kb, or 100 kb of an endogenous promoter or enhancer. In some embodiments, the heterologous object sequence of the template nucleic acid (e.g., template RNA) can be, e.g., 50-50,000 base pairs (e.g., between 50-40,000 bp, between 500-30,000 bp between 500-20,000 bp, between 100-15,000 bp, between 500-10,000 bp, between 50-10,000 bp, between 50-5,000 bp.

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).

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 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-thio-2'-O-methyluridine
2,6-diaminopurine	3-(3-amino-3-carboxypropyl)uridine
7-deaza-adenine	5-methoxyuridine
7-deaza-8-aza-adenine	uridine 5-oxyacetic acid
7-deaza-2-aminopurine	uridine 5-oxyacetic acid methyl ester
7-deaza-8-aza-2-aminopurine	5-(carboxyhydroxymethyl)uridine)
7-deaza-2,6- diaminopurine	5-(carboxyhydroxymethyl)uridine methyl ester
7-deaza-8-aza-2,6-diarninopurine	5-methoxycarbonylmethyluridine
1-methyladenosine	5-methoxycarbonylmethyl-2'-O-methyluridine
N6-isopentenyladenosine	5-methoxycarbonylmethyl-2-thiouridine
N6-(cis-hydroxyisopentenyl)adenosine	5-aminomethyl-2-thiouridine
2-methylthio-N6-(cis-hydroxyisopentenyl) adenosine	5-methylaminomethyluridine
N6-glycinylcarbamoyladenosine	5-methylaminomethyl-2-thiouridine
N6-threonylcarbamoyladenosine	5-methylaminomethyl-2-selenouridine
2-methylthio-N6-threonyl carbamoyladenosine	5-carbamoylmethyluridine
N6,N6-dimethyladenosine	5-carbamoylmethyl-2'-O-methyluridine
7-methyladenine	5-carboxymethylaminomethyluridine
2-methylthio-adenine	5-carboxymethylaminomethyl-2'-O-methyluridine
2-methoxy-adenine	5-carboxymethylaminomethyl-2-thiouridine
inosine	N4,2'-O-dimethylcytidine
1-methyl-inosine	5-carboxymethyluridine
wyosine	N6,2'-O-dimethyladenosine
wybutosine	N,N6,O-2'-trimethyladenosine
7-deaza-guanosine	N2,7-dimethylguanosine
7-deaza-8-aza-guanosine	N2,N2,7-trimethylguanosine
6-thio-guanosine	3,2'-O-dimethyluridine
6-thio-7-deaza-guanosine	5-methyldihydrouridine
6-thio-7-deaza-8-aza-guanosine	5-formyl-2'-O-methylcytidine
7-methyl-guanosine	1,2'-O-dimethylguanosine
6-thio-7-methyl-guanosine	4-demethylwyosine
7-methylinosine	Isowyosine
6-methoxy-guanosine	N6-acetyladenosine
1-methylguanosine	
N2-methylguanosine	
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, 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.

In some embodiments, an insertion, deletion, substitution, or combination thereof, increases or decreases expression (e.g. transcription or translation) of a target gene. In some embodiments, an insertion, deletion, substitution, or combination thereof, increases or decreases expression (e.g. transcription or translation) of a target 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 target 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 target 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, increases, decreases the activity of a target gene, e.g. a protein encoded by the target gene.

Compensatory edits

In some embodiments, the systems or methods provided herein can be used to introduce a compensatory edit. In some embodiments, the compensatory edit is at a position of a gene associated with a disease or disorder, which is different from the position of a disease-causing mutation. In some embodiments, the compensatory mutation is not in the gene containing the causative mutation. In some embodiments, the compensatory edit can negate or compensate for a disease-causing mutation. In some embodiments, the compensatory edit can be introduced by the systems or methods provided herein to suppress or reverse the mutant effect of a disease-causing mutation.

Regulatory edits

In some embodiments, the systems or methods provided herein can be used to introduce a regulatory edit. In some embodiments, the regulatory edit is introduced to a regulatory sequence of a gene, for example, a gene promoter, gene enhancer, gene repressor, or a sequence that regulates gene splicing. In some embodiments, the regulatory edit increases or decreases the expression level of a target gene. In some embodiments, the target gene is the same as the gene containing a disease-causing mutation. In some embodiments, the target gene is different from the gene containing a disease-causing mutation.

Repeat expansion diseases

In some embodiments, the systems or methods provided herein can be used to treat a repeat expansion disease. In some embodiments, the systems or methods provided herein, for example, those comprising gene modifying polypeptides, can be used to treat repeat expansion diseases by resetting the number of repeats at the locus according to a customized RNA template.

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

Promoter	Target 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)
SERPINA1 (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)
ITNNI3 (cTnI)	Troponin I type 3 (cardiac)	Cardiomyocytes (from immature state)
ITNNI3 (cTnI)	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

Promoter	Gene Description	Gene Specificity
CNS specific promoters		
Promoter	**Gene Description**	**Gene Specificity**
SYN1 (hSyn)	Synapsin I	Neurons
GFAP	Glial fibrillary acidic protein	Astrocytes
INA	Internexin 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)	Integrin, 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

Promoter	Gene Description	Gene Specificity
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, an 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) (CACTCCTCCCCATCCTCTCCCTCTGTCCCTCTGTCCCTCTGACCCTGCACTGTCCCAGCACC; SEQ ID NO: 11,004) or orosomucoid 1 (ORM1) (CAGGACACAGCCTTGGATCAGGACAGAGACTTGGGGGCCATCCTGCCCCTCCAACCCGACATGTGTACCTCAGCTTTTTCCCTCACTTGCATCAATAAAGCTTCTGTGTTTGGAACAGCTAA; 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 UGAUAAUAGGCUGGAGCCUCGGUGGCCAUGCUUCUUGCCCCUUGGGCCUCCCCCCAGCCCCUCCUCCCCUUCCU

GCACCCGUACCCCCGUGGUCUUUGAAUAAAGUCUGA (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′-
UGAUAAUAGGCUGGAGCCUCGGUGGCCAUGCUUCUUGCCCCUUGGGCCUCCCCCCAGCCCCUCCUCCCCUUCCU
GCACCCGUACCCCCGUGGUCUUUGAAUAAAGUCUGA-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.

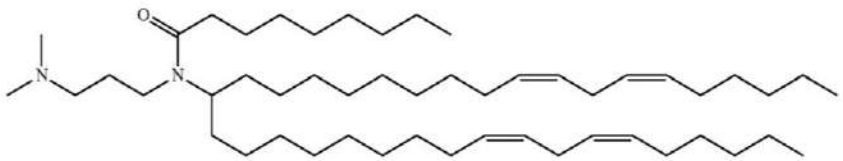
In some embodiments, the lipid to nucleic acid ratio (mass/mass ratio; w/w ratio) can be in the range of from about 1 : 1 to about 25: 1, from about 10: 1 to about 14: 1, from about 3 : 1 to about 15: 1, from about 4: 1 to about 10: 1, from about 5: 1 to about 9: 1, or about 6: 1 to about 9: 1. The amounts 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)-

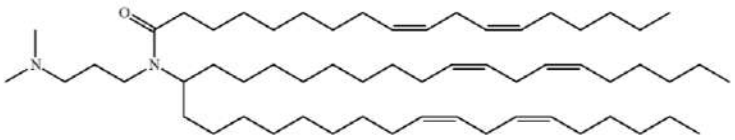
A,A-dimethyl-3- nonyldocosa-l3, l6-dien-l-amine (Compound 32), e.g., as described in Example 11 of WO2019051289A9 (incorporated by reference herein in its entirety). In some embodiments, the ionizable lipid is Compound 6 or Compound 22, e.g., as described in Example 12 of WO2019051289A9 (incorporated 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,



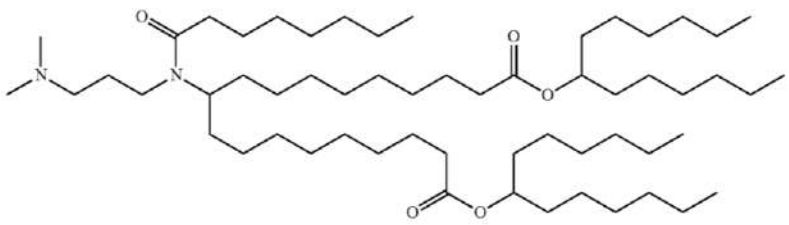
(i)

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.



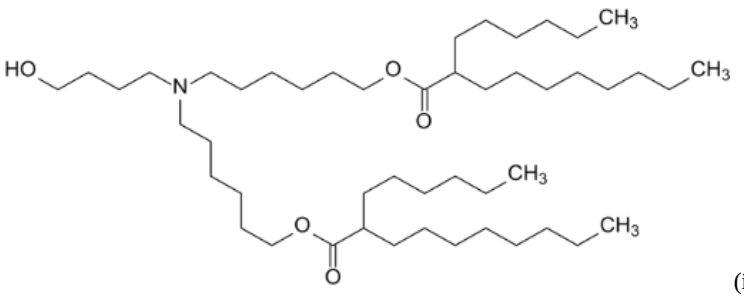
(ii)

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.

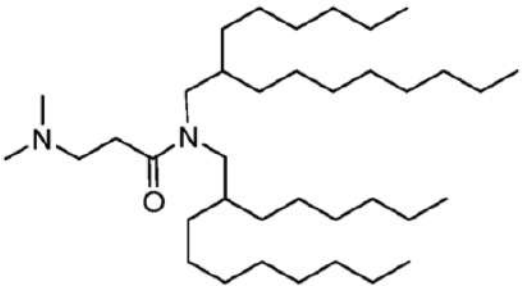


(iii)

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.

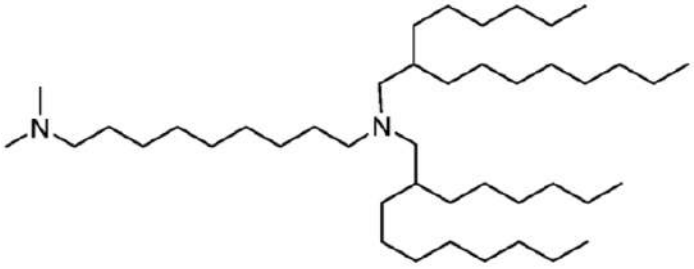


(iv)



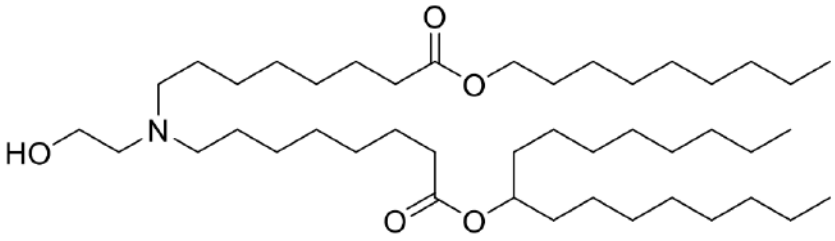
(v)

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.

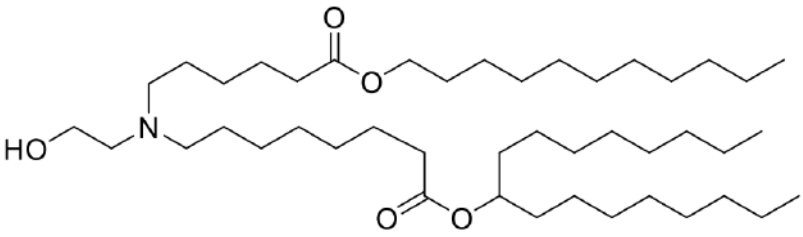


(vi)

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.

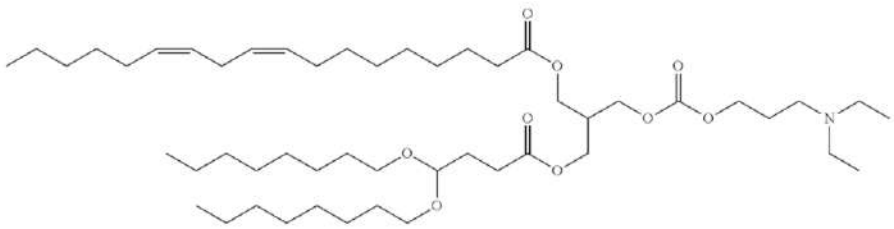


(vii)



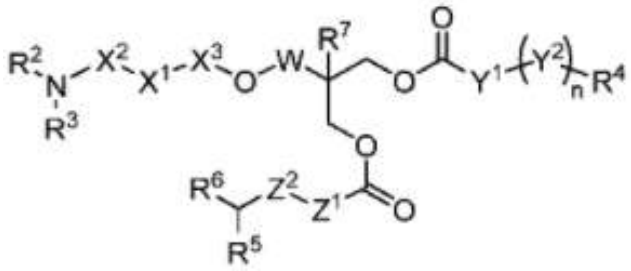
(viii)

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)

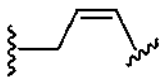
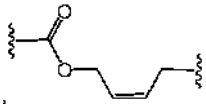
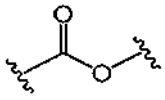
In some embodiments an LNP comprising Formula (ix) is used to deliver a gene modifying composition described herein to the liver and/or hepatocyte cells.



(x)

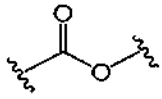
wherein

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

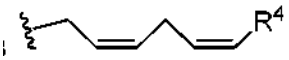
(in either orientation), (in either orientation), (in either orientation),

n is 0 to 3, R^4 is Ci-15 alkyl, Z^1 is Ci-6 alkylene or a direct bond,

Z^2 is 

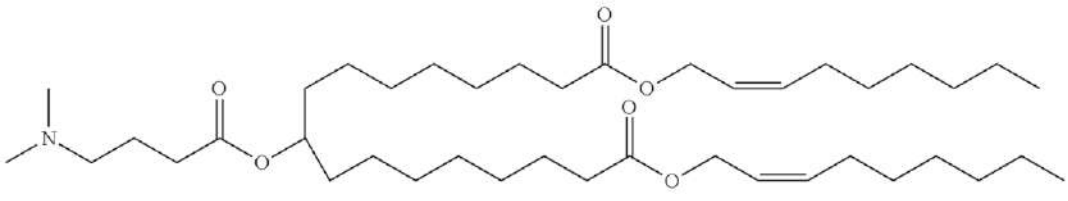
(in either orientation) or absent, provided that if Z^1 is a direct bond, Z^2 is absent;

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



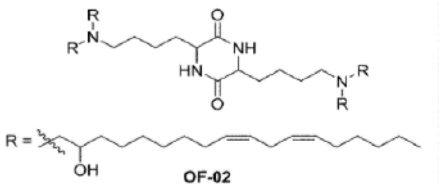
, R^4 is linear C5 alkyl, Z^1 is C2 alkylene, Z^2 is absent, W is methylene, and R^7 is H, then R^5 and R^6 are not Cx alkoxy.

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.



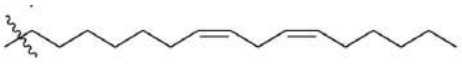
(xi)

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.

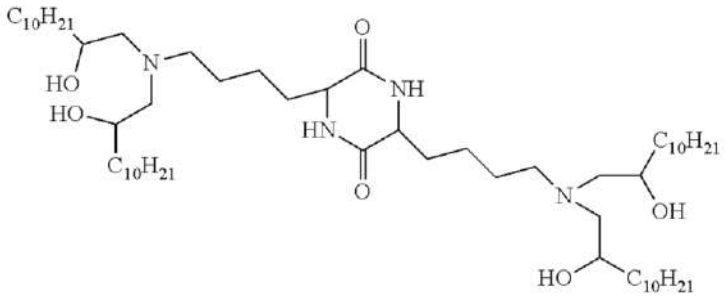


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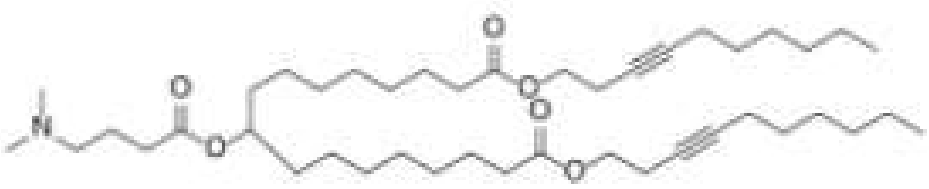
where R=



(xii)

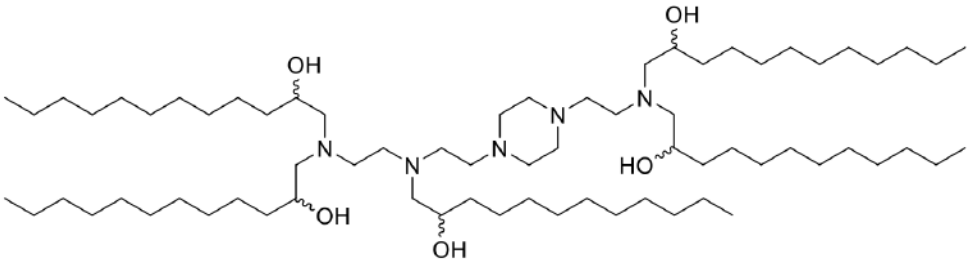


(xiii)



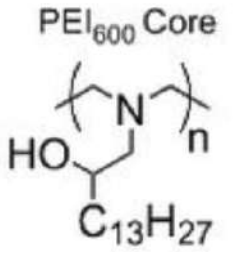
(xiv)

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.

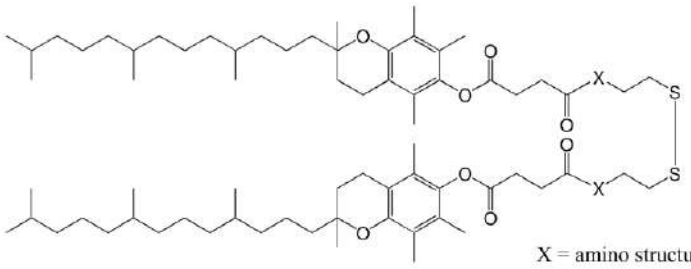


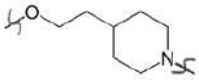
(xvi)

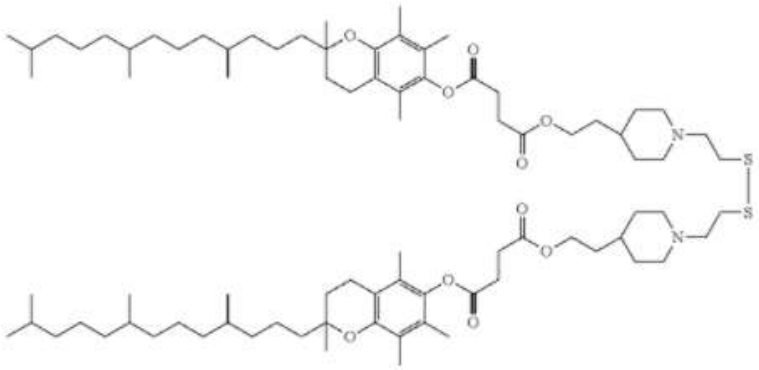
In some embodiments an LNP comprising a formulation of Formula (xvi) is used to deliver a gene modifying composition described herein to the lung endothelial cells.



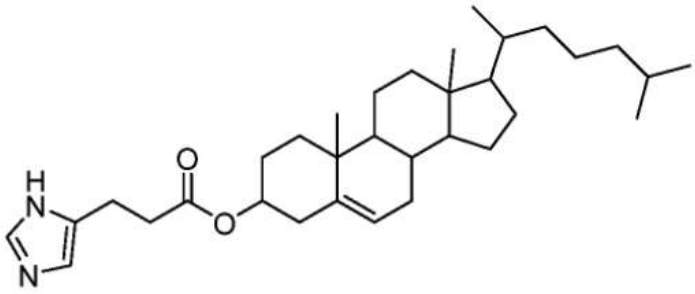
(xvii)



where X=  (xviii) (a)

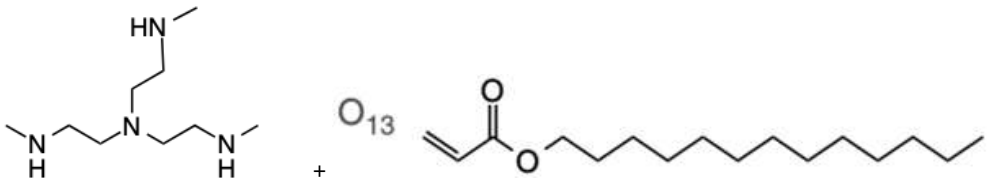


(xviii)(b)

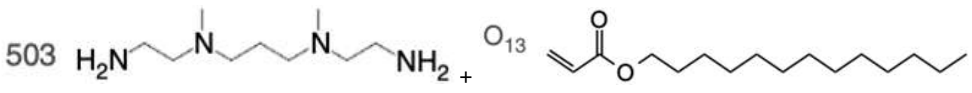


(xix)

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:



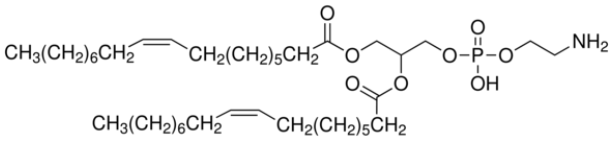
(xx) (a)



(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).

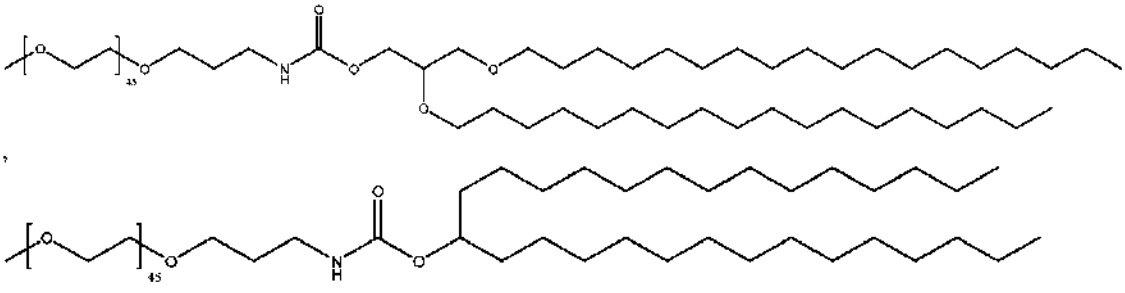
In some embodiments, the lipid nanoparticles do not comprise any phospholipids.

In some embodiments, 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.

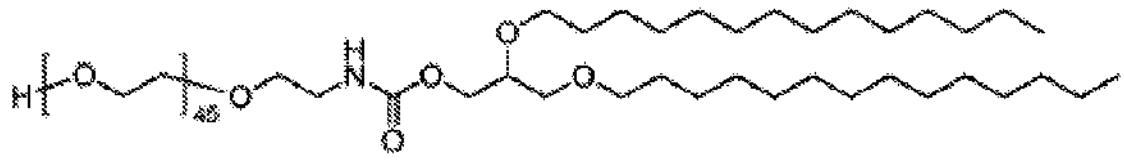
In some embodiments, the component providing membrane integrity, such as a sterol, can comprise 0-50% (mol) (e.g., 0-10%, 10-20%, 20-30%, 30-40%, or 40-50%) of the total lipid present in the lipid nanoparticle. In some embodiments, such a component is 20-50% (mol) 30-40% (mol) of the total lipid content 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.

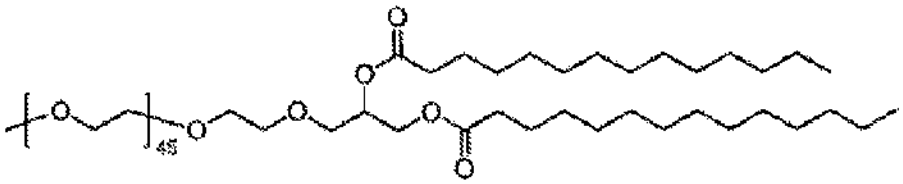
Exemplary PEG-lipid conjugates include, but are not limited to, PEG-diacylglycerol (DAG) (such as l-(monomethoxy-polyethyleneglycol)-2,3-dimyristoylglycerol (PEG-DMG)), PEG-dialkyloxypropyl (DAA), PEG-phospholipid, PEG-ceramide (Cer), a pegylated phosphatidylethanoloamine (PEG-PE), 1,2-dimyristoyl-sn-glycerol, 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:



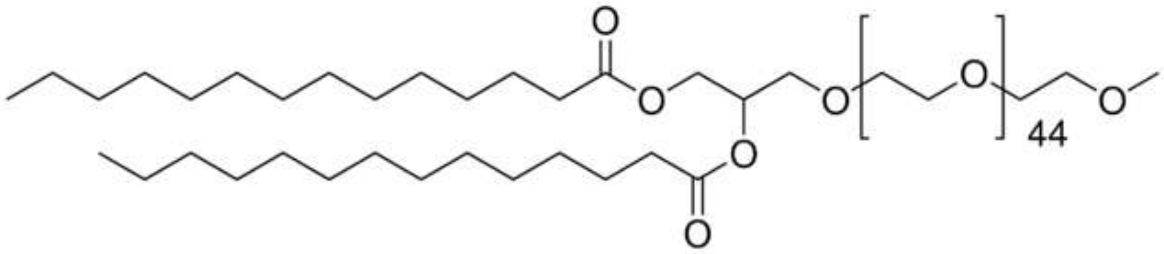
(xxii),



(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.

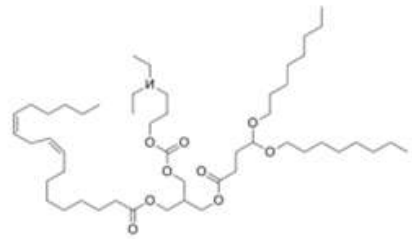
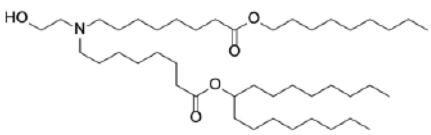
In some embodiments, LNPs are directed to specific tissues by the addition of targeting domains. For example, biological ligands may be displayed on the surface of LNPs to enhance interaction with cells displaying cognate receptors, thus driving association with and cargo delivery to tissues wherein 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.

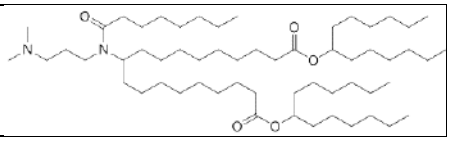
In some embodiments, LNPs are selected for tissue-specific activity by the addition of a Selective ORgan Targeting (SORT) molecule to a formulation comprising traditional components, such as ionizable cationic lipids, amphipathic phospholipids, cholesterol and poly(ethylene glycol) (PEG) lipids. The 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: 15471));

(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: Quantifying activity of a gene editing polypeptide using a GFP/BFP assay in human cells

This example describes the use of gene modifying system containing an exemplary gene modifying polypeptide and an exemplary template RNA. In this example, the template RNA contains:

(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 comprises the following sequence:
GCCGAAGCACTGCACGCCGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTG AAAAAGTGGCACCGAGTCGGTGCACCCTGACGTACGGCGTGCAGTGCTT (SEQ ID NO: 11,010).

A gene modifying system comprising a given gene modifying polypeptide (e.g., one described herein) and the template RNA is transfected into the HEK293T BFP-expressing cell line. The gene modifying polypeptide and the template RNA are delivered by nucleofection in DNA format. Specifically, 800 ng of gene modifying polypeptide plasmid DNA is combined with 200 ng template RNA in plasmid format. The modifying polypeptide and template RNA in plasmid DNA format are added to 25µL SF buffer containing 250,000 HEK293T BFP-expressing cells, and cells are nucleofected using program DS-150. After nucleofection, cells are 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 BFP locus can be used to amplify across the locus. Amplicons are analyzed via short read sequencing using an Illumina MiSeq. Conversion of the BFP gene sequence to the GFP gene sequence indicate successful editing. In some embodiments, the assay will indicate that at least 10%, 20%, 30%, 40%, 50%, 60%, or 70% of copies of the BFP gene in the sample are converted to the GFP gene.

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 *Streptococcus pyogenes* (*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, based on exemplary RT domains listed in Table 2 (FIG. 2A). In total, 17,446 Cas-linker-RT gene modifying polypeptides (also referred to, in the context of the experiment, as individual elements or candidates) were tested. RT domains of the present disclosure can be grouped into families (each an “RT family”), each RT family comprising a wild type or reference RT sequence from a retrovirus and any variants of that RT wild type or

reference sequence, e.g., RT sequences comprising one or more amino acid differences relative to the reference RT sequence. RT family candidates, accordingly, as used herein, refers to all gene modifying polypeptide candidates as described above, in which the RT sequence is selected from identified RT family.

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 (<u>underline</u>) (ACCCTGACC<u>T</u>ACGGCGTGCAGTGCTTCGGCCGCTACCCCGA**T**CACAT; 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 (FIG. 3). 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 as listed in Example 7).

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 1. 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. A subset of the gene modifying polypeptide candidates tested were selected for further analysis (amino acid sequences listed Table A1).

Table 1. 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: of Linker	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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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
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
EAAAKEAAAKEAAAKEAAAKEAAAK	12,283	FLV_P10273_3mutA
PAPGGSEAAAK	12,284	MLVAV_P03356_3mutA

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
GGGGSSPAP	12,429	PERV_Q4VFZ2_3mut
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
GGGEAAAKPAP	12,549	PERV_Q4VFZ2_3mutA_WS
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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
EAAAKGGGGGS	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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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
GSSEAAAK	12,670	MLVMS_P03355_3mut
GGSGSSEAAAK	12,671	MLVMS_P03355_PLV919
GGSEAAAKGGG	12,672	MLVFF_P26809_3mutA

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
EAAAKGGGPAP	12,868	MLVFF_P26809_3mut
GSSPAP	12,869	PERV_Q4VFZ2_3mutA_WS
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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
EAAAKPAP	12,990	MLVMS_P03355_3mut

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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
GSSGSS	13,110	KORV_Q9TTC1-Pro_3mut
GGGPAPGSS	13,111	MLVMS_P03355_3mutA_WS
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	13,112	FOAMV_P14350
PAPGSSGGG	13,113	MLVMS_P03355_PLV919
GGSEAAAKPAP	13,114	BAEVM_P10272_3mutA

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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
GGGGSGGGGSGGGGSGGGGSGGGGSGGGGS	13,150	SFV3L_P27401_2mutA
GGGEAAAKGSS	13,151	MLVMS_P03355_PLV919
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
EAAAKGGGPAP	13,189	MLVBM_Q7SVK7_3mutA_WS
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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
GGGGG	13,310	MLVMS_P03355_3mutA_WS
EAAAK	13,311	PERV_Q4VFZ2_3mut
GSS		FLV_P10273_3mutA

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
EAAAKEAAAKEAAAK	13,387	PERV_Q4VFZ2
GGSGGGEAAAK	13,388	MLVMS_P03355_3mutA_WS
GGGGSGGGGSGGGGSGGGGS	13,389	BAEVM_P10272_3mut
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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: of Linker	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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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
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
EAAAKGGGGS	13,683	MLVBM_Q7SVK7_3mutA_WS

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
EAAAKEAAAKEAAAKEAAAK	13,708	FFV_O93209_2mut
GSSGGSGGG	13,709	MLVMS_P03355_3mutA_WS
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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: of Linker	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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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
EAAAKGGGGS	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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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
GGGG	13,950	BAEVM_P10272_3mutA
EAAAKGGGGSS	13,951	MLVCB_P08361_3mutA
EAAAKEAAAKEAAAK	13,952	GALV_P21414_3mutA
PAPGGGEAAAK	13,953	KORV_Q9TTC1

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
PAPGSS	14,027	MLVFF_P26809_3mutA
PAPGSS	14,028	BAEVM_P10272_3mutA
GGSPAPGSS	14,029	AVIRE_P03360_3mut
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
SGSETPGTSESATPES	14,148	FOAMV_P14350-Pro_2mutA
EAAAKPAPGGS	14,149	AVIRE_P03360_3mut
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
SGGSSGGSSGSETPGTSESATPESSGGSSGGSS	14,268	SFV3L_P27401-Pro_2mutA
EAAAKGGGPAP	14,269	BAEVM_P10272_3mutA
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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
GGGGSS	14,390	KORV_Q9TTC1-Pro_3mut
GGGGSSEAAAK	14,391	KORV_Q9TTC1

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
EAAAK	14,467	SFV3L_P27401_2mut
EAAAKGGGGSS	14,468	BAEVM_P10272_3mut
GGGGGSEAAAK	14,469	MLVBM_Q7SVK7_3mut
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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: of Linker	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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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
GGGGG	14,710	FLV_P10273_3mut
GGGEAAAKGSS	14,711	SFV3L_P27401

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
GGGGGSGSS	14,907	MMTVB_P03365
GSSPAPGGS	14,908	FOAMV_P14350_2mutA
EAAAKGSS	14,909	MLVMS_P03355
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
GSSPAPGGS	15,029	FOAMV_P14350-Pro_2mut
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
SGSETPGTSESATPES	15,149	SFVCP_Q87040-Pro_2mutA
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
EAAAKGGGPAP	15,269	MMTVB_P03365
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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
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

Linker amino acid sequence	SEQ ID NO: of Linker	RT domain name
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: Sequencing Analysis of Pooled Screening of Gene Modifying Polypeptides in HEK293T and U2OS Cells

This example describes identification and characterization of several classes of gene modifying polypeptides capable of editing genomic DNA.

Genomic DNA was extracted from pools of the sorted and unsorted cell populations in Example 2 and analysed as described in Example 1. Specifically, DNA libraries were prepared by PCR amplification of candidate gene modifying polypeptide sequences. Libraries were sequenced using long read sequencing using an Oxford Nanopore Technologies sequencer protocol Amplicons by Ligation SQK-LSK110. Raw sequencing reads were processed using MinKNOW (Oxford Nanopore Technologies) to perform base-calling and standard quality filtering. The filtered sequencing reads were then mapped against a reference consisting of full-length DNA sequences for all

possible library candidates. Following mapping, the data were further processed to remove reads not satisfying requirements for minimum and maximum length, excessive truncation, chimerism, and minimum sequence identity to improve mapping confidence. The surviving data were then normalized to counts-per-million to adjust for sequencing depth. Normalized counts from unsorted populations were used as baseline for their respective sorted populations to calculate fold-change enrichment for each candidate. Finally, fold-change values were $\log_2$ transformed and Z-score normalized.

Cells infected with lentiviral pools encoding gene modifying polypeptides comprising MLVMS RT having high editing activity with several linkers were used as a positive control and cells infected with lentiviral pools encoding gene modifying polypeptides comprising MMTVB RT having low editing activity were used as a negative control to confirm that sequencing analyses were consistent with known editing assay results (FIGS. 4A-4C). The results showed that the assay distinguishes between gene modifying polypeptides containing high activity RTs and low activity RTs (FIGS. 4A-4B). The results further showed that the activity trends associated with the positive control RT and negative control RT selected are consistent across all members of a given RT family tested, e.g., for each of the MLVMS RT sequences and each of the MMTVB RT sequences across multiple linkers tested (FIG. 4C). These data indicate that the identity of the RT domain plays a significant role in determining editing activity of a gene modifying polypeptide.

The genome-editing capacity of gene modifying library candidates tested was assessed across four conditions, using two different templates and two different cell lines: template g4 in HEK293T cells (condition 1), template g4 in U2OS cells (condition 2), template g10 in HEK293T cells (condition 3), and template g10 in U2OS cells (condition 4). Genome editing activity was plotted as log2(Fold Change CPM) in a violin plot and the data for candidates were sorted by RT family (FIGS. 5A-5D). The results showed editing activity for gene modifying candidates containing linkers paired with RT sequences from across 17 different retroviral RT families tested in the assay: AVIRE, BAEVM, FFV, FLV, FOAMV, GALV, KORV, MLVAV, MLVBM, MLVCB, MLVFF, MLVMS, PERV, SFV1, SFV3L, WMSV, and XMRV6. In contrast, gene modifying candidates with RT sequences from other RT families tested lacked editing activity or had lower levels of editing activity. Regression analysis showed that editing activity of gene modifying polypeptide candidates was correlated across HEK293T and U2OS conditions (FIG. 6), as well as across templates g4 and g10 (FIG. 7). The overall activity trends of all candidate gene modifying polypeptides showed that editing activity remained consistent across the four conditions tested, suggesting that gene modifying polypeptide editing activity may translate across different cell types and templates.

Data from the four conditions tested were analyzed to select subsets of gene modifying polypeptide candidates displaying consistent and robust evidence of genome editing activity. Namely, selected candidates were required to exhibit an enrichment Z-score of 1 or higher in one or more of the template g4 conditions in HEK293T and U2OS cells (conditions 1 and 2, respectively) and the test template g10 condition in HEK293T cells (condition 3). Data from the test template g10 condition (condition 4) in U2OS cells were omitted from initial analysis. An exemplary selection analysis is depicted graphically in FIG. 14 which displays gene modifying candidates showing high genome editing activity across both cells types for test template g4 and in HEK293T cells for test template g10 in HEK293T cells.

Approximately 3180 gene modifying polypeptide candidates within the library had a Z-score of at least 1 or greater in any one of conditions 1, 2, or 3. These results show that this subset of gene modifying polypeptides had editing activity in at least one condition of the screening assay (FIG. 14, light and dark dots). The subset of these gene modifying polypeptides are encoded by amino acid sequences of any one of the SEQ ID NOs listed in Table D1 below.

Table D1. Gene modifying polypeptide candidates having a Z-score of at least 1 or greater in any one of conditions 1, 2, or 3.

SEQ ID NOs															
1	255	631	964	1208	1551	1803	2028	2324	2563	2781	3001	4524	6434	6879	7296
2	256	636	965	1209	1552	1804	2029	2325	2564	2782	3002	4525	6439	6881	7298
3	257	645	966	1210	1553	1805	2030	2326	2565	2783	3003	4526	6442	6882	7299
4	258	647	967	1211	1555	1806	2031	2327	2566	2784	3005	4527	6443	6883	7301
5	259	648	968	1212	1556	1808	2033	2328	2567	2785	3007	4528	6444	6884	7302
6	261	649	969	1213	1557	1809	2034	2329	2568	2786	3008	4529	6445	6885	7305
7	262	650	970	1214	1558	1810	2035	2330	2569	2787	3009	4530	6449	6886	7306
9	263	651	971	1215	1559	1811	2037	2331	2570	2788	3010	4531	6453	6887	7307
10	264	652	972	1216	1561	1813	2038	2332	2571	2789	3011	4532	6454	6890	7311
13	265	653	973	1217	1563	1816	2039	2333	2572	2790	3012	4533	6457	6891	7312
14	268	656	974	1218	1564	1817	2041	2334	2573	2791	3014	4534	6458	6896	7313
17	269	657	975	1219	1565	1818	2042	2335	2574	2792	3015	4535	6462	6897	7314
19	270	659	976	1220	1566	1819	2045	2336	2575	2793	3016	4536	6465	6898	7317
22	271	661	977	1221	1567	1824	2048	2337	2576	2794	3017	4537	6478	6901	7320
33	273	662	978	1222	1568	1825	2049	2338	2577	2795	3018	4538	6479	6902	7322
34	274	663	979	1223	1570	1827	2050	2339	2578	2796	3019	4539	6480	6904	7323
35	278	664	980	1224	1571	1828	2051	2340	2579	2797	3020	4540	6486	6905	7326
36	279	667	981	1225	1572	1829	2052	2341	2580	2798	3021	4541	6488	6907	7328
37	280	668	982	1226	1573	1831	2053	2342	2581	2799	3022	6001	6491	6908	7329
38	281	670	983	1227	1574	1834	2054	2343	2582	2800	3025	6004	6492	6910	7335
39	283	677	984	1228	1576	1838	2055	2344	2583	2801	3026	6007	6495	6911	7336
40	285	679	985	1229	1577	1840	2056	2345	2584	2802	3027	6008	6497	6915	7339
41	290	687	986	1230	1578	1842	2057	2346	2585	2803	3028	6012	6499	6917	7342
42	293	689	987	1231	1579	1843	2058	2347	2586	2804	3030	6013	6501	6919	7343
43	294	690	988	1232	1580	1844	2060	2348	2587	2805	3031	6014	6502	6923	7345
44	295	694	989	1233	1581	1845	2061	2349	2588	2806	3033	6015	6503	6925	7346
45	298	700	990	1234	1582	1846	2062	2350	2589	2807	3034	6021	6505	6928	7347
46	300	707	991	1235	1583	1847	2069	2351	2590	2808	3035	6022	6511	6930	7349
47	302	711	992	1236	1585	1848	2070	2352	2591	2809	3036	6023	6512	6932	7350
48	303	715	993	1237	1588	1849	2071	2353	2592	2810	3037	6024	6515	6933	7352
49	304	716	994	1238	1590	1850	2074	2354	2593	2811	3038	6025	6520	6942	7357

50	305	717	996	1239	1593	1851	2075	2355	2594	2812	3039	6026	6524	6943	7358
51	306	720	997	1240	1594	1852	2076	2356	2595	2813	3040	6028	6525	6951	7360
52	308	726	999	1241	1597	1853	2081	2357	2596	2814	3041	6029	6527	6952	7361
53	309	727	1000	1242	1598	1855	2082	2358	2597	2815	3042	6030	6529	6963	7362
54	310	728	1002	1243	1600	1856	2084	2359	2598	2816	3043	6031	6530	6966	7364
55	311	729	1003	1245	1604	1857	2086	2360	2599	2817	3044	6036	6531	6968	7368
56	312	731	1004	1246	1605	1858	2089	2361	2600	2818	3045	6043	6532	6969	7369
57	313	738	1005	1247	1606	1859	2090	2362	2601	2819	3046	6045	6533	6972	7370
58	315	739	1006	1248	1607	1860	2091	2363	2603	2820	3047	6048	6535	6978	7371
59	316	745	1007	1250	1608	1861	2092	2364	2604	2821	3048	6051	6540	6980	7372
60	317	765	1008	1251	1610	1862	2093	2365	2605	2822	3049	6054	6542	6982	7374
61	318	766	1009	1252	1611	1863	2094	2366	2606	2823	3050	6056	6549	6984	7377
62	319	767	1010	1253	1612	1864	2095	2367	2608	2824	3051	6057	6551	6990	7378
63	320	768	1011	1254	1616	1865	2096	2368	2610	2825	3052	6058	6552	6993	7381
64	321	769	1012	1255	1617	1866	2103	2369	2611	2826	3053	6059	6555	6998	7383
65	322	770	1013	1256	1618	1867	2104	2370	2612	2827	3054	6061	6558	6999	7384
66	323	771	1014	1257	1619	1868	2105	2371	2613	2828	3055	6063	6559	7001	7387
67	324	772	1015	1258	1620	1869	2108	2372	2614	2829	3056	6067	6561	7006	7388
68	325	773	1016	1259	1621	1870	2111	2373	2615	2830	3057	6068	6563	7009	7389
69	327	774	1017	1261	1622	1871	2112	2374	2616	2831	3058	6071	6565	7013	7393
70	328	775	1018	1262	1623	1872	2113	2375	2617	2832	3059	6072	6567	7015	7394
72	329	776	1019	1263	1625	1873	2114	2376	2618	2833	3060	6073	6568	7023	7396
73	330	780	1020	1264	1626	1874	2115	2377	2619	2834	3061	6074	6572	7024	7397
74	331	782	1021	1265	1627	1875	2117	2378	2620	2835	3062	6079	6575	7025	7402
75	332	783	1022	1266	1628	1876	2121	2379	2621	2836	3063	6080	6577	7026	7403
76	333	784	1023	1267	1629	1877	2122	2380	2622	2837	3064	6084	6578	7027	7404
77	334	789	1024	1269	1630	1878	2123	2381	2623	2838	3065	6089	6579	7030	7412
78	335	797	1025	1270	1631	1879	2125	2382	2624	2839	3066	6091	6580	7031	7415
79	336	798	1026	1272	1632	1880	2126	2383	2625	2840	3067	6093	6581	7033	7416
80	337	799	1027	1274	1633	1881	2128	2384	2626	2841	3070	6094	6582	7034	7417
81	338	800	1028	1275	1634	1882	2130	2385	2627	2842	3071	6096	6583	7035	7418
83	339	801	1029	1278	1635	1883	2132	2386	2628	2843	3072	6099	6584	7036	7419
86	340	802	1030	1279	1636	1884	2136	2387	2629	2844	3073	6103	6585	7037	7430
87	341	803	1031	1280	1638	1885	2137	2388	2630	2845	3074	6106	6587	7038	7431
88	342	804	1032	1282	1639	1886	2138	2389	2631	2846	3075	6107	6591	7043	7433
89	343	805	1033	1288	1641	1887	2141	2390	2632	2847	3076	6108	6594	7045	7434
90	344	806	1034	1290	1642	1888	2143	2391	2633	2848	3077	6112	6595	7046	7435
92	345	807	1035	1295	1644	1889	2144	2392	2634	2849	3078	6115	6596	7047	7436
94	346	808	1036	1298	1645	1890	2145	2393	2635	2850	3079	6117	6598	7048	7441
96	348	809	1037	1299	1646	1891	2147	2394	2636	2851	3080	6121	6600	7051	7443
97	349	810	1038	1301	1647	1892	2148	2395	2637	2852	3081	6123	6601	7055	7444

98	350	811	1039	1302	1648	1893	2149	2396	2638	2853	3082	6130	6602	7056	7445
99	351	812	1040	1305	1649	1894	2150	2397	2639	2854	3083	6133	6603	7058	7448
100	352	813	1041	1308	1651	1895	2152	2398	2640	2855	3084	6136	6606	7060	7449
101	353	814	1042	1311	1653	1896	2153	2399	2641	2856	3085	6139	6607	7064	7450
102	354	815	1043	1312	1656	1897	2154	2400	2642	2857	3086	6142	6608	7065	7453
103	355	816	1044	1314	1657	1898	2155	2401	2643	2858	3087	6144	6610	7067	7455
104	356	817	1045	1315	1658	1899	2156	2402	2644	2859	3088	6147	6611	7068	7458
105	357	818	1046	1320	1659	1900	2158	2403	2645	2860	3089	6148	6612	7070	7461
106	359	819	1047	1322	1661	1901	2159	2404	2646	2861	3090	6150	6615	7071	7466
107	360	820	1048	1324	1662	1902	2161	2405	2647	2862	3091	6151	6616	7072	7469
108	361	821	1049	1326	1663	1903	2162	2406	2648	2865	3092	6152	6617	7074	7471
110	362	822	1050	1327	1664	1905	2163	2407	2649	2866	3093	6155	6621	7075	7472
112	363	824	1051	1328	1665	1906	2164	2408	2650	2867	3094	6163	6622	7077	7473
113	364	825	1052	1338	1666	1907	2165	2409	2651	2868	3096	6165	6624	7078	7474
114	365	826	1053	1340	1667	1908	2166	2410	2652	2869	3097	6168	6627	7079	7476
115	367	827	1054	1342	1668	1909	2167	2411	2653	2870	3098	6171	6630	7080	7488
116	368	828	1055	1347	1669	1910	2170	2413	2654	2871	3099	6172	6635	7081	7489
117	369	829	1056	1348	1670	1911	2172	2414	2656	2872	3101	6176	6639	7082	7496
118	370	830	1057	1349	1671	1912	2173	2417	2657	2873	3102	6180	6642	7085	7497
119	371	831	1058	1350	1672	1913	2174	2418	2658	2874	3103	6185	6644	7087	7499
120	372	832	1059	1354	1673	1914	2175	2422	2659	2875	3104	6188	6645	7088	7500
121	373	833	1060	1359	1674	1915	2176	2423	2660	2877	3107	6190	6646	7089	7501
122	374	834	1061	1366	1675	1916	2177	2425	2661	2878	3108	6191	6648	7091	7508
123	376	835	1062	1369	1676	1917	2178	2426	2662	2879	3109	6193	6650	7096	7509
124	377	836	1063	1370	1677	1918	2179	2431	2663	2881	3110	6196	6651	7098	7511
125	378	837	1065	1371	1678	1920	2182	2436	2664	2882	3111	6197	6652	7100	7515
126	380	839	1066	1372	1679	1921	2184	2438	2665	2884	3112	6201	6654	7103	7519
127	382	840	1067	1373	1680	1922	2185	2440	2666	2885	3113	6204	6655	7105	7520
128	384	841	1068	1374	1681	1923	2186	2441	2667	2886	3114	6205	6656	7110	7523
129	385	842	1069	1375	1682	1924	2191	2442	2668	2887	3115	6207	6659	7115	7525
130	386	843	1070	1376	1683	1925	2192	2443	2669	2888	3116	6208	6665	7116	7526
131	388	844	1071	1377	1684	1926	2193	2444	2670	2889	3117	6211	6666	7120	7527
132	389	845	1072	1378	1685	1927	2195	2445	2671	2890	3118	6216	6668	7121	7530
133	391	846	1073	1379	1686	1929	2196	2446	2672	2891	3119	6218	6671	7122	7531
134	392	847	1074	1380	1687	1931	2197	2447	2673	2892	3120	6219	6672	7123	7536
135	394	849	1075	1381	1688	1932	2198	2448	2674	2893	3121	6223	6674	7125	7537
136	395	852	1076	1382	1689	1934	2201	2449	2675	2894	3122	6227	6675	7127	7538
137	396	853	1077	1383	1690	1935	2202	2450	2676	2895	3123	6234	6676	7128	7539
138	397	854	1078	1384	1691	1936	2205	2451	2677	2896	3124	6236	6680	7129	7540
139	398	856	1079	1385	1693	1937	2206	2452	2679	2897	3125	6240	6681	7131	7541
140	399	860	1080	1386	1694	1938	2207	2453	2680	2898	3126	6243	6683	7135	7543

141	400	861	1081	1387	1695	1939	2213	2454	2681	2900	3127	6244	6684	7136	7545
142	402	862	1082	1388	1696	1940	2214	2455	2682	2901	3128	6247	6685	7138	7547
143	403	863	1083	1389	1697	1941	2219	2456	2683	2902	3129	6248	6686	7140	7549
144	404	866	1084	1390	1698	1942	2224	2457	2684	2903	3130	6250	6688	7141	7550
145	407	867	1085	1391	1699	1943	2225	2458	2685	2904	3131	6253	6690	7142	7555
146	408	868	1086	1392	1700	1944	2226	2459	2687	2905	3133	6254	6692	7143	7556
147	409	871	1087	1393	1701	1945	2227	2460	2688	2906	3134	6257	6693	7144	7558
148	413	872	1088	1394	1702	1946	2228	2461	2689	2907	3135	6258	6695	7147	7565
149	415	873	1089	1395	1703	1947	2229	2462	2690	2908	3136	6263	6698	7148	7566
150	416	874	1090	1396	1704	1948	2230	2463	2692	2909	3138	6264	6705	7150	7567
151	423	875	1091	1397	1705	1949	2231	2464	2693	2910	3139	6265	6706	7151	7568
153	426	876	1092	1398	1706	1950	2232	2465	2695	2911	3144	6266	6708	7153	7569
154	428	877	1093	1399	1707	1951	2233	2468	2696	2912	3146	6267	6709	7154	7570
156	438	878	1094	1400	1708	1952	2234	2469	2697	2913	3149	6268	6710	7157	7574
157	449	879	1095	1401	1709	1953	2235	2470	2700	2914	3152	6269	6713	7158	7576
158	450	880	1097	1402	1710	1954	2236	2471	2701	2915	3154	6271	6715	7160	7578
159	452	881	1103	1403	1711	1955	2238	2472	2702	2916	3155	6272	6716	7163	7580
160	460	882	1115	1404	1712	1956	2239	2474	2703	2917	3157	6273	6717	7164	7582
161	461	883	1116	1405	1713	1957	2240	2477	2706	2918	3167	6275	6718	7167	7585
162	462	884	1117	1406	1714	1958	2241	2478	2708	2919	3169	6278	6719	7169	7587
164	464	885	1118	1407	1715	1959	2242	2480	2709	2920	3171	6281	6724	7170	7588
165	469	886	1120	1408	1716	1960	2244	2488	2710	2921	3172	6284	6726	7171	7589
166	470	887	1121	1409	1717	1961	2245	2489	2711	2922	3173	6285	6728	7172	7590
167	472	888	1123	1410	1718	1962	2246	2490	2712	2923	3176	6286	6730	7174	7591
168	480	889	1126	1411	1719	1963	2247	2497	2713	2925	3177	6287	6731	7175	7593
169	481	890	1131	1412	1720	1964	2248	2498	2714	2926	3180	6289	6732	7176	7594
170	483	891	1136	1413	1721	1965	2249	2503	2715	2927	3181	6290	6733	7180	7597
171	484	892	1137	1414	1722	1966	2250	2504	2716	2928	3184	6292	6736	7181	7599
172	502	893	1138	1415	1723	1967	2251	2505	2717	2929	3190	6293	6738	7184	7600
173	503	894	1139	1416	1725	1968	2252	2506	2718	2930	3196	6294	6744	7186	7606
175	504	895	1140	1417	1726	1969	2253	2507	2719	2931	3198	6300	6746	7187	7607
176	523	896	1141	1418	1729	1970	2254	2508	2720	2932	3199	6304	6751	7188	7610
180	524	897	1142	1419	1735	1971	2255	2509	2721	2933	3208	6305	6754	7189	7612
181	527	898	1143	1420	1736	1972	2256	2510	2722	2934	3214	6307	6756	7191	7613
183	534	899	1144	1421	1738	1973	2257	2511	2723	2935	3233	6309	6757	7192	7615
184	535	900	1145	1422	1739	1974	2259	2512	2724	2936	3247	6310	6758	7193	7617
185	537	901	1146	1423	1741	1975	2260	2513	2725	2937	3248	6311	6760	7194	7621
190	538	902	1147	1424	1742	1976	2261	2514	2726	2938	3251	6312	6761	7197	7625
191	539	903	1148	1425	1743	1977	2262	2515	2727	2939	3252	6313	6762	7198	7629
192	540	904	1149	1426	1747	1978	2263	2516	2728	2940	3253	6317	6765	7203	7632
194	541	905	1150	1427	1751	1979	2264	2517	2729	2941	3254	6318	6770	7204	7633

195	543	906	1151	1429	1752	1980	2265	2518	2730	2942	3256	6322	6772	7205	7634
196	544	907	1152	1430	1753	1981	2266	2519	2731	2943	3259	6323	6773	7206	7635
198	545	908	1153	1431	1754	1982	2268	2520	2732	2945	3260	6324	6776	7207	7636
199	547	909	1154	1432	1755	1983	2270	2521	2733	2947	3261	6325	6777	7209	7638
200	550	910	1155	1433	1756	1984	2271	2522	2734	2948	3262	6327	6778	7214	7644
201	553	911	1156	1434	1757	1985	2273	2523	2735	2950	3263	6328	6783	7215	7646
203	554	912	1157	1435	1758	1986	2275	2524	2736	2951	3264	6329	6784	7216	7649
205	555	913	1158	1436	1759	1987	2276	2525	2737	2953	3266	6339	6785	7217	7650
206	557	914	1159	1439	1760	1988	2277	2526	2738	2954	3268	6340	6786	7218	7651
207	559	915	1160	1440	1761	1989	2278	2527	2739	2955	3269	6343	6788	7222	7652
208	561	916	1161	1441	1762	1990	2279	2528	2740	2957	3270	6344	6793	7226	7653
209	563	917	1163	1442	1764	1991	2280	2529	2741	2959	3272	6346	6794	7227	7654
210	565	918	1164	1444	1765	1992	2282	2530	2742	2960	3277	6349	6795	7228	7656
211	567	919	1165	1446	1766	1993	2286	2531	2743	2962	3286	6351	6796	7240	7657
212	568	920	1166	1447	1767	1994	2287	2532	2744	2965	3302	6356	6797	7242	7658
213	570	921	1167	1449	1768	1995	2288	2533	2745	2966	3303	6363	6798	7243	7659
215	571	922	1168	1452	1769	1996	2291	2534	2746	2967	3305	6364	6801	7244	7660
216	572	923	1169	1455	1770	1997	2292	2535	2747	2970	3310	6367	6802	7246	7662
217	575	924	1170	1456	1771	1998	2294	2536	2748	2971	3313	6370	6808	7247	7663
218	583	925	1171	1460	1772	1999	2295	2537	2749	2972	3315	6377	6809	7250	7665
219	584	926	1172	1471	1773	2000	2299	2538	2750	2973	3316	6378	6811	7251	7667
223	585	927	1173	1497	1774	2001	2300	2539	2751	2974	3326	6381	6815	7252	7668
225	589	928	1174	1499	1775	2002	2301	2540	2752	2975	3329	6384	6816	7253	7670
227	590	929	1176	1504	1776	2003	2302	2541	2755	2976	4501	6387	6823	7255	7674
228	591	931	1177	1505	1777	2004	2303	2542	2756	2977	4502	6389	6826	7258	7675
229	592	933	1178	1506	1778	2005	2304	2543	2757	2979	4503	6394	6827	7261	7676
230	594	934	1179	1507	1779	2006	2305	2544	2758	2980	4505	6395	6832	7262	7677
232	595	936	1181	1508	1780	2007	2306	2545	2760	2981	4506	6402	6834	7263	7679
234	596	937	1184	1519	1781	2008	2307	2546	2761	2982	4507	6403	6841	7264	7681
235	597	938	1185	1521	1783	2009	2308	2547	2762	2983	4508	6407	6842	7267	7682
236	598	939	1186	1523	1784	2011	2309	2548	2764	2984	4509	6409	6845	7273	7685
237	599	944	1187	1527	1785	2012	2310	2549	2765	2985	4510	6410	6850	7274	7694
238	600	945	1190	1529	1786	2013	2311	2550	2766	2986	4511	6412	6852	7275	7695
239	602	946	1193	1539	1787	2014	2312	2551	2767	2987	4512	6415	6855	7276	7698
240	604	948	1197	1540	1788	2015	2313	2552	2768	2988	4513	6417	6859	7280	7702
241	605	950	1198	1541	1789	2017	2314	2553	2769	2989	4514	6418	6861	7281	7706
242	606	951	1199	1542	1790	2018	2315	2554	2772	2990	4515	6419	6864	7282	7707
243	607	952	1200	1543	1792	2019	2316	2555	2773	2991	4516	6421	6866	7284	7714
244	610	957	1201	1544	1793	2020	2317	2556	2774	2992	4517	6423	6870	7286	7717
245	613	958	1202	1545	1794	2021	2318	2557	2775	2993	4518	6424	6872	7288	7719
248	614	959	1203	1546	1795	2022	2319	2558	2776	2994	4519	6425	6873	7290	7723

249	616	960	1204	1547	1796	2023	2320	2559	2777	2995	4520	6426	6874	7291	7724
252	617	961	1205	1548	1799	2024	2321	2560	2778	2997	4521	6427	6876	7292	7728
253	618	962	1206	1549	1801	2025	2322	2561	2779	2998	4522	6429	6877	7293	
254	624	963	1207	1550	1802	2027	2323	2562	2780	2999	4523	6432	6878	7294	

A further analysis identified a subset of approximately 320 gene modifying polypeptide candidates having a Z-score of at least 1 or greater across all of conditions 1, 2, and 3. These results show that this subset of gene modifying polypeptides had editing activity in all analyzed conditions of the screening assay (FIG. 14, magenta colored dots). These include gene modifying polypeptides having amino acid sequences according to any one of the SEQ ID NOs listed in Table D2 below.

Table D2. Gene modifying polypeptide candidates having a Z-score of at least 1 or greater across all of conditions 1, 2, and 3.

SEQ ID NOs						
34	874	1377	1945	2370	2711	3014
35	878	1380	1953	2371	2712	3015
36	882	1381	1961	2449	2713	3018
37	883	1382	1970	2503	2714	3026
38	884	1383	1976	2504	2715	3035
39	890	1384	1992	2505	2718	3039
40	900	1385	2048	2506	2721	3042
41	901	1389	2086	2507	2726	3053
49	912	1390	2091	2508	2734	3059
62	958	1394	2093	2510	2780	3067
97	960	1397	2115	2511	2781	3076
113	963	1400	2144	2512	2782	3079
117	964	1401	2158	2513	2783	3084
121	966	1404	2192	2514	2784	3091
139	987	1405	2225	2515	2787	3093
140	1006	1406	2227	2518	2788	3094
141	1007	1410	2231	2519	2789	3096
142	1008	1540	2299	2521	2790	3108
190	1012	1543	2300	2525	2792	3111
191	1015	1550	2301	2526	2794	3112
192	1016	1616	2302	2527	2795	3116
195	1017	1618	2303	2528	2797	3120
199	1018	1619	2304	2530	2798	3125
212	1019	1666	2305	2534	2800	3126
213	1020	1668	2308	2536	2801	3130
228	1022	1672	2309	2542	2802	

232	1023	1677	2311	2544	2804	
239	1025	1679	2312	2548	2813	
268	1038	1682	2314	2559	2817	
303	1049	1686	2315	2568	2818	
313	1059	1754	2316	2610	2826	
316	1137	1759	2317	2611	2835	
318	1168	1770	2319	2612	2865	
332	1171	1856	2322	2614	2874	
341	1197	1857	2323	2615	2877	
363	1198	1861	2325	2618	2886	
396	1202	1863	2326	2619	2888	
480	1203	1864	2327	2622	2890	
550	1216	1865	2328	2623	2895	
590	1219	1868	2329	2624	2901	
647	1225	1870	2331	2627	2904	
715	1235	1877	2335	2629	2920	
800	1242	1883	2338	2632	2932	
801	1371	1889	2342	2633	2937	
804	1372	1937	2346	2636	2943	
806	1373	1938	2353	2638	2950	
871	1374	1940	2363	2644	2966	
872	1375	1942	2364	2648	2972	
873	1376	1943	2365	2653	2982	

Additional sequencing data were generated for same DNA libraries for the test template g10 condition in HEK293T cells (condition 3) to improve detection sensitivity and confidence in evidence of genome editing activity. This further analysis including the revised dataset for condition 3 identified a subset of approximately 420 gene modifying polypeptide candidates having a Z score of at least 1 or greater across all of conditions 1, 2, and 3. These results show that this subset of gene modifying polypeptides had editing activity in all conditions of the screening assay under this revised analysis. These include gene modifying polypeptides having amino acid sequences according to any one of the SEQ ID NOs listed in Table D3 below.

Table D3. Gene modifying polypeptide candidates having a Z-score of at least 1 or greater across all of conditions 1, 2, or 3.

SEQ ID NOs:						
34	961	1616	2301	2568	2822	4522
35	963	1618	2302	2578	2826	4532
36	964	1619	2303	2585	2833	6312
37	966	1666	2304	2592	2835	6505
38	967	1672	2305	2610	2838	6761

39	978	1679	2308	2611	2840	6925
48	1006	1682	2309	2612	2865	7036
49	1007	1686	2311	2614	2871	7067
62	1008	1690	2312	2615	2874	7397
97	1012	1691	2314	2618	2877	
113	1015	1695	2315	2619	2878	
121	1016	1698	2316	2622	2886	
123	1017	1721	2317	2623	2887	
139	1018	1754	2319	2624	2888	
140	1019	1759	2322	2627	2890	
142	1020	1769	2323	2629	2895	
144	1022	1770	2325	2632	2901	
147	1023	1772	2326	2633	2904	
190	1025	1773	2327	2636	2905	
191	1029	1856	2328	2638	2909	
192	1038	1857	2329	2639	2920	
195	1043	1861	2331	2644	2922	
213	1049	1863	2335	2647	2928	
219	1052	1864	2338	2648	2932	
232	1059	1865	2342	2649	2937	
239	1061	1868	2347	2653	2943	
252	1115	1870	2353	2654	2948	
258	1137	1874	2363	2666	2950	
268	1168	1877	2364	2667	2966	
303	1171	1881	2365	2675	2967	
316	1197	1883	2370	2676	2972	
318	1198	1889	2371	2681	2976	
320	1202	1899	2382	2711	2982	
332	1203	1937	2395	2712	2991	
363	1210	1938	2403	2713	3014	
384	1216	1939	2449	2714	3015	
386	1219	1940	2503	2715	3018	
392	1225	1942	2504	2716	3026	
396	1235	1943	2505	2718	3035	
480	1242	1945	2506	2721	3039	
550	1371	1953	2507	2723	3042	
590	1373	1961	2508	2726	3052	
647	1374	1968	2510	2731	3053	
715	1375	1970	2511	2734	3059	
800	1376	1976	2512	2744	3067	
801	1377	1978	2513	2745	3076	

804	1380	1991	2514	2780	3079	
805	1381	1992	2515	2781	3084	
806	1382	2048	2518	2782	3087	
818	1383	2086	2519	2783	3091	
819	1384	2091	2521	2784	3093	
871	1385	2092	2525	2787	3094	
872	1389	2093	2526	2788	3096	
873	1390	2115	2527	2789	3108	
874	1394	2137	2528	2790	3111	
876	1397	2144	2530	2791	3112	
878	1399	2148	2531	2792	3116	
880	1400	2158	2534	2794	3120	
883	1401	2172	2536	2795	3121	
884	1402	2174	2542	2797	3124	
890	1405	2192	2544	2798	3125	
898	1406	2225	2547	2800	3126	
900	1410	2226	2548	2801	3130	
901	1415	2227	2551	2802	3136	
912	1419	2231	2556	2804	4505	
915	1422	2235	2559	2808	4508	
929	1424	2236	2561	2813	4514	
958	1543	2299	2562	2817	4519	
960	1550	2300	2566	2818	4521	

Approximately 3680 gene modifying polypeptide candidates within the library had a Z-score of at least 1 or greater in any one of conditions 1, 2, or 3 using this further analysis. These results show that this subset of gene modifying polypeptides had editing activity in at least one analyzed condition of the screening assay under this revised analysis. The subset of these gene modifying polypeptides are encoded by amino acid sequences of any one of the SEQ ID NOs listed in Table D4 below.

Table D4. Gene modifying polypeptide candidates having a Z-score of at least 1 or greater in any one of conditions 1, 2, or 3 according to the above further analysis.

SEQ ID NOs:												
1	343	846	1197	1624	1955	2294	2616	2929	4523	6495	7046	7570
2	344	847	1198	1625	1956	2295	2617	2930	4524	6497	7047	7574
3	345	848	1199	1626	1957	2299	2618	2931	4525	6499	7049	7575
4	346	849	1200	1627	1958	2300	2619	2932	4526	6501	7050	7576
5	348	850	1201	1628	1959	2301	2620	2933	4527	6502	7051	7580
6	349	852	1202	1629	1960	2302	2621	2934	4528	6503	7052	7582
7	350	853	1203	1630	1961	2303	2622	2935	4529	6505	7053	7585

9	351	854	1204	1631	1962	2304	2623	2936	4530	6506	7055	7587
10	352	855	1205	1632	1963	2305	2624	2937	4531	6511	7056	7588
12	353	856	1206	1633	1964	2306	2625	2938	4532	6512	7058	7590
13	354	857	1207	1634	1965	2307	2626	2939	4533	6515	7059	7591
14	355	860	1208	1635	1966	2308	2627	2940	4534	6524	7060	7592
17	356	861	1209	1636	1967	2309	2628	2941	4535	6525	7062	7595
18	357	862	1210	1637	1968	2310	2629	2942	4536	6526	7063	7596
19	358	863	1211	1638	1969	2311	2630	2943	4537	6527	7064	7597
22	359	866	1212	1639	1970	2312	2631	2944	4538	6529	7065	7599
24	360	867	1213	1640	1971	2313	2632	2945	4539	6530	7067	7600
28	361	868	1214	1641	1972	2314	2633	2946	4540	6531	7068	7603
33	362	869	1215	1642	1973	2315	2634	2947	4541	6532	7070	7606
34	363	870	1216	1644	1974	2316	2635	2948	6001	6533	7072	7607
35	364	871	1217	1645	1975	2317	2636	2950	6004	6535	7073	7610
36	365	872	1218	1646	1976	2318	2637	2951	6007	6538	7074	7612
37	366	873	1219	1648	1977	2319	2638	2952	6008	6540	7075	7613
38	367	874	1220	1649	1978	2320	2639	2953	6010	6542	7078	7615
39	368	875	1221	1651	1979	2321	2640	2954	6012	6543	7079	7620
40	369	876	1222	1652	1980	2322	2641	2955	6013	6544	7080	7621
41	370	877	1223	1653	1981	2323	2642	2957	6014	6545	7081	7624
42	371	878	1224	1654	1982	2324	2643	2958	6015	6549	7082	7625
43	372	879	1225	1655	1983	2325	2644	2959	6021	6551	7084	7626
44	373	880	1226	1656	1984	2326	2645	2960	6022	6552	7085	7629
45	374	881	1227	1657	1985	2327	2646	2962	6023	6555	7087	7631
46	375	882	1228	1658	1986	2328	2647	2965	6025	6557	7088	7632
47	376	883	1229	1659	1987	2329	2648	2966	6026	6559	7089	7633
48	377	884	1230	1660	1988	2330	2649	2967	6028	6561	7091	7634
49	380	885	1231	1661	1989	2331	2650	2968	6029	6563	7092	7635
50	382	886	1232	1662	1990	2332	2651	2969	6030	6564	7095	7636
51	383	887	1233	1663	1991	2333	2652	2971	6031	6565	7096	7638
52	384	888	1234	1664	1992	2334	2653	2972	6036	6566	7098	7643
53	385	889	1235	1665	1993	2335	2654	2973	6038	6567	7100	7644
54	386	890	1236	1666	1994	2336	2655	2974	6040	6568	7103	7646
55	387	891	1237	1667	1995	2337	2656	2975	6041	6572	7104	7649
56	388	892	1238	1668	1996	2338	2657	2976	6043	6575	7105	7650
57	389	893	1239	1669	1997	2339	2658	2979	6045	6577	7109	7651
58	391	894	1240	1670	1998	2340	2659	2981	6048	6579	7110	7652
59	392	895	1241	1671	1999	2341	2660	2982	6049	6580	7111	7653
60	393	896	1242	1672	2000	2342	2661	2983	6051	6581	7114	7654
61	394	897	1243	1673	2001	2343	2662	2984	6054	6582	7115	7656
62	395	898	1244	1674	2002	2344	2663	2985	6055	6583	7116	7657

63	396	899	1245	1675	2003	2345	2664	2986	6056	6584	7120	7658
64	397	900	1246	1676	2004	2346	2665	2987	6057	6585	7121	7659
65	398	901	1247	1677	2005	2347	2666	2988	6058	6587	7123	7660
66	399	902	1248	1678	2006	2348	2667	2989	6059	6589	7125	7662
67	400	903	1249	1679	2007	2349	2668	2990	6060	6590	7127	7663
68	401	904	1250	1680	2008	2350	2669	2991	6061	6591	7128	7665
69	402	905	1251	1681	2009	2351	2670	2992	6063	6594	7129	7667
70	403	906	1252	1682	2010	2352	2671	2993	6064	6595	7131	7668
71	404	907	1253	1683	2011	2353	2672	2994	6067	6596	7133	7669
72	406	908	1254	1684	2012	2354	2673	2995	6068	6598	7134	7670
73	407	909	1255	1685	2013	2355	2674	2997	6069	6600	7135	7674
74	408	910	1256	1686	2014	2356	2675	2998	6071	6601	7136	7675
75	409	911	1257	1687	2015	2357	2676	2999	6072	6602	7140	7676
76	410	912	1258	1688	2017	2358	2677	3001	6073	6603	7141	7677
77	413	913	1259	1689	2018	2359	2678	3002	6074	6606	7142	7679
78	415	914	1261	1690	2019	2360	2679	3003	6076	6607	7143	7681
79	416	915	1262	1691	2020	2361	2680	3004	6079	6608	7144	7682
80	419	916	1263	1692	2021	2362	2681	3005	6080	6609	7147	7685
81	420	917	1264	1693	2022	2363	2682	3006	6081	6610	7148	7686
82	421	918	1265	1694	2023	2364	2683	3007	6083	6611	7149	7689
83	424	919	1266	1695	2024	2365	2684	3008	6084	6612	7150	7693
85	426	920	1267	1696	2025	2366	2685	3009	6089	6613	7151	7694
86	427	921	1269	1697	2026	2367	2687	3010	6090	6614	7153	7695
87	428	922	1270	1698	2027	2368	2688	3011	6091	6615	7154	7698
88	429	923	1271	1699	2028	2369	2689	3012	6092	6617	7155	7700
89	432	924	1272	1700	2029	2370	2690	3014	6093	6618	7156	7701
90	433	925	1273	1701	2030	2371	2691	3015	6094	6619	7158	7702
91	438	926	1274	1702	2031	2372	2692	3016	6096	6621	7159	7706
92	441	927	1275	1703	2033	2373	2693	3018	6097	6622	7160	7707
94	446	928	1277	1704	2034	2374	2694	3019	6099	6623	7163	7708
95	449	929	1278	1705	2035	2375	2695	3020	6103	6624	7164	7713
96	450	930	1279	1706	2036	2376	2697	3021	6105	6625	7167	7715
97	452	931	1280	1707	2037	2377	2698	3022	6106	6627	7169	7717
98	460	932	1282	1708	2038	2378	2699	3023	6107	6629	7170	7719
99	461	933	1288	1709	2039	2379	2700	3025	6108	6630	7171	7721
100	462	934	1290	1710	2040	2380	2701	3026	6112	6632	7172	7722
101	464	936	1295	1711	2041	2381	2702	3027	6115	6635	7174	7723
102	465	937	1296	1712	2042	2382	2703	3028	6117	6639	7175	7724
103	469	938	1298	1713	2043	2383	2704	3029	6121	6642	7176	7726
104	470	939	1299	1714	2044	2384	2708	3030	6122	6644	7180	7727
105	472	940	1301	1715	2045	2385	2709	3031	6123	6645	7181	7729

106	475	942	1302	1716	2046	2386	2710	3033	6129	6646	7184	7730
107	476	943	1304	1717	2047	2387	2711	3034	6130	6648	7186	7731
108	480	944	1305	1718	2048	2388	2712	3035	6133	6650	7187	7732
110	481	945	1308	1719	2049	2389	2713	3036	6136	6651	7188	7737
112	483	946	1311	1720	2050	2390	2714	3037	6138	6652	7191	7740
113	484	948	1312	1721	2051	2391	2715	3038	6139	6654	7192	7741
114	486	950	1314	1722	2052	2392	2716	3039	6142	6655	7194	
115	488	951	1315	1723	2053	2393	2717	3040	6143	6656	7196	
116	489	952	1320	1725	2054	2394	2718	3041	6144	6659	7197	
117	495	957	1322	1726	2055	2395	2719	3042	6147	6664	7198	
118	502	958	1324	1728	2056	2396	2720	3043	6148	6665	7201	
119	503	959	1326	1729	2057	2397	2721	3044	6150	6666	7203	
120	504	960	1327	1730	2058	2398	2722	3045	6151	6671	7204	
121	510	961	1328	1731	2059	2399	2723	3046	6152	6674	7206	
122	517	962	1329	1733	2060	2400	2724	3047	6153	6675	7209	
123	522	963	1338	1734	2061	2401	2725	3048	6155	6676	7212	
124	523	964	1340	1735	2062	2402	2726	3049	6158	6679	7214	
125	524	965	1342	1736	2063	2403	2727	3050	6160	6680	7215	
126	527	966	1346	1737	2064	2404	2728	3051	6164	6681	7216	
127	534	967	1347	1738	2066	2405	2729	3052	6165	6683	7217	
128	535	968	1348	1739	2069	2406	2730	3053	6168	6684	7218	
129	536	969	1349	1741	2070	2407	2731	3054	6169	6685	7220	
130	537	970	1350	1742	2071	2408	2732	3055	6171	6686	7221	
131	538	971	1351	1743	2072	2409	2733	3056	6172	6687	7222	
132	539	972	1354	1744	2074	2410	2734	3057	6173	6688	7226	
133	540	973	1359	1745	2075	2411	2735	3058	6174	6690	7227	
134	541	974	1362	1747	2076	2412	2736	3059	6175	6691	7228	
135	542	975	1365	1748	2079	2413	2737	3060	6176	6692	7230	
136	543	976	1366	1750	2080	2414	2738	3061	6177	6693	7232	
137	544	977	1369	1751	2081	2415	2739	3062	6178	6695	7236	
138	545	978	1370	1752	2082	2416	2740	3063	6179	6698	7240	
139	546	979	1371	1753	2084	2417	2741	3064	6180	6705	7242	
140	547	980	1372	1754	2086	2418	2742	3065	6181	6706	7243	
141	548	981	1373	1755	2089	2419	2743	3066	6182	6708	7244	
142	549	982	1374	1756	2090	2420	2744	3067	6184	6709	7246	
143	550	983	1375	1757	2091	2422	2745	3070	6185	6713	7247	
144	553	984	1376	1758	2092	2423	2746	3071	6188	6715	7250	
145	554	985	1377	1759	2093	2424	2747	3072	6189	6716	7251	
146	555	986	1378	1760	2094	2425	2748	3073	6190	6717	7252	
147	556	987	1379	1761	2095	2426	2750	3074	6191	6718	7253	
148	557	988	1380	1762	2096	2427	2751	3075	6193	6719	7255	

149	558	989	1381	1764	2097	2431	2752	3076	6196	6720	7258	
150	559	990	1382	1765	2098	2436	2753	3077	6197	6722	7260	
151	560	991	1383	1766	2099	2438	2754	3078	6200	6724	7261	
153	561	992	1384	1767	2100	2440	2755	3079	6201	6726	7262	
154	562	993	1385	1769	2101	2441	2756	3080	6203	6728	7263	
155	563	994	1386	1770	2102	2442	2757	3081	6204	6730	7264	
156	565	996	1387	1771	2103	2443	2758	3082	6205	6731	7266	
157	566	997	1388	1772	2104	2444	2759	3083	6207	6732	7267	
158	567	999	1389	1773	2105	2445	2760	3084	6208	6733	7273	
159	568	1000	1390	1774	2106	2446	2761	3085	6215	6736	7274	
160	570	1001	1391	1775	2107	2447	2762	3086	6216	6738	7275	
161	571	1003	1392	1776	2108	2448	2763	3087	6218	6744	7276	
162	572	1004	1393	1777	2109	2449	2764	3088	6219	6746	7281	
163	575	1006	1394	1778	2111	2450	2765	3089	6223	6750	7282	
164	581	1007	1395	1779	2112	2451	2766	3090	6227	6751	7284	
165	583	1008	1396	1780	2113	2452	2767	3091	6234	6754	7286	
166	584	1009	1397	1781	2114	2453	2768	3092	6235	6756	7288	
167	585	1010	1398	1782	2115	2454	2769	3093	6236	6757	7291	
168	587	1011	1399	1783	2116	2455	2771	3094	6237	6758	7292	
169	589	1012	1400	1784	2117	2456	2772	3096	6240	6760	7293	
170	590	1013	1401	1785	2118	2457	2773	3097	6244	6761	7294	
171	591	1014	1402	1786	2119	2458	2774	3098	6247	6762	7297	
172	592	1015	1403	1787	2120	2459	2775	3099	6248	6765	7298	
173	593	1016	1404	1788	2121	2460	2776	3100	6250	6772	7299	
174	594	1017	1405	1789	2122	2461	2778	3101	6253	6773	7301	
175	595	1018	1406	1790	2123	2462	2779	3102	6254	6774	7302	
176	596	1019	1407	1792	2125	2463	2780	3103	6255	6776	7303	
178	597	1020	1408	1793	2126	2464	2781	3104	6257	6777	7305	
179	598	1021	1409	1794	2128	2465	2782	3107	6258	6778	7306	
180	599	1022	1410	1795	2129	2466	2783	3108	6263	6782	7307	
181	600	1023	1411	1796	2130	2467	2784	3109	6264	6783	7311	
182	601	1024	1412	1797	2132	2468	2785	3110	6265	6784	7312	
183	602	1025	1413	1799	2133	2469	2786	3111	6266	6785	7313	
184	604	1026	1414	1800	2135	2470	2787	3112	6267	6786	7317	
185	605	1027	1415	1801	2136	2471	2788	3113	6268	6788	7320	
186	606	1028	1416	1802	2137	2472	2789	3114	6269	6792	7322	
187	607	1029	1417	1803	2138	2473	2790	3115	6271	6793	7323	
188	610	1030	1418	1804	2140	2474	2791	3116	6272	6794	7326	
190	611	1031	1419	1805	2141	2476	2792	3117	6273	6795	7327	
191	614	1032	1420	1806	2142	2477	2793	3118	6275	6796	7328	
192	616	1033	1421	1808	2143	2478	2794	3119	6277	6797	7329	

194	617	1034	1422	1809	2144	2479	2795	3120	6278	6798	7331	
195	618	1035	1423	1810	2145	2480	2796	3121	6279	6800	7335	
196	624	1036	1424	1811	2146	2481	2797	3122	6280	6801	7336	
197	625	1037	1425	1812	2147	2482	2798	3123	6281	6802	7339	
198	628	1038	1426	1813	2148	2483	2799	3124	6282	6803	7342	
199	631	1039	1427	1815	2149	2484	2800	3125	6284	6808	7343	
200	633	1040	1428	1816	2150	2485	2801	3126	6285	6809	7345	
201	634	1041	1429	1818	2151	2488	2802	3127	6286	6811	7346	
203	636	1042	1430	1819	2152	2489	2803	3128	6287	6815	7347	
204	645	1043	1431	1824	2153	2490	2804	3129	6288	6822	7348	
205	647	1044	1432	1825	2154	2491	2805	3130	6290	6824	7349	
206	648	1045	1433	1827	2155	2492	2806	3131	6292	6826	7350	
207	649	1046	1434	1828	2156	2497	2807	3133	6293	6827	7352	
208	650	1047	1435	1829	2158	2498	2808	3134	6294	6829	7357	
209	652	1048	1436	1831	2159	2501	2809	3135	6298	6832	7358	
210	653	1049	1437	1834	2161	2502	2810	3136	6299	6833	7360	
211	654	1050	1439	1835	2162	2503	2811	3138	6304	6834	7361	
212	655	1051	1440	1838	2163	2504	2812	3139	6305	6835	7362	
213	656	1052	1441	1840	2164	2505	2813	3141	6307	6837	7364	
214	657	1053	1442	1842	2165	2506	2814	3142	6308	6841	7368	
215	659	1054	1443	1843	2166	2507	2815	3144	6309	6842	7369	
216	661	1055	1444	1844	2167	2508	2816	3146	6310	6845	7370	
217	662	1056	1445	1845	2168	2509	2817	3152	6311	6850	7371	
218	663	1057	1446	1846	2170	2510	2818	3153	6312	6852	7372	
219	664	1058	1447	1847	2171	2511	2819	3154	6313	6855	7374	
220	666	1059	1449	1848	2172	2512	2820	3155	6314	6857	7375	
222	667	1060	1450	1849	2173	2513	2821	3157	6315	6858	7377	
223	668	1061	1451	1850	2174	2514	2822	3162	6317	6859	7378	
225	669	1062	1452	1851	2175	2515	2823	3166	6319	6861	7379	
226	670	1063	1455	1852	2176	2516	2824	3167	6320	6863	7380	
227	673	1064	1456	1853	2177	2517	2825	3169	6322	6864	7381	
228	677	1065	1460	1855	2178	2518	2826	3171	6324	6865	7384	
229	678	1066	1462	1856	2179	2519	2827	3172	6325	6866	7387	
230	679	1067	1471	1857	2180	2520	2828	3173	6327	6867	7388	
232	680	1068	1473	1858	2182	2521	2829	3175	6328	6868	7389	
234	681	1069	1475	1859	2183	2522	2830	3176	6329	6869	7390	
235	687	1070	1488	1860	2184	2523	2831	3177	6334	6870	7392	
236	689	1071	1489	1861	2185	2524	2832	3180	6335	6872	7393	
237	690	1072	1491	1862	2186	2525	2833	3181	6339	6873	7394	
238	692	1073	1492	1863	2188	2526	2834	3183	6340	6874	7396	
239	694	1074	1493	1864	2189	2527	2835	3184	6343	6876	7397	

240	700	1075	1497	1865	2190	2528	2836	3188	6344	6877	7400	
241	702	1076	1499	1866	2191	2529	2837	3190	6345	6878	7402	
242	706	1077	1504	1867	2192	2530	2838	3196	6347	6879	7403	
243	711	1078	1505	1868	2193	2531	2839	3198	6349	6881	7404	
244	715	1079	1506	1869	2194	2532	2840	3199	6350	6882	7412	
245	716	1080	1507	1870	2195	2533	2841	3201	6351	6883	7413	
248	717	1081	1508	1871	2196	2534	2842	3202	6352	6885	7415	
249	720	1082	1510	1872	2197	2535	2843	3203	6353	6886	7416	
251	724	1083	1513	1873	2198	2536	2844	3204	6355	6890	7417	
252	726	1084	1515	1874	2199	2537	2845	3205	6356	6891	7418	
253	727	1085	1519	1875	2200	2538	2846	3206	6358	6892	7419	
254	729	1086	1521	1876	2201	2539	2847	3207	6359	6894	7424	
255	731	1087	1523	1877	2202	2540	2848	3208	6360	6896	7430	
256	738	1088	1524	1878	2204	2541	2849	3209	6363	6897	7431	
257	739	1089	1527	1879	2205	2542	2850	3211	6364	6898	7433	
258	740	1090	1529	1880	2206	2543	2851	3213	6366	6902	7434	
259	745	1091	1531	1881	2207	2544	2852	3214	6367	6906	7435	
261	747	1092	1539	1882	2210	2545	2853	3219	6370	6907	7436	
262	755	1093	1540	1883	2211	2546	2854	3220	6374	6908	7441	
263	756	1094	1541	1884	2212	2547	2855	3223	6377	6910	7442	
264	759	1095	1542	1885	2213	2548	2856	3225	6378	6911	7443	
265	765	1097	1543	1886	2214	2549	2857	3228	6380	6915	7444	
268	766	1103	1544	1887	2218	2550	2858	3233	6381	6917	7445	
269	767	1110	1545	1888	2219	2551	2859	3235	6384	6919	7448	
270	768	1115	1546	1889	2222	2552	2860	3240	6389	6920	7449	
271	769	1116	1547	1890	2223	2553	2861	3247	6390	6923	7450	
272	770	1117	1548	1891	2224	2554	2862	3248	6393	6925	7452	
273	771	1118	1549	1892	2225	2555	2864	3251	6394	6928	7453	
274	772	1119	1550	1893	2226	2556	2865	3252	6395	6930	7455	
275	773	1120	1551	1894	2227	2557	2866	3253	6396	6931	7458	
276	774	1121	1552	1895	2228	2558	2867	3254	6397	6932	7461	
277	775	1122	1553	1896	2229	2559	2868	3256	6402	6933	7466	
278	776	1124	1554	1897	2230	2560	2869	3259	6403	6934	7469	
279	780	1126	1555	1898	2231	2561	2870	3260	6407	6939	7471	
280	782	1131	1556	1899	2232	2562	2871	3261	6409	6942	7472	
281	783	1134	1557	1900	2233	2563	2872	3262	6410	6943	7473	
283	784	1136	1558	1901	2234	2564	2873	3263	6411	6944	7474	
284	789	1137	1559	1902	2235	2565	2874	3264	6412	6948	7476	
285	790	1138	1560	1903	2236	2566	2875	3266	6415	6950	7477	
286	797	1139	1561	1904	2237	2567	2876	3268	6417	6951	7479	
287	798	1140	1563	1905	2238	2568	2877	3269	6418	6952	7483	

290	799	1141	1564	1906	2239	2569	2878	3270	6419	6954	7485	
293	800	1142	1565	1907	2240	2570	2880	3272	6420	6961	7488	
294	801	1143	1566	1908	2241	2571	2881	3276	6421	6965	7489	
295	802	1144	1567	1909	2242	2572	2882	3277	6423	6966	7493	
296	803	1145	1568	1910	2244	2573	2884	3279	6424	6968	7496	
297	804	1146	1570	1911	2245	2574	2885	3282	6425	6969	7497	
298	805	1147	1571	1912	2246	2575	2886	3283	6426	6972	7499	
300	806	1148	1572	1913	2247	2576	2887	3286	6427	6974	7500	
301	807	1149	1573	1914	2248	2577	2888	3294	6431	6978	7501	
302	808	1150	1574	1915	2249	2578	2889	3296	6432	6979	7502	
303	809	1151	1575	1916	2250	2579	2890	3298	6433	6980	7507	
304	810	1152	1576	1917	2251	2580	2891	3300	6434	6982	7508	
305	811	1153	1577	1918	2252	2581	2892	3302	6435	6984	7509	
306	812	1154	1578	1920	2253	2582	2893	3303	6439	6985	7510	
308	813	1155	1579	1921	2254	2583	2894	3305	6440	6990	7511	
309	814	1156	1580	1922	2255	2584	2895	3306	6441	6993	7513	
310	815	1157	1581	1923	2256	2585	2896	3310	6442	6998	7515	
312	816	1158	1582	1924	2257	2586	2897	3313	6443	6999	7516	
313	817	1159	1583	1925	2259	2587	2898	3315	6444	7001	7518	
315	818	1160	1584	1926	2260	2588	2900	3316	6445	7003	7519	
316	819	1161	1585	1927	2261	2589	2901	3318	6449	7005	7520	
317	820	1162	1588	1928	2262	2590	2903	3323	6451	7006	7523	
318	821	1163	1590	1929	2263	2591	2904	3326	6453	7008	7525	
319	822	1164	1592	1931	2264	2592	2905	3329	6454	7009	7526	
320	823	1165	1593	1932	2265	2593	2906	4501	6455	7012	7529	
321	824	1166	1594	1934	2266	2594	2907	4502	6456	7013	7530	
322	825	1167	1597	1935	2268	2595	2908	4503	6457	7014	7532	
323	826	1168	1598	1936	2270	2596	2909	4504	6458	7015	7536	
324	827	1169	1599	1937	2271	2597	2910	4505	6459	7017	7537	
325	828	1170	1600	1938	2272	2598	2911	4506	6460	7021	7538	
327	829	1171	1604	1939	2273	2599	2912	4507	6461	7023	7540	
328	830	1172	1605	1940	2274	2600	2913	4508	6462	7024	7541	
329	831	1173	1606	1941	2275	2601	2914	4509	6465	7025	7545	
330	832	1174	1607	1942	2276	2602	2915	4510	6467	7026	7547	
331	833	1176	1608	1943	2277	2603	2916	4511	6469	7027	7548	
332	834	1177	1610	1944	2278	2604	2917	4512	6474	7030	7549	
333	835	1178	1611	1945	2279	2605	2918	4513	6476	7031	7550	
334	836	1181	1612	1946	2280	2606	2919	4514	6477	7033	7555	
335	837	1182	1616	1947	2281	2607	2920	4515	6478	7034	7556	
336	839	1184	1617	1948	2282	2608	2921	4516	6479	7035	7558	
337	840	1185	1618	1949	2286	2610	2922	4517	6480	7036	7560	

338	841	1186	1619	1950	2287	2611	2923	4518	6486	7037	7562	
339	842	1187	1620	1951	2288	2612	2925	4519	6488	7038	7565	
340	843	1188	1621	1952	2289	2613	2926	4520	6491	7040	7566	
341	844	1190	1622	1953	2291	2614	2927	4521	6492	7043	7567	
342	845	1193	1623	1954	2293	2615	2928	4522	6493	7045	7569	

Sequencing libraries were re-generated for the original DNA extracted from the test template g10 in U2OS cells (condition 4) and yielded a new dataset amenable to integration into the analyses of genome editing activity. The expanded analysis identified a subset of approximately 200 gene modifying polypeptide candidates having a Z-score of at least 1 or greater across all of conditions 1, 2, 3, and 4. These results show that this subset of gene modifying polypeptides had editing activity in all conditions of the screening assay under this revised analysis. These include gene modifying polypeptides having amino acid sequences according to any one of the SEQ ID NOs listed in Table D5 below.

Table D5. Gene modifying polypeptide candidates having a Z-score of at least 1 or greater in all of conditions 1, 2, 3, and 4.

SEQ ID NOs						
34	1012	1415	2309	2515	2675	2928
36	1016	1419	2314	2519	2681	2932
37	1017	1422	2316	2526	2731	2937
39	1018	1666	2319	2536	2780	2943
123	1019	1686	2322	2542	2782	2948
140	1022	1690	2325	2544	2784	2950
142	1023	1691	2326	2551	2787	3053
190	1029	1863	2327	2556	2789	3059
192	1038	1870	2328	2566	2791	3067
232	1052	1937	2329	2578	2800	3076
252	1059	1939	2331	2585	2801	3093
303	1061	1940	2338	2592	2802	3108
316	1137	1942	2342	2610	2804	3111
332	1198	1953	2347	2611	2813	3116
386	1210	1961	2353	2612	2817	3120
647	1225	1968	2363	2615	2826	3121
800	1242	1970	2364	2618	2833	3124
804	1371	1976	2365	2623	2835	3126
876	1374	1978	2371	2624	2838	3130
878	1375	2048	2382	2627	2865	4514
880	1376	2086	2395	2629	2874	4519
884	1382	2093	2403	2632	2877	4522
901	1383	2137	2449	2633	2887	6761

915	1384	2172	2504	2636	2888	6925
929	1385	2174	2505	2638	2890	7067
961	1390	2300	2508	2639	2901	
964	1394	2301	2510	2644	2904	
967	1397	2302	2511	2647	2909	
1006	1400	2303	2512	2666	2922	

Approximately 4030 gene modifying polypeptide candidates within the library had a Z-score of at least 1 or greater in any one of conditions 1, 2, 3, or 4 using this further analysis. These results show that this subset of gene modifying polypeptides had editing activity in at least one analyzed condition of the screening assay under this revised analysis. The subset of these gene modifying polypeptides are encoded by amino acid sequences of any one of the SEQ ID NOs listed in Table D6 below.

Table D6. Gene modifying polypeptide candidates having a Z-score of at least 1 or greater in any one of conditions 1, 2, 3, or 4.

SEQ ID NOs:									
1	486	1065	1642	2097	2560	2994	6192	6784	7361
2	488	1066	1644	2098	2561	2995	6193	6785	7362
3	489	1067	1645	2099	2562	2997	6195	6786	7364
4	495	1068	1646	2100	2563	2998	6196	6787	7368
5	499	1069	1648	2101	2564	2999	6197	6788	7369
6	502	1070	1649	2102	2565	3001	6200	6791	7370
7	503	1071	1651	2103	2566	3002	6201	6792	7371
9	504	1072	1652	2104	2567	3003	6203	6793	7372
10	510	1073	1653	2105	2568	3004	6204	6794	7374
12	517	1074	1654	2106	2569	3005	6205	6795	7375
13	522	1075	1655	2107	2570	3006	6206	6796	7377
14	523	1076	1656	2108	2571	3007	6207	6797	7378
17	524	1077	1657	2109	2572	3008	6208	6798	7379
18	527	1078	1658	2110	2573	3009	6210	6799	7380
19	532	1079	1659	2111	2574	3010	6212	6800	7381
22	534	1080	1660	2112	2575	3011	6213	6801	7382
24	535	1081	1661	2113	2576	3012	6214	6802	7384
28	536	1082	1662	2114	2577	3013	6215	6803	7386
33	537	1083	1663	2115	2578	3014	6216	6804	7387
34	538	1084	1664	2116	2579	3015	6217	6805	7388
35	539	1085	1665	2117	2580	3016	6218	6806	7389
36	540	1086	1666	2118	2581	3018	6219	6807	7390
37	541	1087	1667	2119	2582	3019	6222	6808	7391
38	542	1088	1668	2120	2583	3020	6223	6809	7392

39	543	1089	1669	2121	2584	3021	6226	6810	7393
40	544	1090	1670	2122	2585	3022	6227	6811	7394
41	545	1091	1671	2123	2586	3023	6229	6814	7396
42	546	1092	1672	2125	2587	3025	6234	6815	7397
43	547	1093	1673	2126	2588	3026	6235	6820	7398
44	548	1094	1674	2127	2589	3027	6236	6822	7400
45	549	1095	1675	2128	2590	3028	6237	6824	7402
46	550	1097	1676	2129	2591	3029	6239	6826	7403
47	553	1103	1677	2130	2592	3030	6240	6827	7404
48	554	1110	1678	2132	2593	3031	6241	6829	7406
49	555	1115	1679	2133	2594	3032	6243	6830	7409
50	556	1116	1680	2134	2595	3033	6244	6832	7412
51	557	1117	1681	2135	2596	3034	6245	6833	7413
52	558	1118	1682	2136	2597	3035	6247	6834	7414
53	559	1119	1683	2137	2598	3036	6248	6835	7415
54	560	1120	1684	2138	2599	3037	6249	6836	7416
55	561	1121	1685	2139	2600	3038	6250	6837	7417
56	562	1122	1686	2140	2601	3039	6253	6838	7418
57	563	1124	1687	2141	2602	3040	6254	6841	7419
58	564	1126	1688	2142	2603	3041	6255	6842	7420
59	565	1131	1689	2143	2604	3042	6257	6843	7424
60	566	1134	1690	2144	2605	3043	6258	6844	7426
61	567	1136	1691	2145	2606	3044	6261	6845	7427
62	568	1137	1692	2146	2607	3045	6263	6846	7428
63	570	1138	1693	2147	2608	3046	6264	6847	7430
64	571	1139	1694	2148	2610	3047	6265	6848	7431
65	572	1140	1695	2149	2611	3048	6266	6849	7432
66	575	1141	1696	2150	2612	3049	6267	6850	7433
67	581	1142	1697	2151	2613	3050	6268	6851	7434
68	583	1143	1698	2152	2614	3051	6269	6852	7435
69	584	1144	1699	2153	2615	3052	6271	6853	7436
70	585	1145	1700	2154	2616	3053	6272	6854	7438
71	587	1146	1701	2155	2617	3054	6273	6855	7441
72	589	1147	1702	2156	2618	3055	6275	6857	7442
73	590	1148	1703	2158	2619	3056	6277	6858	7443
74	591	1149	1704	2159	2620	3057	6278	6859	7444
75	592	1150	1705	2161	2621	3058	6279	6860	7445
76	593	1151	1706	2162	2622	3059	6280	6861	7446
77	594	1152	1707	2163	2623	3060	6281	6863	7448
78	595	1153	1708	2164	2624	3061	6282	6864	7449
79	596	1154	1709	2165	2625	3062	6284	6865	7450

80	597	1155	1710	2166	2626	3063	6285	6866	7451
81	598	1156	1711	2167	2627	3064	6286	6867	7452
82	599	1157	1712	2168	2628	3065	6287	6868	7453
83	600	1158	1713	2170	2629	3066	6288	6869	7455
84	601	1159	1714	2171	2630	3067	6290	6870	7457
85	602	1160	1715	2172	2631	3068	6292	6871	7458
86	604	1161	1716	2173	2632	3070	6293	6872	7461
87	605	1162	1717	2174	2633	3071	6294	6873	7462
88	606	1163	1718	2175	2634	3072	6295	6874	7464
89	607	1164	1719	2176	2635	3073	6298	6876	7466
90	610	1165	1720	2177	2636	3074	6299	6877	7467
91	611	1166	1721	2178	2637	3075	6302	6878	7469
92	614	1167	1722	2179	2638	3076	6304	6879	7470
94	616	1168	1723	2180	2639	3077	6305	6880	7471
95	617	1169	1724	2181	2640	3078	6306	6881	7472
96	618	1170	1725	2182	2641	3079	6307	6882	7473
97	624	1171	1726	2183	2642	3080	6308	6883	7474
98	625	1172	1728	2184	2643	3081	6309	6885	7475
99	626	1173	1729	2185	2644	3082	6310	6886	7476
100	628	1174	1730	2186	2645	3083	6311	6890	7477
101	631	1176	1731	2188	2646	3084	6312	6891	7479
102	632	1177	1733	2189	2647	3085	6313	6892	7483
103	633	1178	1734	2190	2648	3086	6314	6893	7484
104	634	1181	1735	2191	2649	3087	6315	6894	7485
105	636	1182	1736	2192	2650	3088	6316	6895	7488
106	640	1184	1737	2193	2651	3089	6317	6896	7489
107	645	1185	1738	2194	2652	3090	6319	6897	7491
108	647	1186	1739	2195	2653	3091	6320	6898	7492
110	648	1187	1740	2196	2654	3092	6321	6899	7493
112	649	1188	1741	2197	2655	3093	6322	6900	7494
113	650	1190	1742	2198	2656	3094	6324	6902	7495
114	652	1193	1743	2199	2657	3095	6325	6903	7496
115	653	1197	1744	2200	2658	3096	6326	6906	7497
116	654	1198	1745	2201	2659	3097	6327	6907	7499
117	655	1199	1747	2202	2660	3098	6328	6908	7500
118	656	1200	1748	2203	2661	3099	6329	6910	7501
119	657	1201	1750	2204	2662	3100	6331	6911	7502
120	659	1202	1751	2205	2663	3101	6334	6913	7503
121	660	1203	1752	2206	2664	3102	6335	6915	7505
122	661	1204	1753	2207	2665	3103	6336	6917	7507
123	662	1205	1754	2210	2666	3104	6337	6918	7508

124	663	1206	1755	2211	2667	3105	6338	6919	7509
125	664	1207	1756	2212	2668	3106	6339	6920	7510
126	666	1208	1757	2213	2669	3107	6340	6921	7511
127	667	1209	1758	2214	2670	3108	6343	6923	7512
128	668	1210	1759	2218	2671	3109	6344	6924	7513
129	669	1211	1760	2219	2672	3110	6345	6925	7514
130	670	1212	1761	2222	2673	3111	6347	6928	7515
131	673	1213	1762	2223	2674	3112	6349	6929	7516
132	677	1214	1764	2224	2675	3113	6350	6930	7517
133	678	1215	1765	2225	2676	3114	6351	6931	7518
134	679	1216	1766	2226	2677	3115	6352	6932	7519
135	680	1217	1767	2227	2678	3116	6353	6933	7520
136	681	1218	1769	2228	2679	3117	6355	6934	7521
137	684	1219	1770	2229	2680	3118	6356	6939	7523
138	687	1220	1771	2230	2681	3119	6357	6942	7525
139	689	1221	1772	2231	2682	3120	6358	6943	7526
140	690	1222	1773	2232	2683	3121	6359	6944	7528
141	692	1223	1774	2233	2684	3122	6360	6947	7529
142	694	1224	1775	2234	2685	3123	6363	6948	7530
143	700	1225	1776	2235	2686	3124	6364	6950	7532
144	702	1226	1777	2236	2687	3125	6366	6951	7534
145	706	1227	1778	2237	2688	3126	6367	6952	7535
146	711	1228	1779	2238	2689	3127	6368	6953	7536
147	715	1229	1780	2239	2690	3128	6369	6954	7537
148	716	1230	1781	2240	2691	3129	6370	6957	7538
149	717	1231	1782	2241	2692	3130	6372	6961	7540
150	719	1232	1783	2242	2693	3131	6374	6962	7541
151	720	1233	1784	2244	2694	3132	6377	6965	7542
152	724	1234	1785	2245	2695	3133	6378	6966	7545
153	726	1235	1786	2246	2696	3134	6379	6968	7547
154	727	1236	1787	2247	2697	3135	6380	6969	7548
155	729	1237	1788	2248	2698	3136	6381	6970	7549
156	731	1238	1789	2249	2699	3138	6383	6971	7550
157	738	1239	1790	2250	2700	3139	6384	6972	7555
158	739	1240	1792	2251	2701	3141	6385	6973	7556
159	740	1241	1793	2252	2702	3142	6389	6974	7558
160	745	1242	1794	2253	2703	3144	6390	6976	7560
161	747	1243	1795	2254	2704	3146	6393	6978	7561
162	755	1244	1796	2255	2708	3147	6394	6979	7562
163	756	1245	1797	2256	2709	3152	6395	6980	7563
164	759	1246	1799	2257	2710	3153	6396	6982	7564

165	765	1247	1800	2259	2711	3154	6397	6984	7565
166	766	1248	1801	2260	2712	3155	6398	6985	7566
167	767	1249	1802	2261	2713	3157	6399	6989	7567
168	768	1250	1803	2262	2714	3162	6400	6990	7568
169	769	1251	1804	2263	2715	3163	6401	6993	7569
170	770	1252	1805	2264	2716	3166	6402	6996	7570
171	771	1253	1806	2265	2717	3167	6403	6998	7574
172	772	1254	1808	2266	2718	3169	6404	6999	7575
173	773	1255	1809	2268	2719	3171	6406	7001	7576
174	774	1256	1810	2270	2720	3172	6407	7002	7579
175	775	1257	1811	2271	2721	3173	6409	7003	7580
176	776	1258	1812	2272	2722	3175	6410	7004	7581
177	780	1259	1813	2273	2723	3176	6411	7005	7582
178	781	1261	1815	2274	2724	3177	6412	7006	7585
179	782	1262	1816	2275	2725	3180	6415	7007	7586
180	783	1263	1818	2276	2726	3181	6417	7008	7587
181	784	1264	1819	2277	2727	3183	6418	7009	7588
182	785	1265	1824	2278	2728	3184	6419	7012	7590
183	789	1266	1825	2279	2729	3188	6420	7013	7591
184	790	1267	1827	2280	2730	3190	6421	7014	7592
185	794	1268	1828	2281	2731	3196	6423	7015	7595
186	797	1269	1829	2282	2732	3198	6424	7016	7596
187	798	1270	1831	2286	2733	3199	6425	7017	7597
188	799	1271	1832	2287	2734	3201	6426	7020	7599
190	800	1272	1834	2288	2735	3202	6427	7021	7600
191	801	1273	1835	2289	2736	3203	6431	7023	7603
192	802	1274	1838	2291	2737	3204	6432	7024	7606
193	803	1275	1840	2293	2738	3205	6433	7025	7607
194	804	1276	1842	2294	2739	3206	6434	7026	7610
195	805	1277	1843	2295	2740	3207	6435	7027	7612
196	806	1278	1844	2299	2741	3208	6437	7028	7613
197	807	1279	1845	2300	2742	3209	6439	7030	7615
198	808	1280	1846	2301	2743	3211	6440	7031	7620
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200	810	1288	1848	2303	2745	3214	6442	7033	7622
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202	812	1295	1850	2305	2747	3219	6444	7035	7625
203	813	1296	1851	2306	2748	3220	6445	7036	7626
204	814	1298	1852	2307	2750	3223	6446	7037	7627
205	815	1299	1853	2308	2751	3225	6448	7038	7628
206	816	1301	1855	2309	2752	3228	6449	7040	7629

207	817	1302	1856	2310	2753	3233	6451	7043	7631
208	818	1304	1857	2311	2754	3234	6453	7045	7632
209	819	1305	1858	2312	2755	3235	6454	7046	7633
210	820	1308	1859	2313	2756	3240	6455	7047	7634
211	821	1311	1860	2314	2757	3247	6456	7049	7635
212	822	1312	1861	2315	2758	3248	6457	7050	7636
213	823	1314	1862	2316	2759	3251	6458	7051	7638
214	824	1315	1863	2317	2760	3252	6459	7052	7643
215	825	1320	1864	2318	2761	3253	6460	7053	7644
216	826	1322	1865	2319	2762	3254	6461	7054	7645
217	827	1324	1866	2320	2763	3256	6462	7055	7646
218	828	1326	1867	2321	2764	3259	6463	7056	7649
219	829	1327	1868	2322	2765	3260	6465	7058	7650
220	830	1328	1869	2323	2766	3261	6467	7059	7651
221	831	1329	1870	2324	2767	3262	6469	7060	7652
222	832	1338	1871	2325	2768	3263	6473	7062	7653
223	833	1340	1872	2326	2769	3264	6474	7063	7654
224	834	1342	1873	2327	2770	3265	6475	7064	7656
225	835	1346	1874	2328	2771	3266	6476	7065	7657
226	836	1347	1875	2329	2772	3268	6477	7067	7658
227	837	1348	1876	2330	2773	3269	6478	7068	7659
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229	840	1350	1878	2332	2775	3272	6480	7072	7662
230	841	1351	1879	2333	2776	3276	6484	7073	7663
231	842	1354	1880	2334	2778	3277	6486	7074	7665
232	843	1357	1881	2335	2779	3279	6488	7075	7666
233	844	1359	1882	2336	2780	3282	6490	7077	7667
234	845	1362	1883	2337	2781	3283	6491	7078	7668
235	846	1365	1884	2338	2782	3286	6492	7079	7669
236	847	1366	1885	2339	2783	3294	6493	7080	7670
237	848	1369	1886	2340	2784	3296	6495	7081	7674
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239	850	1371	1888	2342	2786	3299	6497	7083	7676
240	852	1372	1889	2343	2787	3300	6499	7084	7677
241	853	1373	1890	2344	2788	3302	6501	7085	7678
242	854	1374	1891	2345	2789	3303	6502	7087	7679
243	855	1375	1892	2346	2790	3305	6503	7088	7681
244	856	1376	1893	2347	2791	3306	6505	7089	7682
245	857	1377	1894	2348	2792	3310	6506	7090	7685
246	860	1378	1895	2349	2793	3313	6507	7091	7686
247	861	1379	1896	2350	2794	3315	6509	7092	7689

248	862	1380	1897	2351	2795	3316	6510	7093	7693
249	863	1381	1898	2352	2796	3318	6511	7095	7694
250	866	1382	1899	2353	2797	3323	6512	7096	7695
251	867	1383	1900	2354	2798	3326	6515	7097	7698
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253	869	1385	1902	2356	2800	4501	6524	7099	7701
254	870	1386	1903	2357	2801	4502	6525	7100	7702
255	871	1387	1904	2358	2802	4503	6526	7103	7705
256	872	1388	1905	2359	2803	4504	6527	7104	7706
257	873	1389	1906	2360	2804	4505	6529	7105	7707
258	874	1390	1907	2361	2805	4506	6530	7106	7708
259	875	1391	1908	2362	2806	4507	6531	7109	7713
261	876	1392	1909	2363	2807	4508	6532	7110	7715
262	877	1393	1910	2364	2808	4509	6533	7111	7717
263	878	1394	1911	2365	2809	4510	6535	7112	7718
264	879	1395	1912	2366	2810	4511	6538	7114	7719
265	880	1396	1913	2367	2811	4512	6540	7115	7720
266	881	1397	1914	2368	2812	4513	6541	7116	7721
267	882	1398	1915	2369	2813	4514	6542	7118	7722
268	883	1399	1916	2370	2814	4515	6543	7119	7723
269	884	1400	1917	2371	2815	4516	6544	7120	7724
270	885	1401	1918	2372	2816	4517	6545	7121	7726
271	886	1402	1919	2373	2817	4518	6547	7123	7727
272	887	1403	1920	2374	2818	4519	6548	7125	7728
273	888	1404	1921	2375	2819	4520	6549	7127	7729
274	889	1405	1922	2376	2820	4521	6551	7128	7730
275	890	1406	1923	2377	2821	4522	6552	7129	7731
276	891	1407	1924	2378	2822	4523	6554	7131	7732
277	892	1408	1925	2379	2823	4524	6555	7133	7733
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283	897	1413	1931	2384	2828	4529	6564	7141	7739
284	898	1414	1932	2385	2829	4530	6565	7142	7740
285	899	1415	1933	2386	2830	4531	6566	7143	7741
286	900	1416	1934	2387	2831	4532	6567	7144	
287	901	1417	1935	2388	2832	4533	6568	7147	
290	902	1418	1936	2389	2833	4534	6569	7148	
293	903	1419	1937	2390	2834	4535	6572	7149	
294	904	1420	1938	2391	2835	4536	6573	7150	

295	905	1421	1939	2392	2836	4537	6575	7151	
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298	908	1424	1942	2395	2839	4540	6580	7154	
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305	915	1431	1949	2402	2846	6010	6587	7162	
306	916	1432	1950	2403	2847	6011	6588	7163	
307	917	1433	1951	2404	2848	6012	6589	7164	
308	918	1434	1952	2405	2849	6013	6590	7166	
309	919	1435	1953	2406	2850	6014	6591	7167	
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313	922	1439	1956	2409	2853	6018	6595	7170	
314	923	1440	1957	2410	2854	6019	6596	7171	
315	924	1441	1958	2411	2855	6021	6597	7172	
316	925	1442	1959	2412	2856	6022	6598	7174	
317	926	1443	1960	2413	2857	6023	6599	7175	
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323	932	1449	1966	2419	2863	6030	6606	7183	
324	933	1450	1967	2420	2864	6031	6607	7184	
325	934	1451	1968	2422	2865	6033	6608	7186	
326	936	1452	1969	2423	2866	6035	6609	7187	
327	937	1455	1970	2424	2867	6036	6610	7188	
328	938	1456	1971	2425	2868	6038	6611	7191	
329	939	1460	1972	2426	2869	6040	6612	7192	
330	940	1462	1973	2427	2870	6041	6613	7194	
331	941	1471	1974	2431	2871	6043	6614	7195	
332	942	1473	1975	2436	2872	6045	6615	7196	
333	943	1475	1976	2438	2873	6046	6617	7197	
334	944	1488	1977	2440	2874	6048	6618	7198	
335	945	1489	1978	2441	2875	6049	6619	7201	
336	946	1491	1979	2442	2876	6050	6621	7203	

337	948	1492	1980	2443	2877	6051	6622	7204	
338	950	1493	1981	2444	2878	6054	6623	7206	
339	951	1497	1982	2445	2880	6055	6624	7208	
340	952	1499	1983	2446	2881	6056	6625	7209	
341	957	1504	1984	2447	2882	6057	6627	7210	
342	958	1505	1985	2448	2884	6058	6628	7212	
343	959	1506	1986	2449	2885	6059	6629	7214	
344	960	1507	1987	2450	2886	6060	6630	7215	
345	961	1508	1988	2451	2887	6061	6632	7216	
346	962	1510	1989	2452	2888	6063	6635	7217	
347	963	1513	1990	2453	2889	6064	6637	7218	
348	964	1515	1991	2454	2890	6066	6639	7220	
349	965	1519	1992	2455	2891	6067	6642	7221	
350	966	1521	1993	2456	2892	6068	6644	7222	
351	967	1523	1994	2457	2893	6069	6645	7223	
352	968	1524	1995	2458	2894	6071	6646	7226	
353	969	1527	1996	2459	2895	6072	6648	7227	
354	970	1529	1997	2460	2896	6073	6650	7228	
355	971	1531	1998	2461	2897	6074	6651	7230	
356	972	1539	1999	2462	2898	6075	6652	7231	
357	973	1540	2000	2463	2899	6076	6654	7232	
358	974	1541	2001	2464	2900	6079	6655	7233	
359	975	1542	2002	2465	2901	6080	6656	7235	
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362	978	1545	2005	2468	2904	6083	6664	7238	
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365	981	1548	2008	2471	2907	6088	6669	7242	
366	982	1549	2009	2472	2908	6089	6671	7243	
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368	984	1551	2011	2474	2910	6091	6674	7246	
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370	986	1553	2013	2477	2912	6093	6676	7250	
371	987	1554	2014	2478	2913	6094	6679	7251	
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373	989	1556	2016	2480	2915	6097	6681	7253	
374	990	1557	2017	2481	2916	6099	6683	7255	
375	991	1558	2018	2482	2917	6101	6684	7258	
376	992	1559	2019	2483	2918	6102	6685	7260	
377	993	1560	2020	2484	2919	6103	6686	7261	

379	994	1561	2021	2485	2920	6105	6687	7262	
380	996	1563	2022	2488	2921	6106	6688	7263	
381	997	1564	2023	2489	2922	6107	6689	7264	
382	999	1565	2024	2490	2923	6108	6690	7265	
383	1000	1566	2025	2491	2924	6109	6691	7266	
384	1001	1567	2026	2492	2925	6110	6692	7267	
385	1003	1568	2027	2497	2926	6112	6693	7270	
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389	1008	1573	2031	2503	2930	6118	6703	7276	
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392	1011	1576	2034	2506	2933	6123	6708	7282	
393	1012	1577	2035	2507	2934	6124	6709	7284	
394	1013	1578	2036	2508	2935	6125	6713	7286	
395	1014	1579	2037	2509	2936	6129	6715	7288	
396	1015	1580	2038	2510	2937	6130	6716	7289	
397	1016	1581	2039	2511	2938	6131	6717	7291	
398	1017	1582	2040	2512	2939	6133	6718	7292	
399	1018	1583	2041	2513	2940	6136	6719	7293	
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416	1032	1605	2055	2527	2954	6153	6739	7312	
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441	1045	1622	2071	2540	2972	6172	6757	7335	
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446	1047	1624	2074	2542	2974	6174	6760	7337	
449	1048	1625	2075	2543	2975	6175	6761	7339	
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464	1054	1631	2084	2549	2983	6181	6773	7346	
465	1055	1632	2085	2550	2984	6182	6774	7347	
469	1056	1633	2086	2551	2985	6183	6775	7348	
470	1057	1634	2089	2552	2986	6184	6776	7349	
472	1058	1635	2090	2553	2987	6185	6777	7350	
475	1059	1636	2091	2554	2988	6186	6778	7351	
476	1060	1637	2092	2555	2989	6187	6779	7352	
480	1061	1638	2093	2556	2990	6188	6780	7354	
481	1062	1639	2094	2557	2991	6189	6781	7357	
483	1063	1640	2095	2558	2992	6190	6782	7358	
484	1064	1641	2096	2559	2993	6191	6783	7360	

To characterize the reproducibility of the selected candidates without cell-type and test template confounders, two additional full experimental replicates were executed for the test template g4 condition in HEK293T cells (herein conditions 1b and 1c; original condition 1 hereafter became condition 1a) following the same experimental procedures detailed above. The analysis of the three condition 1 replicates identified a subset of approximately 260 gene modifying polypeptide candidates having a Z-score of at least 1 or greater across all of replicates 1a, 1b, and 1c. These results show that this subset of gene modifying polypeptides had reproducible editing activity in all condition 1 replicates of the screening assay under this revised analysis. These include gene modifying polypeptides having amino acid sequences according to any one of the SEQ ID NOs listed in Table D7 below.

Table D7. Gene modifying polypeptide candidates having a Z-score of at least 1 or greater across all of replicates 1a, 1b, and 1c.

SEQ ID NOs						
156	1376	2320	2678	2927	4511	6760
300	1401	2324	2700	2929	4512	6761
317	1423	2327	2701	2930	4513	6783
346	1441	2329	2711	2933	4514	6788
352	1553	2331	2712	2937	4515	6876
591	1860	2332	2737	2953	4516	6883
647	1863	2333	2741	2957	4517	6998
801	1867	2338	2748	2972	4518	7067
871	1871	2343	2760	2983	4520	7103
898	1874	2345	2772	2995	4522	7121
933	1875	2359	2780	3007	4523	7142
1007	1876	2360	2781	3039	4524	7154
1008	1939	2370	2784	3044	4525	7242
1009	1943	2382	2786	3045	4526	7262
1011	1949	2400	2787	3057	4527	7267
1018	1951	2405	2788	3063	4528	7293
1021	1967	2510	2790	3065	4529	7335
1029	2060	2514	2791	3067	4530	7443
1033	2086	2527	2795	3076	4531	7476
1034	2092	2529	2797	3079	4533	7496
1037	2094	2535	2800	3083	4534	7509
1039	2104	2536	2810	3084	4535	7555
1044	2112	2539	2815	3085	4536	7587
1046	2114	2550	2820	3093	4537	7588
1047	2117	2553	2823	3096	4538	7660
1052	2132	2573	2825	3099	4539	7667
1056	2145	2583	2826	3103	4540	
1059	2148	2599	2830	3107	4541	
1060	2149	2610	2835	3111	6030	
1076	2161	2615	2836	3123	6073	
1083	2165	2620	2850	4501	6091	
1093	2172	2631	2880	4502	6181	
1197	2174	2634	2881	4503	6402	
1198	2196	2636	2888	4504	6434	
1219	2249	2644	2893	4506	6505	
1242	2280	2654	2903	4507	6567	
1262	2301	2656	2913	4508	6568	
1372	2311	2657	2914	4509	6591	
1373	2313	2660	2916	4510	6738	

Approximately 3070 gene modifying polypeptide candidates within the library had a Z-score of at least 1 or greater in any one of conditions 1a, 1b, or 1c using this further analysis. These results show that this subset of gene modifying polypeptides had editing activity in at least one replicate of condition 1 of the screening assay under this revised analysis. The subset of these gene modifying polypeptides are encoded by amino acid sequences of any one of the SEQ ID NOs listed in Table D8 below.

Table D8. Gene modifying polypeptide candidates having a Z-score of at least 1 or greater in any one of conditions 1a, 1b, or 1c.

SEQ ID NOs										
1	731	1242	1882	2326	2690	3059	6301	6729	7174	7620
34	746	1243	1883	2327	2691	3060	6303	6730	7176	7621
35	765	1244	1884	2328	2692	3061	6304	6731	7178	7623
36	770	1245	1885	2329	2695	3062	6305	6732	7179	7625
37	772	1246	1886	2330	2697	3063	6307	6733	7180	7626
38	777	1247	1887	2331	2699	3064	6308	6734	7182	7627
39	780	1250	1889	2332	2700	3065	6310	6735	7183	7629
40	799	1253	1890	2333	2701	3066	6311	6737	7184	7630
45	800	1254	1891	2334	2702	3067	6312	6738	7185	7632
46	801	1255	1892	2335	2703	3068	6313	6742	7186	7633
47	802	1256	1893	2336	2711	3069	6314	6744	7187	7634
48	803	1257	1894	2337	2712	3070	6315	6746	7190	7635
49	804	1258	1896	2338	2713	3071	6316	6748	7191	7636
50	805	1259	1898	2339	2714	3072	6317	6749	7192	7637
51	806	1260	1899	2340	2715	3073	6320	6751	7194	7638
52	807	1261	1900	2341	2716	3074	6322	6752	7195	7639
55	808	1262	1901	2342	2717	3075	6324	6753	7196	7640
56	809	1263	1903	2343	2718	3076	6325	6754	7197	7641
57	811	1264	1905	2344	2719	3077	6327	6755	7198	7642
59	812	1265	1906	2345	2720	3078	6328	6758	7199	7643
61	813	1266	1907	2346	2721	3079	6329	6759	7200	7644
62	814	1267	1908	2347	2722	3080	6330	6760	7201	7646
63	817	1268	1909	2348	2723	3081	6332	6761	7202	7647
64	818	1269	1912	2349	2724	3082	6333	6763	7203	7648
65	819	1270	1913	2350	2726	3083	6336	6765	7204	7649
67	820	1272	1915	2351	2727	3084	6339	6766	7206	7650
68	821	1273	1916	2352	2728	3085	6340	6767	7209	7651
69	824	1274	1917	2353	2729	3086	6341	6768	7211	7653
70	825	1276	1918	2354	2730	3087	6342	6769	7212	7654

71	827	1278	1920	2355	2731	3088	6343	6772	7213	7655
72	828	1279	1921	2356	2732	3090	6344	6773	7216	7656
76	829	1281	1922	2357	2734	3091	6348	6774	7219	7658
78	830	1288	1923	2358	2736	3093	6349	6776	7222	7660
79	833	1298	1924	2359	2737	3094	6351	6777	7224	7661
81	834	1311	1925	2360	2739	3095	6352	6778	7225	7662
83	835	1319	1926	2361	2740	3096	6354	6780	7226	7664
85	836	1330	1927	2362	2741	3097	6355	6781	7227	7665
86	837	1343	1929	2363	2742	3098	6356	6782	7229	7666
88	839	1346	1932	2364	2743	3099	6357	6783	7230	7667
89	843	1348	1934	2365	2744	3100	6359	6784	7232	7670
90	844	1353	1935	2366	2745	3101	6360	6785	7234	7671
93	847	1354	1936	2367	2746	3102	6361	6786	7235	7672
94	848	1370	1937	2368	2747	3103	6362	6788	7240	7673
96	849	1371	1938	2369	2748	3104	6363	6789	7241	7675
97	850	1372	1939	2370	2750	3105	6364	6790	7242	7676
100	851	1373	1940	2371	2751	3106	6365	6793	7244	7678
103	852	1374	1941	2372	2753	3107	6366	6796	7245	7679
106	853	1375	1942	2373	2754	3108	6367	6797	7246	7680
108	854	1376	1943	2374	2755	3109	6368	6798	7248	7682
110	861	1377	1944	2375	2758	3110	6370	6801	7249	7683
111	862	1379	1945	2376	2760	3111	6371	6802	7250	7684
114	863	1380	1946	2377	2761	3112	6372	6803	7253	7687
115	866	1381	1947	2378	2764	3113	6373	6804	7254	7688
116	867	1383	1948	2379	2768	3114	6374	6808	7256	7689
117	870	1384	1949	2380	2769	3116	6375	6809	7257	7690
118	871	1385	1950	2381	2772	3117	6376	6810	7258	7691
119	872	1386	1951	2382	2773	3118	6377	6811	7259	7692
120	873	1387	1952	2383	2775	3119	6380	6812	7260	7693
121	874	1388	1953	2384	2776	3120	6381	6813	7261	7694
122	876	1389	1954	2385	2777	3121	6382	6815	7262	7695
123	877	1390	1955	2386	2780	3122	6383	6816	7263	7696
124	878	1391	1956	2387	2781	3123	6385	6817	7264	7697
125	879	1393	1957	2388	2782	3124	6386	6818	7266	7698
126	880	1394	1958	2389	2783	3125	6387	6819	7267	7699
127	881	1395	1959	2390	2784	3126	6388	6820	7268	7701
130	883	1396	1960	2391	2785	3127	6390	6821	7269	7702
131	884	1397	1961	2392	2786	3128	6391	6822	7271	7703
134	885	1398	1962	2393	2787	3129	6392	6825	7272	7704
137	886	1399	1964	2394	2788	3130	6394	6828	7273	7706
138	887	1400	1965	2395	2789	3131	6395	6829	7274	7707

139	888	1401	1966	2396	2790	3133	6402	6831	7275	7709
143	890	1402	1967	2397	2791	3134	6405	6833	7276	7710
144	891	1403	1968	2398	2792	3135	6407	6835	7277	7711
145	892	1404	1969	2399	2793	3136	6408	6837	7279	7712
146	893	1405	1970	2400	2794	3194	6409	6839	7281	7716
147	894	1406	1972	2401	2795	3231	6410	6840	7282	7717
150	897	1408	1973	2402	2796	3317	6412	6844	7283	7719
153	898	1409	1974	2403	2797	4501	6413	6845	7284	7725
154	899	1410	1975	2404	2798	4502	6414	6846	7285	7728
156	900	1411	1976	2405	2799	4503	6416	6847	7286	7730
157	901	1412	1977	2406	2800	4504	6417	6850	7287	7736
158	902	1414	1978	2407	2801	4505	6419	6852	7291	7740
159	903	1415	1979	2408	2802	4506	6421	6855	7292	7742
160	905	1416	1980	2409	2803	4507	6422	6856	7293	7743
161	907	1417	1981	2410	2804	4508	6424	6858	7294	
162	908	1418	1982	2412	2805	4509	6425	6859	7295	
163	909	1419	1983	2413	2806	4510	6426	6861	7298	
164	910	1420	1984	2414	2807	4511	6428	6862	7299	
165	912	1422	1985	2415	2808	4512	6429	6863	7300	
167	914	1423	1986	2416	2809	4513	6430	6864	7301	
168	915	1424	1987	2440	2810	4514	6431	6866	7302	
170	916	1425	1988	2443	2811	4515	6432	6867	7303	
171	917	1426	1989	2444	2812	4516	6434	6868	7305	
172	918	1427	1990	2447	2813	4517	6436	6869	7306	
174	919	1428	1991	2448	2814	4518	6438	6870	7308	
176	920	1430	1992	2449	2815	4519	6439	6872	7309	
177	921	1433	1993	2451	2816	4520	6440	6874	7310	
180	922	1434	1994	2452	2817	4521	6441	6875	7311	
181	923	1437	1995	2453	2818	4522	6443	6876	7312	
182	924	1439	1996	2454	2820	4523	6444	6878	7313	
184	925	1440	1998	2455	2821	4524	6445	6883	7316	
190	928	1441	1999	2456	2822	4525	6447	6885	7317	
191	929	1442	2000	2457	2823	4526	6450	6886	7318	
192	933	1443	2002	2458	2824	4527	6452	6888	7319	
195	934	1444	2003	2459	2825	4528	6455	6889	7320	
196	935	1445	2004	2460	2826	4529	6458	6890	7321	
199	936	1446	2006	2461	2827	4530	6464	6891	7322	
200	938	1447	2009	2462	2828	4531	6465	6892	7323	
203	940	1448	2010	2465	2829	4532	6466	6896	7324	
204	942	1454	2011	2466	2830	4533	6467	6897	7325	
206	943	1460	2012	2467	2831	4534	6468	6898	7326	

208	944	1465	2013	2469	2832	4535	6469	6902	7329	
209	946	1469	2014	2470	2833	4536	6470	6906	7330	
210	947	1475	2016	2471	2834	4537	6471	6908	7333	
213	948	1504	2017	2480	2835	4538	6472	6909	7334	
215	951	1542	2018	2481	2836	4539	6476	6910	7335	
216	959	1543	2020	2483	2837	4540	6477	6911	7336	
217	960	1544	2023	2485	2838	4541	6478	6912	7338	
218	961	1546	2024	2486	2839	6001	6479	6914	7339	
219	962	1547	2025	2488	2840	6002	6480	6915	7341	
220	963	1549	2027	2489	2841	6003	6481	6916	7342	
222	964	1550	2028	2496	2842	6005	6482	6919	7343	
223	965	1552	2029	2502	2843	6008	6483	6920	7345	
224	966	1553	2030	2503	2844	6009	6485	6922	7346	
225	967	1556	2031	2504	2845	6010	6486	6923	7348	
226	968	1565	2033	2505	2846	6012	6487	6924	7349	
227	969	1566	2034	2506	2847	6013	6488	6925	7351	
229	970	1567	2035	2507	2848	6014	6489	6926	7352	
231	971	1568	2036	2508	2849	6016	6491	6927	7353	
232	972	1570	2037	2509	2850	6020	6493	6928	7355	
234	975	1573	2041	2510	2851	6022	6494	6930	7356	
236	976	1576	2043	2511	2852	6027	6498	6931	7357	
237	977	1577	2045	2512	2853	6028	6499	6933	7358	
238	978	1579	2047	2513	2854	6029	6500	6935	7359	
239	979	1580	2048	2514	2856	6030	6501	6936	7360	
240	980	1584	2050	2515	2857	6032	6502	6937	7363	
241	981	1585	2051	2516	2858	6034	6503	6938	7364	
248	982	1588	2052	2517	2859	6036	6504	6939	7365	
252	983	1590	2055	2518	2860	6037	6505	6940	7366	
253	985	1593	2060	2519	2861	6038	6508	6941	7367	
254	986	1595	2071	2520	2862	6039	6509	6942	7368	
255	987	1596	2072	2521	2863	6041	6511	6943	7369	
257	988	1599	2084	2522	2864	6042	6512	6945	7370	
258	989	1616	2086	2523	2865	6043	6513	6946	7371	
259	990	1617	2087	2524	2866	6044	6514	6948	7372	
260	993	1618	2088	2525	2867	6045	6515	6949	7373	
261	994	1619	2089	2526	2868	6047	6516	6952	7376	
262	995	1620	2091	2527	2869	6048	6517	6954	7378	
265	996	1621	2092	2528	2870	6049	6518	6955	7381	
266	998	1622	2093	2529	2871	6052	6519	6956	7384	
267	999	1625	2094	2530	2872	6053	6521	6957	7385	
268	1001	1628	2096	2531	2873	6054	6522	6958	7387	

269	1002	1629	2100	2532	2874	6057	6523	6959	7389	
270	1003	1632	2101	2533	2875	6059	6524	6960	7393	
271	1005	1633	2102	2534	2877	6062	6525	6961	7394	
272	1006	1634	2103	2535	2878	6063	6526	6963	7395	
273	1007	1635	2104	2536	2880	6065	6527	6964	7397	
283	1008	1636	2107	2537	2881	6067	6528	6966	7399	
284	1009	1638	2108	2538	2882	6070	6530	6967	7400	
286	1010	1639	2109	2539	2883	6071	6531	6968	7401	
287	1011	1640	2111	2540	2884	6073	6532	6969	7402	
288	1012	1644	2112	2541	2885	6074	6534	6973	7403	
292	1014	1646	2114	2542	2886	6077	6536	6975	7405	
295	1015	1652	2115	2543	2887	6078	6537	6977	7407	
297	1016	1655	2116	2544	2888	6079	6539	6979	7408	
298	1017	1659	2117	2545	2890	6082	6540	6980	7410	
300	1018	1660	2121	2546	2891	6083	6542	6981	7411	
301	1019	1662	2124	2547	2893	6084	6543	6982	7412	
302	1020	1663	2125	2548	2894	6086	6546	6983	7416	
304	1021	1664	2126	2549	2895	6087	6549	6985	7417	
305	1022	1665	2128	2550	2896	6091	6550	6986	7418	
306	1023	1666	2131	2551	2897	6093	6551	6987	7421	
307	1024	1667	2132	2552	2898	6095	6552	6988	7422	
309	1025	1669	2133	2553	2899	6097	6553	6989	7423	
310	1027	1670	2135	2554	2900	6098	6555	6990	7424	
312	1028	1671	2136	2555	2901	6100	6556	6991	7425	
313	1029	1672	2137	2556	2903	6104	6558	6992	7429	
314	1030	1673	2142	2557	2904	6105	6559	6993	7430	
315	1031	1675	2143	2558	2905	6106	6560	6994	7433	
317	1032	1679	2144	2559	2906	6108	6561	6995	7435	
318	1033	1680	2145	2560	2907	6111	6562	6997	7436	
319	1034	1681	2146	2561	2908	6113	6564	6998	7437	
320	1035	1682	2147	2562	2909	6114	6566	7000	7439	
321	1037	1686	2148	2563	2911	6115	6567	7003	7440	
322	1038	1687	2149	2564	2912	6117	6568	7005	7443	
323	1039	1688	2153	2565	2913	6118	6570	7008	7444	
324	1040	1689	2157	2566	2914	6119	6571	7009	7447	
326	1041	1690	2158	2567	2916	6120	6572	7010	7453	
328	1042	1691	2159	2568	2917	6121	6574	7011	7454	
329	1043	1694	2160	2569	2918	6123	6575	7012	7456	
330	1044	1695	2161	2570	2919	6126	6576	7013	7459	
331	1045	1698	2165	2571	2920	6127	6578	7014	7460	
332	1046	1699	2166	2572	2921	6128	6579	7015	7462	

334	1047	1700	2167	2573	2922	6129	6581	7017	7463	
335	1049	1701	2168	2574	2924	6130	6582	7018	7465	
336	1050	1702	2169	2575	2925	6132	6584	7019	7468	
337	1051	1704	2171	2576	2926	6133	6585	7022	7469	
339	1052	1705	2172	2577	2927	6134	6587	7023	7470	
343	1053	1706	2174	2578	2928	6135	6588	7024	7473	
344	1054	1707	2175	2579	2929	6141	6591	7029	7474	
345	1055	1708	2176	2580	2930	6142	6592	7031	7476	
346	1056	1709	2177	2582	2931	6143	6594	7032	7477	
347	1057	1711	2178	2583	2932	6144	6595	7033	7478	
348	1058	1713	2179	2584	2933	6145	6599	7036	7480	
350	1059	1714	2180	2585	2935	6146	6601	7038	7481	
351	1060	1716	2187	2586	2936	6147	6603	7039	7482	
352	1061	1717	2189	2587	2937	6148	6604	7041	7485	
354	1062	1719	2192	2588	2938	6149	6607	7042	7486	
355	1063	1720	2193	2589	2940	6150	6609	7044	7487	
356	1064	1721	2194	2590	2942	6151	6610	7045	7488	
357	1065	1722	2196	2591	2943	6152	6613	7046	7490	
360	1066	1724	2199	2592	2944	6155	6615	7047	7493	
361	1068	1726	2201	2593	2945	6156	6617	7050	7496	
362	1069	1727	2204	2594	2948	6161	6618	7051	7497	
363	1070	1733	2208	2595	2949	6162	6619	7054	7498	
364	1071	1734	2209	2596	2950	6166	6620	7055	7499	
366	1072	1735	2213	2598	2951	6169	6621	7057	7500	
368	1074	1736	2214	2599	2952	6170	6622	7058	7504	
369	1075	1737	2215	2600	2953	6171	6623	7059	7506	
370	1076	1738	2220	2601	2954	6175	6624	7060	7507	
372	1077	1740	2222	2602	2955	6176	6625	7061	7508	
374	1078	1741	2223	2603	2957	6177	6626	7062	7509	
375	1079	1742	2224	2605	2965	6180	6627	7064	7510	
376	1080	1743	2225	2606	2966	6181	6630	7065	7513	
377	1081	1744	2226	2607	2967	6182	6631	7066	7516	
382	1082	1746	2227	2608	2969	6183	6632	7067	7519	
384	1083	1747	2228	2610	2970	6189	6633	7068	7520	
386	1084	1748	2230	2611	2971	6190	6634	7069	7522	
388	1085	1751	2231	2612	2972	6194	6636	7070	7523	
389	1086	1752	2232	2614	2973	6196	6638	7072	7524	
390	1088	1754	2233	2615	2974	6198	6639	7073	7525	
391	1089	1756	2235	2616	2975	6199	6640	7075	7526	
392	1091	1759	2236	2617	2976	6200	6641	7076	7530	
393	1092	1764	2237	2618	2977	6202	6642	7079	7531	

394	1093	1765	2239	2619	2978	6203	6643	7080	7532	
395	1096	1767	2241	2620	2981	6205	6644	7082	7533	
397	1115	1768	2243	2621	2982	6206	6645	7084	7535	
398	1116	1769	2244	2622	2983	6208	6646	7085	7536	
399	1118	1770	2245	2623	2984	6209	6647	7086	7537	
403	1127	1771	2246	2624	2985	6211	6648	7087	7538	
404	1129	1772	2247	2625	2987	6213	6649	7088	7541	
405	1137	1773	2248	2626	2989	6216	6650	7089	7544	
406	1138	1774	2249	2627	2990	6219	6651	7091	7545	
407	1143	1777	2250	2628	2991	6220	6652	7092	7546	
413	1145	1778	2252	2629	2992	6221	6653	7093	7547	
460	1150	1780	2253	2630	2994	6224	6654	7094	7548	
474	1154	1781	2255	2631	2995	6225	6657	7095	7550	
480	1155	1782	2256	2632	2996	6228	6658	7096	7551	
489	1156	1785	2257	2633	2997	6229	6659	7100	7552	
498	1157	1786	2260	2634	2998	6230	6660	7101	7553	
517	1159	1789	2261	2635	2999	6231	6662	7102	7554	
519	1161	1790	2262	2636	3002	6232	6663	7103	7555	
524	1163	1791	2263	2637	3005	6233	6664	7104	7556	
528	1164	1793	2265	2638	3006	6234	6666	7105	7557	
534	1168	1794	2266	2639	3007	6235	6667	7106	7558	
536	1169	1796	2270	2640	3008	6237	6670	7107	7559	
541	1170	1799	2271	2641	3009	6238	6673	7108	7560	
550	1171	1800	2272	2642	3010	6242	6674	7110	7562	
555	1172	1801	2273	2643	3011	6246	6675	7111	7567	
556	1176	1802	2275	2644	3012	6247	6676	7113	7569	
564	1193	1804	2276	2645	3013	6248	6677	7117	7570	
568	1195	1805	2278	2646	3014	6251	6678	7120	7571	
569	1196	1810	2280	2647	3015	6252	6679	7121	7572	
571	1197	1811	2281	2648	3018	6253	6682	7122	7573	
580	1198	1812	2282	2649	3019	6256	6683	7124	7574	
581	1199	1813	2283	2650	3020	6257	6684	7126	7575	
586	1200	1816	2286	2651	3021	6258	6685	7127	7576	
587	1201	1823	2287	2652	3022	6259	6686	7129	7577	
588	1202	1824	2289	2653	3024	6260	6687	7130	7578	
590	1203	1827	2291	2654	3025	6262	6688	7131	7582	
591	1204	1829	2294	2655	3026	6263	6690	7132	7583	
592	1205	1831	2295	2656	3027	6265	6691	7134	7584	
593	1206	1835	2299	2657	3028	6267	6692	7135	7585	
594	1207	1854	2300	2658	3030	6268	6695	7137	7586	
595	1208	1855	2301	2659	3031	6269	6696	7139	7587	

599	1209	1856	2302	2660	3035	6270	6697	7141	7588	
602	1210	1857	2303	2661	3036	6271	6698	7142	7590	
603	1212	1858	2304	2662	3037	6272	6699	7144	7592	
611	1213	1859	2305	2663	3038	6273	6700	7145	7594	
613	1214	1860	2306	2664	3039	6274	6701	7146	7596	
616	1215	1861	2307	2665	3040	6275	6702	7147	7597	
628	1216	1862	2308	2666	3041	6276	6704	7148	7598	
638	1217	1863	2309	2667	3042	6278	6706	7149	7599	
645	1218	1864	2310	2670	3043	6279	6707	7150	7600	
647	1219	1865	2311	2672	3044	6280	6708	7151	7601	
648	1220	1866	2312	2673	3045	6282	6709	7152	7602	
649	1222	1867	2313	2674	3046	6283	6711	7153	7603	
651	1223	1868	2314	2675	3047	6284	6712	7154	7604	
654	1224	1869	2315	2676	3048	6285	6714	7155	7605	
659	1225	1870	2316	2677	3049	6286	6715	7156	7606	
660	1227	1871	2317	2678	3050	6287	6716	7158	7608	
662	1228	1872	2318	2679	3051	6288	6717	7159	7609	
674	1230	1874	2319	2681	3052	6290	6719	7160	7610	
675	1232	1875	2320	2684	3053	6291	6720	7164	7611	
676	1233	1876	2321	2685	3054	6293	6721	7165	7614	
677	1235	1877	2322	2686	3055	6294	6725	7169	7615	
681	1237	1878	2323	2687	3056	6296	6726	7171	7616	
704	1238	1880	2324	2688	3057	6297	6727	7172	7618	
722	1239	1881	2325	2689	3058	6299	6728	7173	7619	

Taken together, the various analyses identified approximately 625 gene modifying polypeptides within the library that had a Z-score of at least 1 or greater in 3 or more conditions or replicates tested, and approximately 4625 gene modifying polypeptides within the library that had a Z-score of at least 1 or greater in at least one condition (these include gene modifying polypeptides having amino amino acid sequences according to any one of the SEQ ID NOs listed in Tables D9 and D10, respectively).

Table D9. Gene modifying polypeptide candidates having a Z-score of at least 1 or greater in 3 or more conditions or replicates tested.

SEQ ID NOs								
34	883	1376	1942	2332	2619	2817	3076	6567
35	884	1377	1943	2333	2620	2818	3079	6568
36	890	1380	1945	2335	2622	2820	3083	6591
37	898	1381	1949	2338	2623	2822	3084	6738
38	900	1382	1951	2342	2624	2823	3085	6760
39	901	1383	1953	2343	2627	2825	3087	6761
40	912	1384	1961	2345	2629	2826	3091	6783

41	915	1385	1967	2346	2631	2830	3093	6788
48	929	1389	1968	2347	2632	2833	3094	6876
49	933	1390	1970	2353	2633	2835	3096	6883
62	958	1394	1976	2359	2634	2836	3099	6925
97	960	1397	1978	2360	2636	2838	3103	6998
113	961	1399	1991	2363	2638	2840	3107	7036
117	963	1400	1992	2364	2639	2850	3108	7067
121	964	1401	2048	2365	2644	2865	3111	7103
123	966	1402	2060	2370	2647	2871	3112	7121
139	967	1404	2086	2371	2648	2874	3116	7142
140	978	1405	2091	2382	2649	2877	3120	7154
141	987	1406	2092	2395	2653	2878	3121	7242
142	1006	1410	2093	2400	2654	2880	3123	7262
144	1007	1415	2094	2403	2656	2881	3124	7267
147	1008	1419	2104	2405	2657	2886	3125	7293
156	1009	1422	2112	2449	2660	2887	3126	7335
190	1011	1423	2114	2503	2666	2888	3130	7397
191	1012	1424	2115	2504	2667	2890	3136	7443
192	1015	1441	2117	2505	2675	2893	4501	7476
195	1016	1540	2132	2506	2676	2895	4502	7496
199	1017	1543	2137	2507	2678	2901	4503	7509
212	1018	1550	2144	2508	2681	2903	4504	7555
213	1019	1553	2145	2510	2700	2904	4505	7587
219	1020	1616	2148	2511	2701	2905	4506	7588
228	1021	1618	2149	2512	2711	2909	4507	7660
232	1022	1619	2158	2513	2712	2913	4508	7667
239	1023	1666	2161	2514	2713	2914	4509	
252	1025	1668	2165	2515	2714	2916	4510	
258	1029	1672	2172	2518	2715	2920	4511	
268	1033	1677	2174	2519	2716	2922	4512	
300	1034	1679	2192	2521	2718	2927	4513	
303	1037	1682	2196	2525	2721	2928	4514	
313	1038	1686	2225	2526	2723	2929	4515	
316	1039	1690	2226	2527	2726	2930	4516	
317	1043	1691	2227	2528	2731	2932	4517	
318	1044	1695	2231	2529	2734	2933	4518	
320	1046	1698	2235	2530	2737	2937	4519	
332	1047	1721	2236	2531	2741	2943	4520	
341	1049	1754	2249	2534	2744	2948	4521	
346	1052	1759	2280	2535	2745	2950	4522	
352	1056	1769	2299	2536	2748	2953	4523	

363	1059	1770	2300	2539	2760	2957	4524	
384	1060	1772	2301	2542	2772	2966	4525	
386	1061	1773	2302	2544	2780	2967	4526	
392	1076	1856	2303	2547	2781	2972	4527	
396	1083	1857	2304	2548	2782	2976	4528	
480	1093	1860	2305	2550	2783	2982	4529	
550	1115	1861	2308	2551	2784	2983	4530	
590	1137	1863	2309	2553	2786	2991	4531	
591	1168	1864	2311	2556	2787	2995	4532	
647	1171	1865	2312	2559	2788	3007	4533	
715	1197	1867	2313	2561	2789	3014	4534	
800	1198	1868	2314	2562	2790	3015	4535	
801	1202	1870	2315	2566	2791	3018	4536	
804	1203	1871	2316	2568	2792	3026	4537	
805	1210	1874	2317	2573	2794	3035	4538	
806	1216	1875	2319	2578	2795	3039	4539	
818	1219	1876	2320	2583	2797	3042	4540	
819	1225	1877	2322	2585	2798	3044	4541	
871	1235	1881	2323	2592	2800	3045	6030	
872	1242	1883	2324	2599	2801	3052	6073	
873	1262	1889	2325	2610	2802	3053	6091	
874	1371	1899	2326	2611	2804	3057	6181	
876	1372	1937	2327	2612	2808	3059	6312	
878	1373	1938	2328	2614	2810	3063	6402	
880	1374	1939	2329	2615	2813	3065	6434	
882	1375	1940	2331	2618	2815	3067	6505	

Table D10. Gene modifying polypeptide candidates having a Z-score of at least 1 or greater in at least one condition.

SEQ ID NOs:									
1	596	1217	1846	2365	2884	6111	6610	7109	7608
2	597	1218	1847	2366	2885	6112	6611	7110	7609
3	598	1219	1848	2367	2886	6113	6612	7111	7610
4	599	1220	1849	2368	2887	6114	6613	7112	7611
5	600	1221	1850	2369	2888	6115	6614	7113	7612
6	601	1222	1851	2370	2889	6116	6615	7114	7613
7	602	1223	1852	2371	2890	6117	6616	7115	7614
9	603	1224	1853	2372	2891	6118	6617	7116	7615
10	604	1225	1854	2373	2892	6119	6618	7117	7616
12	605	1226	1855	2374	2893	6120	6619	7118	7617
13	606	1227	1856	2375	2894	6121	6620	7119	7618
14	607	1228	1857	2376	2895	6122	6621	7120	7619

17	610	1229	1858	2377	2896	6123	6622	7121	7620
18	611	1230	1859	2378	2897	6124	6623	7122	7621
19	613	1231	1860	2379	2898	6125	6624	7123	7622
22	614	1232	1861	2380	2899	6126	6625	7124	7623
24	616	1233	1862	2381	2900	6127	6626	7125	7624
28	617	1234	1863	2382	2901	6128	6627	7126	7625
33	618	1235	1864	2383	2902	6129	6628	7127	7626
34	624	1236	1865	2384	2903	6130	6629	7128	7627
35	625	1237	1866	2385	2904	6131	6630	7129	7628
36	626	1238	1867	2386	2905	6132	6631	7130	7629
37	628	1239	1868	2387	2906	6133	6632	7131	7630
38	631	1240	1869	2388	2907	6134	6633	7132	7631
39	632	1241	1870	2389	2908	6135	6634	7133	7632
40	633	1242	1871	2390	2909	6136	6635	7134	7633
41	634	1243	1872	2391	2910	6137	6636	7135	7634
42	636	1244	1873	2392	2911	6138	6637	7136	7635
43	638	1245	1874	2393	2912	6139	6638	7137	7636
44	640	1246	1875	2394	2913	6140	6639	7138	7637
45	645	1247	1876	2395	2914	6141	6640	7139	7638
46	647	1248	1877	2396	2915	6142	6641	7140	7639
47	648	1249	1878	2397	2916	6143	6642	7141	7640
48	649	1250	1879	2398	2917	6144	6643	7142	7641
49	650	1251	1880	2399	2918	6145	6644	7143	7642
50	651	1252	1881	2400	2919	6146	6645	7144	7643
51	652	1253	1882	2401	2920	6147	6646	7145	7644
52	653	1254	1883	2402	2921	6148	6647	7146	7645
53	654	1255	1884	2403	2922	6149	6648	7147	7646
54	655	1256	1885	2404	2923	6150	6649	7148	7647
55	656	1257	1886	2405	2924	6151	6650	7149	7648
56	657	1258	1887	2406	2925	6152	6651	7150	7649
57	659	1259	1888	2407	2926	6153	6652	7151	7650
58	660	1260	1889	2408	2927	6154	6653	7152	7651
59	661	1261	1890	2409	2928	6155	6654	7153	7652
60	662	1262	1891	2410	2929	6156	6655	7154	7653
61	663	1263	1892	2411	2930	6157	6656	7155	7654
62	664	1264	1893	2412	2931	6158	6657	7156	7655
63	666	1265	1894	2413	2932	6159	6658	7157	7656
64	667	1266	1895	2414	2933	6160	6659	7158	7657
65	668	1267	1896	2415	2934	6161	6660	7159	7658
66	669	1268	1897	2416	2935	6162	6661	7160	7659
67	670	1269	1898	2417	2936	6163	6662	7161	7660

68	673	1270	1899	2418	2937	6164	6663	7162	7661
69	674	1271	1900	2419	2938	6165	6664	7163	7662
70	675	1272	1901	2420	2939	6166	6665	7164	7663
71	676	1273	1902	2422	2940	6167	6666	7165	7664
72	677	1274	1903	2423	2941	6168	6667	7166	7665
73	678	1275	1904	2424	2942	6169	6668	7167	7666
74	679	1276	1905	2425	2943	6170	6669	7168	7667
75	680	1277	1906	2426	2944	6171	6670	7169	7668
76	681	1278	1907	2427	2945	6172	6671	7170	7669
77	684	1279	1908	2431	2946	6173	6672	7171	7670
78	687	1280	1909	2436	2947	6174	6673	7172	7671
79	689	1281	1910	2438	2948	6175	6674	7173	7672
80	690	1282	1911	2440	2949	6176	6675	7174	7673
81	692	1288	1912	2441	2950	6177	6676	7175	7674
82	694	1290	1913	2442	2951	6178	6677	7176	7675
83	700	1295	1914	2443	2952	6179	6678	7177	7676
84	702	1296	1915	2444	2953	6180	6679	7178	7677
85	704	1298	1916	2445	2954	6181	6680	7179	7678
86	706	1299	1917	2446	2955	6182	6681	7180	7679
87	707	1301	1918	2447	2957	6183	6682	7181	7680
88	711	1302	1919	2448	2958	6184	6683	7182	7681
89	715	1304	1920	2449	2959	6185	6684	7183	7682
90	716	1305	1921	2450	2960	6186	6685	7184	7683
91	717	1308	1922	2451	2962	6187	6686	7185	7684
92	719	1311	1923	2452	2965	6188	6687	7186	7685
93	720	1312	1924	2453	2966	6189	6688	7187	7686
94	722	1314	1925	2454	2967	6190	6689	7188	7687
95	724	1315	1926	2455	2968	6191	6690	7189	7688
96	726	1319	1927	2456	2969	6192	6691	7190	7689
97	727	1320	1928	2457	2970	6193	6692	7191	7690
98	728	1322	1929	2458	2971	6194	6693	7192	7691
99	729	1324	1931	2459	2972	6195	6694	7193	7692
100	731	1326	1932	2460	2973	6196	6695	7194	7693
101	738	1327	1933	2461	2974	6197	6696	7195	7694
102	739	1328	1934	2462	2975	6198	6697	7196	7695
103	740	1329	1935	2463	2976	6199	6698	7197	7696
104	745	1330	1936	2464	2977	6200	6699	7198	7697
105	746	1338	1937	2465	2978	6201	6700	7199	7698
106	747	1340	1938	2466	2979	6202	6701	7200	7699
107	755	1342	1939	2467	2980	6203	6702	7201	7700
108	756	1343	1940	2468	2981	6204	6703	7202	7701

110	759	1346	1941	2469	2982	6205	6704	7203	7702
111	765	1347	1942	2470	2983	6206	6705	7204	7703
112	766	1348	1943	2471	2984	6207	6706	7205	7704
113	767	1349	1944	2472	2985	6208	6707	7206	7705
114	768	1350	1945	2473	2986	6209	6708	7207	7706
115	769	1351	1946	2474	2987	6210	6709	7208	7707
116	770	1353	1947	2476	2988	6211	6710	7209	7708
117	771	1354	1948	2477	2989	6212	6711	7210	7709
118	772	1357	1949	2478	2990	6213	6712	7211	7710
119	773	1359	1950	2479	2991	6214	6713	7212	7711
120	774	1362	1951	2480	2992	6215	6714	7213	7712
121	775	1365	1952	2481	2993	6216	6715	7214	7713
122	776	1366	1953	2482	2994	6217	6716	7215	7714
123	777	1369	1954	2483	2995	6218	6717	7216	7715
124	780	1370	1955	2484	2996	6219	6718	7217	7716
125	781	1371	1956	2485	2997	6220	6719	7218	7717
126	782	1372	1957	2486	2998	6221	6720	7219	7718
127	783	1373	1958	2488	2999	6222	6721	7220	7719
128	784	1374	1959	2489	3001	6223	6722	7221	7720
129	785	1375	1960	2490	3002	6224	6723	7222	7721
130	789	1376	1961	2491	3003	6225	6724	7223	7722
131	790	1377	1962	2492	3004	6226	6725	7224	7723
132	794	1378	1963	2496	3005	6227	6726	7225	7724
133	797	1379	1964	2497	3006	6228	6727	7226	7725
134	798	1380	1965	2498	3007	6229	6728	7227	7726
135	799	1381	1966	2501	3008	6230	6729	7228	7727
136	800	1382	1967	2502	3009	6231	6730	7229	7728
137	801	1383	1968	2503	3010	6232	6731	7230	7729
138	802	1384	1969	2504	3011	6233	6732	7231	7730
139	803	1385	1970	2505	3012	6234	6733	7232	7731
140	804	1386	1971	2506	3013	6235	6734	7233	7732
141	805	1387	1972	2507	3014	6236	6735	7234	7733
142	806	1388	1973	2508	3015	6237	6736	7235	7734
143	807	1389	1974	2509	3016	6238	6737	7236	7735
144	808	1390	1975	2510	3017	6239	6738	7237	7736
145	809	1391	1976	2511	3018	6240	6739	7238	7737
146	810	1392	1977	2512	3019	6241	6740	7239	7738
147	811	1393	1978	2513	3020	6242	6741	7240	7739
148	812	1394	1979	2514	3021	6243	6742	7241	7740
149	813	1395	1980	2515	3022	6244	6743	7242	7741
150	814	1396	1981	2516	3023	6245	6744	7243	7742

151	815	1397	1982	2517	3024	6246	6745	7244	7743
152	816	1398	1983	2518	3025	6247	6746	7245	
153	817	1399	1984	2519	3026	6248	6747	7246	
154	818	1400	1985	2520	3027	6249	6748	7247	
155	819	1401	1986	2521	3028	6250	6749	7248	
156	820	1402	1987	2522	3029	6251	6750	7249	
157	821	1403	1988	2523	3030	6252	6751	7250	
158	822	1404	1989	2524	3031	6253	6752	7251	
159	823	1405	1990	2525	3032	6254	6753	7252	
160	824	1406	1991	2526	3033	6255	6754	7253	
161	825	1407	1992	2527	3034	6256	6755	7254	
162	826	1408	1993	2528	3035	6257	6756	7255	
163	827	1409	1994	2529	3036	6258	6757	7256	
164	828	1410	1995	2530	3037	6259	6758	7257	
165	829	1411	1996	2531	3038	6260	6759	7258	
166	830	1412	1997	2532	3039	6261	6760	7259	
167	831	1413	1998	2533	3040	6262	6761	7260	
168	832	1414	1999	2534	3041	6263	6762	7261	
169	833	1415	2000	2535	3042	6264	6763	7262	
170	834	1416	2001	2536	3043	6265	6764	7263	
171	835	1417	2002	2537	3044	6266	6765	7264	
172	836	1418	2003	2538	3045	6267	6766	7265	
173	837	1419	2004	2539	3046	6268	6767	7266	
174	839	1420	2005	2540	3047	6269	6768	7267	
175	840	1421	2006	2541	3048	6270	6769	7268	
176	841	1422	2007	2542	3049	6271	6770	7269	
177	842	1423	2008	2543	3050	6272	6771	7270	
178	843	1424	2009	2544	3051	6273	6772	7271	
179	844	1425	2010	2545	3052	6274	6773	7272	
180	845	1426	2011	2546	3053	6275	6774	7273	
181	846	1427	2012	2547	3054	6276	6775	7274	
182	847	1428	2013	2548	3055	6277	6776	7275	
183	848	1429	2014	2549	3056	6278	6777	7276	
184	849	1430	2015	2550	3057	6279	6778	7277	
185	850	1431	2016	2551	3058	6280	6779	7278	
186	851	1432	2017	2552	3059	6281	6780	7279	
187	852	1433	2018	2553	3060	6282	6781	7280	
188	853	1434	2019	2554	3061	6283	6782	7281	
190	854	1435	2020	2555	3062	6284	6783	7282	
191	855	1436	2021	2556	3063	6285	6784	7283	
192	856	1437	2022	2557	3064	6286	6785	7284	

193	857	1439	2023	2558	3065	6287	6786	7285	
194	860	1440	2024	2559	3066	6288	6787	7286	
195	861	1441	2025	2560	3067	6289	6788	7287	
196	862	1442	2026	2561	3068	6290	6789	7288	
197	863	1443	2027	2562	3069	6291	6790	7289	
198	866	1444	2028	2563	3070	6292	6791	7290	
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202	870	1448	2032	2567	3074	6296	6795	7294	
203	871	1449	2033	2568	3075	6297	6796	7295	
204	872	1450	2034	2569	3076	6298	6797	7296	
205	873	1451	2035	2570	3077	6299	6798	7297	
206	874	1452	2036	2571	3078	6300	6799	7298	
207	875	1454	2037	2572	3079	6301	6800	7299	
208	876	1455	2038	2573	3080	6302	6801	7300	
209	877	1456	2039	2574	3081	6303	6802	7301	
210	878	1460	2040	2575	3082	6304	6803	7302	
211	879	1462	2041	2576	3083	6305	6804	7303	
212	880	1465	2042	2577	3084	6306	6805	7304	
213	881	1469	2043	2578	3085	6307	6806	7305	
214	882	1471	2044	2579	3086	6308	6807	7306	
215	883	1473	2045	2580	3087	6309	6808	7307	
216	884	1475	2046	2581	3088	6310	6809	7308	
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221	889	1493	2051	2586	3093	6315	6814	7313	
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223	891	1499	2053	2588	3095	6317	6816	7315	
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226	894	1506	2056	2591	3098	6320	6819	7318	
227	895	1507	2057	2592	3099	6321	6820	7319	
228	896	1508	2058	2593	3100	6322	6821	7320	
229	897	1510	2059	2594	3101	6323	6822	7321	
230	898	1513	2060	2595	3102	6324	6823	7322	
231	899	1515	2061	2596	3103	6325	6824	7323	
232	900	1519	2062	2597	3104	6326	6825	7324	
233	901	1521	2063	2598	3105	6327	6826	7325	

234	902	1523	2064	2599	3106	6328	6827	7326	
235	903	1524	2066	2600	3107	6329	6828	7327	
236	904	1527	2069	2601	3108	6330	6829	7328	
237	905	1529	2070	2602	3109	6331	6830	7329	
238	906	1531	2071	2603	3110	6332	6831	7330	
239	907	1539	2072	2604	3111	6333	6832	7331	
240	908	1540	2074	2605	3112	6334	6833	7332	
241	909	1541	2075	2606	3113	6335	6834	7333	
242	910	1542	2076	2607	3114	6336	6835	7334	
243	911	1543	2079	2608	3115	6337	6836	7335	
244	912	1544	2080	2610	3116	6338	6837	7336	
245	913	1545	2081	2611	3117	6339	6838	7337	
246	914	1546	2082	2612	3118	6340	6839	7338	
247	915	1547	2084	2613	3119	6341	6840	7339	
248	916	1548	2085	2614	3120	6342	6841	7340	
249	917	1549	2086	2615	3121	6343	6842	7341	
250	918	1550	2087	2616	3122	6344	6843	7342	
251	919	1551	2088	2617	3123	6345	6844	7343	
252	920	1552	2089	2618	3124	6346	6845	7344	
253	921	1553	2090	2619	3125	6347	6846	7345	
254	922	1554	2091	2620	3126	6348	6847	7346	
255	923	1555	2092	2621	3127	6349	6848	7347	
256	924	1556	2093	2622	3128	6350	6849	7348	
257	925	1557	2094	2623	3129	6351	6850	7349	
258	926	1558	2095	2624	3130	6352	6851	7350	
259	927	1559	2096	2625	3131	6353	6852	7351	
260	928	1560	2097	2626	3132	6354	6853	7352	
261	929	1561	2098	2627	3133	6355	6854	7353	
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264	932	1565	2101	2630	3136	6358	6857	7356	
265	933	1566	2102	2631	3138	6359	6858	7357	
266	934	1567	2103	2632	3139	6360	6859	7358	
267	935	1568	2104	2633	3141	6361	6860	7359	
268	936	1570	2105	2634	3142	6362	6861	7360	
269	937	1571	2106	2635	3144	6363	6862	7361	
270	938	1572	2107	2636	3146	6364	6863	7362	
271	939	1573	2108	2637	3147	6365	6864	7363	
272	940	1574	2109	2638	3149	6366	6865	7364	
273	941	1575	2110	2639	3152	6367	6866	7365	
274	942	1576	2111	2640	3153	6368	6867	7366	

275	943	1577	2112	2641	3154	6369	6868	7367	
276	944	1578	2113	2642	3155	6370	6869	7368	
277	945	1579	2114	2643	3157	6371	6870	7369	
278	946	1580	2115	2644	3162	6372	6871	7370	
279	947	1581	2116	2645	3163	6373	6872	7371	
280	948	1582	2117	2646	3166	6374	6873	7372	
281	950	1583	2118	2647	3167	6375	6874	7373	
283	951	1584	2119	2648	3169	6376	6875	7374	
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285	957	1587	2121	2650	3172	6378	6877	7376	
286	958	1588	2122	2651	3173	6379	6878	7377	
287	959	1590	2123	2652	3175	6380	6879	7378	
288	960	1592	2124	2653	3176	6381	6880	7379	
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293	963	1595	2127	2656	3181	6384	6883	7382	
294	964	1596	2128	2657	3183	6385	6884	7383	
295	965	1597	2129	2658	3184	6386	6885	7384	
296	966	1598	2130	2659	3188	6387	6886	7385	
297	967	1599	2131	2660	3190	6388	6887	7386	
298	968	1600	2132	2661	3194	6389	6888	7387	
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303	973	1608	2137	2666	3202	6394	6893	7392	
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305	975	1611	2139	2668	3204	6396	6895	7394	
306	976	1612	2140	2669	3205	6397	6896	7395	
307	977	1616	2141	2670	3206	6398	6897	7396	
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310	980	1619	2144	2673	3209	6401	6900	7399	
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313	983	1622	2147	2676	3214	6404	6903	7402	
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315	985	1624	2149	2678	3219	6406	6905	7404	
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317	987	1626	2151	2680	3223	6408	6907	7406	
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326	996	1635	2160	2689	3248	6417	6916	7415	
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329	999	1638	2163	2692	3253	6420	6919	7418	
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331	1001	1640	2165	2694	3256	6422	6921	7420	
332	1002	1641	2166	2695	3259	6423	6922	7421	
333	1003	1642	2167	2696	3260	6424	6923	7422	
334	1004	1644	2168	2697	3261	6425	6924	7423	
335	1005	1645	2169	2698	3262	6426	6925	7424	
336	1006	1646	2170	2699	3263	6427	6926	7425	
337	1007	1647	2171	2700	3264	6428	6927	7426	
338	1008	1648	2172	2701	3265	6429	6928	7427	
339	1009	1649	2173	2702	3266	6430	6929	7428	
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342	1012	1653	2176	2706	3270	6433	6932	7431	
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344	1014	1655	2178	2709	3276	6435	6934	7433	
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346	1016	1657	2180	2711	3279	6437	6936	7435	
347	1017	1658	2181	2712	3282	6438	6937	7436	
348	1018	1659	2182	2713	3283	6439	6938	7437	
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351	1021	1662	2185	2716	3296	6442	6941	7440	
352	1022	1663	2186	2717	3298	6443	6942	7441	
353	1023	1664	2187	2718	3299	6444	6943	7442	
354	1024	1665	2188	2719	3300	6445	6944	7443	
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357	1027	1668	2191	2722	3305	6448	6947	7446	
358	1028	1669	2192	2723	3306	6449	6948	7447	
359	1029	1670	2193	2724	3310	6450	6949	7448	

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363	1033	1674	2197	2728	3317	6454	6953	7452	
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368	1038	1679	2202	2733	4501	6459	6958	7457	
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379	1049	1690	2213	2744	4512	6470	6969	7468	
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416	1083	1724	2250	2778	6005	6504	7003	7502	
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465	1122	1750	2277	2802	6029	6528	7027	7526	
469	1123	1751	2278	2803	6030	6529	7028	7527	
470	1124	1752	2279	2804	6031	6530	7029	7528	
472	1126	1753	2280	2805	6032	6531	7030	7529	
474	1127	1754	2281	2806	6033	6532	7031	7530	

475	1129	1755	2282	2807	6034	6533	7032	7531	
476	1131	1756	2283	2808	6035	6534	7033	7532	
480	1134	1757	2286	2809	6036	6535	7034	7533	
481	1136	1758	2287	2810	6037	6536	7035	7534	
483	1137	1759	2288	2811	6038	6537	7036	7535	
484	1138	1760	2289	2812	6039	6538	7037	7536	
486	1139	1761	2291	2813	6040	6539	7038	7537	
488	1140	1762	2292	2814	6041	6540	7039	7538	
489	1141	1764	2293	2815	6042	6541	7040	7539	
495	1142	1765	2294	2816	6043	6542	7041	7540	
498	1143	1766	2295	2817	6044	6543	7042	7541	
499	1144	1767	2299	2818	6045	6544	7043	7542	
502	1145	1768	2300	2819	6046	6545	7044	7543	
503	1146	1769	2301	2820	6047	6546	7045	7544	
504	1147	1770	2302	2821	6048	6547	7046	7545	
510	1148	1771	2303	2822	6049	6548	7047	7546	
517	1149	1772	2304	2823	6050	6549	7048	7547	
519	1150	1773	2305	2824	6051	6550	7049	7548	
522	1151	1774	2306	2825	6052	6551	7050	7549	
523	1152	1775	2307	2826	6053	6552	7051	7550	
524	1153	1776	2308	2827	6054	6553	7052	7551	
527	1154	1777	2309	2828	6055	6554	7053	7552	
528	1155	1778	2310	2829	6056	6555	7054	7553	
532	1156	1779	2311	2830	6057	6556	7055	7554	
534	1157	1780	2312	2831	6058	6557	7056	7555	
535	1158	1781	2313	2832	6059	6558	7057	7556	
536	1159	1782	2314	2833	6060	6559	7058	7557	
537	1160	1783	2315	2834	6061	6560	7059	7558	
538	1161	1784	2316	2835	6062	6561	7060	7559	
539	1162	1785	2317	2836	6063	6562	7061	7560	
540	1163	1786	2318	2837	6064	6563	7062	7561	
541	1164	1787	2319	2838	6065	6564	7063	7562	
542	1165	1788	2320	2839	6066	6565	7064	7563	
543	1166	1789	2321	2840	6067	6566	7065	7564	
544	1167	1790	2322	2841	6068	6567	7066	7565	
545	1168	1791	2323	2842	6069	6568	7067	7566	
546	1169	1792	2324	2843	6070	6569	7068	7567	
547	1170	1793	2325	2844	6071	6570	7069	7568	
548	1171	1794	2326	2845	6072	6571	7070	7569	
549	1172	1795	2327	2846	6073	6572	7071	7570	
550	1173	1796	2328	2847	6074	6573	7072	7571	

553	1174	1797	2329	2848	6075	6574	7073	7572	
554	1176	1799	2330	2849	6076	6575	7074	7573	
555	1177	1800	2331	2850	6077	6576	7075	7574	
556	1178	1801	2332	2851	6078	6577	7076	7575	
557	1179	1802	2333	2852	6079	6578	7077	7576	
558	1181	1803	2334	2853	6080	6579	7078	7577	
559	1182	1804	2335	2854	6081	6580	7079	7578	
560	1184	1805	2336	2855	6082	6581	7080	7579	
561	1185	1806	2337	2856	6083	6582	7081	7580	
562	1186	1808	2338	2857	6084	6583	7082	7581	
563	1187	1809	2339	2858	6085	6584	7083	7582	
564	1188	1810	2340	2859	6086	6585	7084	7583	
565	1190	1811	2341	2860	6087	6586	7085	7584	
566	1193	1812	2342	2861	6088	6587	7086	7585	
567	1195	1813	2343	2862	6089	6588	7087	7586	
568	1196	1815	2344	2863	6090	6589	7088	7587	
569	1197	1816	2345	2864	6091	6590	7089	7588	
570	1198	1817	2346	2865	6092	6591	7090	7589	
571	1199	1818	2347	2866	6093	6592	7091	7590	
572	1200	1819	2348	2867	6094	6593	7092	7591	
575	1201	1823	2349	2868	6095	6594	7093	7592	
580	1202	1824	2350	2869	6096	6595	7094	7593	
581	1203	1825	2351	2870	6097	6596	7095	7594	
583	1204	1827	2352	2871	6098	6597	7096	7595	
584	1205	1828	2353	2872	6099	6598	7097	7596	
585	1206	1829	2354	2873	6100	6599	7098	7597	
586	1207	1831	2355	2874	6101	6600	7099	7598	
587	1208	1832	2356	2875	6102	6601	7100	7599	
588	1209	1834	2357	2876	6103	6602	7101	7600	
589	1210	1835	2358	2877	6104	6603	7102	7601	
590	1211	1838	2359	2878	6105	6604	7103	7602	
591	1212	1840	2360	2879	6106	6605	7104	7603	
592	1213	1842	2361	2880	6107	6606	7105	7604	
593	1214	1843	2362	2881	6108	6607	7106	7605	
594	1215	1844	2363	2882	6109	6608	7107	7606	
595	1216	1845	2364	2883	6110	6609	7108	7607	

As the results in this example establish, gene modifying polypeptides combining linkers selected from those shown in Table 10 and RTs from 17 retroviral RT families out of the 35 RT families screened have gene editing activity when delivered as DNA to test cells.

Example 4: Evaluating the Effects of RT Domain Mutations on Editing Activity in Pooled Screen

The pooled screen data using the library from Example 3 was further analyzed to evaluate the effect of mutations, within and across RT families, on candidate gene modifying polypeptide editing activity. The RT families included RT domains comprising one or more substitutions at positions corresponding to 200, 603, 330, 524, 562, 583, 51, 67, 67, 197, 204, 302, 309, 313, 435, 454, 594, 671, 69, or 653 of murine leukemia virus reverse transcriptase relative to a wildtype sequence of the RT domain. Without wishing to be bound by theory, it is thought that substitutions at positions corresponding to one or more of these positions may improve stability (e.g., thermostability) and/or editing activity of the RT domain and/or a gene modifying polypeptide comprising the same. Specific combinations of mutations tested included those listed in Table 2.

FIGs. 8A-8F, 9A-9H, and 10A-10C show graphs of average Z score for candidate gene modifying polypeptides grouped by RT variant (X-axis) and RT family (each box).

FIGs. 8A-8F show that for several RT families (MLVAV, MLVBM, BAEVM, FLV, FOAMV, and GALV), gene modifying polypeptide candidates comprising RT variants without mutations have negative or near 0 average Z-scores, whereas those comprising RT variants with one or more mutations at the specified sites have positive average Z-scores which increase with the number of positions substituted. These results show that mutations at one or more of the positions suspected of stabilizing/increasing editing activity rescue RT domains of these families, resulting in active or more active candidate gene modifying polypeptides relative to gene candidates with an RT lacking substitutions.

FIGs. 9A-9H show that for several RT families (KORV, AVIRE, MLVCB, MLVFF, MLVMS, SFV3L, WMSV, and XMRV6), gene modifying polypeptide candidates comprising RT variants without mutations have positive average Z-scores and those comprising RT variants with one or more mutations at the specified sites have higher average Z-scores which increase with the number of positions substituted. These results show that for eight of the RT families tested, mutations at one or more of the positions suspected of stabilizing/increasing editing activity further improve the activity of already active RT domains in these families, resulting in more active candidate gene modifying polypeptides.

FIGs. 10A-10C show that for several RT families that show editing activity in Example 3 (PERV, SFV1, and FFV), gene modifying polypeptide candidates comprising RT variants without mutations have similar average Z-scores to those comprising RT variants with one or more mutations at the specified sites, or have lower average Z-scores that decrease with the number of positions substituted. These results show that the effect of mutations is not predictable as evidenced by the fact that, for some editing-active RT families, mutations at one or more of the positions suspected of stabilizing/increasing editing activity have no or little effect on editing activity, or decrease the editing activity of the gene modifying polypeptide.

These results demonstrate that RT domain mutations at one or more positions corresponding to 200, 603, 330, 524, 562, 583, 51, 67, 67, 197, 204, 302, 309, 313, 435, 454, 594, 671, 69, or 653 of murine leukemia virus reverse transcriptase can increase editing activity of gene modifying polypeptides derived from certain RT families and not others. In particular, editing activity of candidate gene modifying polypeptides containing RT domains of RT families MLVAV, MLVBM, BAEVM, FLV, FOAMV, GALV, KORV, AVIRE, MLVCB, MLVFF, MLVMS, SFV3L, WMSV, and XMRV6 was increased by substitutions at the listed positions, and that the more substitutions in the RT variant, the greater the increase in editing activity. The RT families identified as active in Example 3 where substitutions improved editing activity were nearly all derived from Gammaretroviruses, with one gammaretroviral RT family (PERV) showing no effect on editing activity from the substitutions. Both of the RT families identified as active in Example 3 where substitutions negatively correlated with editing activity were Spumavirus RTs.

Example 5: Evaluating the Effects of Different Linkers on Editing Activity in Pooled Screen

The pooled screen data using the library from Example 3 was further analyzed to evaluate the effect of different linkers, within and across RT families, on candidate gene modifying polypeptide editing activity.

FIG. 11 shows a graph of average Z score for candidate gene modifying polypeptides grouped by linker (Y-axis) for select linkers, with lines indicating the average and standard error of the mean from the highest performing linker. The results show that candidate gene modifying polypeptides containing a AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA (SEQ ID NO: 11,041) linker consistently show high editing activity. The results further suggest that some linkers, e.g., those listed in Table A2, show higher editing activity than some other linkers tested.

Table A2: Exemplary Linkers

Amino Acid Sequence	**SEQ ID NO:**
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	11,041
EAAAKEAAAKEAAAKEAAAKEAAAKEAAAK	11,042
SGGSSGGSSGSETPGTSESATPESSGGSSGGSS	11,043
EAAAKEAAAKEAAAKEAAAKEAAAK	11,044
EAAAKEAAAKEAAAKEAAAK	11,045
GSSGSSGSSGSSGSSGSS	11,046
GGGGSGGGGSGGGGSGGGGSGGGGSGGGGS	11,047
SGSETPGTSESATPES	11,048
PAPAPAPAPAPAP	11,049
EAAAKGGGGSEAAAK	11,050

Example 6: Characterizing Editing Activity of Exemplary Gene Modifying Polypeptides Delivered in RNA Form to Several Model Systems

FIG. 12A-12D show graphs of editing activity of four exemplary gene modifying polypeptides delivered as RNA in different experimental model systems, each gene modifying polypeptide comprising the AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA (SEQ ID NO: 11,041) linker. The amino acid sequences of the exemplary gene modifying polypeptides are given in the below table.

Table A3: Exemplary Gene Modifying Polypeptides

Exemplary Gene Modifying Polypeptide	**Full AA Sequence**
1	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLV EEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENL IAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQL PEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSR FAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVE ISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLI HDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYY LQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQ ILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEIT LANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIM ERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANL DKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAK EAAAKEAAAKAGGTAPLEEEYRLFLEAPIQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSG TSEYRMVQDLREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEEGESGQLTWTRLPQGFKNSPTLFNEALNRDLQGFRLDHPSVSLLQYV DDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAILQIPVPKTKRQVREFLGKIGYCRLFIPGFAELAQPLYAATRPGNDPLVWGEKE EEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSKRLDPVAAGWPRCLRAIAAAALLTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARIT QYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTSTRPDLTDQPLAQAEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKD KSVNIYTDSRYAFATLHVHGMIYRERGWLTAGGKAIKNAPEILALLTAVWLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFEKRTADGSEFE SPKKKAKVE (SEQ ID NO: 11,091)
2	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLV EEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENL IAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQL PEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSR FAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVE ISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLI HDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYY LQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQ ILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEIT LANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIM ERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANL DKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAK EAAAKEAAAKAGGTLQLEEEYRLFEPESTQKQEMDIWLKNFPQAWAETGGMGTAHCQAPVLIQLKATATPISIRQYPMPHEAYQGIKPHIRRMLDQGILKPCQSPWNTPLLPVKKPGT EDYRPVQDLREVNKRVEDIHPTVPNPYNLLSTLPPSHPWYTVLDLKDAFFCLRLHSESQLLFAFEWRDPEIGLSGQLTWTRLPQGFKNSPTLFNEALHSDLADFRVRYPALVLLQYVD DLLLAAATRTECLEGTKALLETLGNKGYRASAKKAQICLQEVTYLGYSLKDGQRWLTKARKEAILSIPVPKNSRQVREFLGKAGYCRLFIPGFAELAAPLYPLTRPGTLFQWGTEQQL AFEDIKKALLSSPALGLPDITKPFELFIDENSGFAKGVLVQKLGPWKRPVAYLSKKLDTVASGWPPCLRMVAAIAILVKDAGKLTLGQPLTILTSHPVEALVRQPPNKWLSNARMTHY QAMLLDAERVHFGPTVSLNPATLLPLPSGGNHHDCLQILAETHGTRPDLTDQPLPDADLTWYTDGSSFIRNGEREAGAAVTTESEVIWAAPLPPGTSAQRAELIALTQALKMAEGKKL TVYTDSRYAFATTHVHGEIYRRRGWLTSEGKEIKNKNEILALLEALFLPKRLSIIHCPGHQKGDSPQAKGNRLADDTAKKAATETHSSLTVLPAGKRTADGSEFEKRTADGSEFESPK KKAKVE (SEQ ID NO: 11,092)
3	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLV EEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENL

	IAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQL PEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSR FAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVE ISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLI HDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYY LQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQ ILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEIT LANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIM ERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANL DKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAK EAAAKEAAAKAGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPG TNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYV DDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQ KAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTH YQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKK LNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESP KKKAKVE (SEQ ID NO: 11,093)
4	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLV EEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENL IAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQL PEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSR FAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVE ISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLI HDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYY LQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQ ILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEIT LANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIM ERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANL DKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAK EAAAKEAAAKAGGMDPLQLLQPLEAEIKGTKLKAHWNSGATITCVPQAFLEEEVPIKNIWIKTIHGEKEQPVYYLTFKIQGRKVEAEVISSPYDYIILVSPSDIPWLMKKPLQLTTLVP LQEYEERLLKQTMLTGSYKEKLQSLFLKYDALWQHWENQVGHRRIKPHHIATGTVNPRPQKQYPINPKAKASIQTVINDLLKQGVLIQQNSIMNTPVYPVPKPDGKWRMVLDYREVNK TIPLIAAQNQHSAGILSSIFRGKYKTTLDLSNGFWAHSITPESYWLTAFTWLGQQYCWTRLPQGFLNSPALFNADVVDLLKEVPNVQVYVDDIYISHDDPREHLEQLEKVFSLLLNAG YVVSLKKSEIAQHEVEFLGFNITKEGRGLTETFKQKLLNITPPRDLKQLQSILGKLNFARNFIPNFSELVKPLYNIIATAPGKYITWTTDNSQQLQNIISMLNSAENLEERNPEVRLI MKVNTSPSAGYIRFYNEFAKRPIMYLNYVYTKAEVKFTNTEKLLTTIHKGLIKALDLGMGQEILVYSPIVSMTKIQKTPLPERKALPIRWITWMSYLEDPRIQFHYDKTLPELQQVPT VTDDIIAKIKHPSEFSMVFYTDGSAIKHPNVNKSHNAGMGIAQVQFKPEFTVINTWSIPLGDHTAQLAEVAAVEFACKKALKIDGPVLIVTDSFYVAESVNKELPYWQSNGFFNNKKK PLKHVSKWKSIADCIQLKPDIIIIHEKGHQPTASTFHTEGNNLADKLATQGSYVVNAGKRTADGSEFEKRTADGSEFESPKKKAKVE (SEQ ID NO: 11,094)

U2OS cells comprising a BFP landing pad (as described in Example 1 for HEK293T cells) were nucleofected with mRNA encoding one of the exemplary gene modifying polypeptides along with a template RNA designed to convert BFP to GFP, as described herein (FIG. 12A). The relative amounts of GFP positive cells (successfully edited) and BFP positive cells (unedited cells) were determined by flow cytometry and used to determine the editing activities of the gene modifying polypeptides in this experimental system. The results showed that all four exemplary gene modifying polypeptides showed high editing activity (from about 60% to over 85%).

U2OS cells were nucleofected with mRNA encoding one of the exemplary gene modifying polypeptides along with a template RNA designed to edit the HEK3 locus and a second strand-targeting gRNA (FIG. 12B). Editing was confirmed by amplicon sequencing using primers specific for the target locus. The results showed that all four exemplary gene modifying polypeptides showed editing activity at the HEK3 locus (from about 1% to about 5%).

Primary murine hepatocytes were nucleofected with mRNA encoding one of the exemplary gene modifying polypeptides along with a second strand-targeting gRNA and a template RNA designed to convert a G nucleotide to an A nucleotide in the endogenous *Fah* locus in wildtype mouse primary hepatocytes (FIG. 12C). A mutation in the last nucleotide of exon 8 of the *Fah* gene leads 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; editing said nucleotide from G to A demonstrates the ability of a gene modifying system to target the mouse model's relevant locus. Editing was confirmed by amplicon sequencing using primers specific for the murine *Fah* target locus. The results showed that three of the four exemplary gene modifying polypeptides showed editing activity at the murine *Fah* locus (from about 6% to about 9%).

The gene modifying system comprising mRNA encoding one of the exemplary gene modifying polypeptides and a template RNA were formulated in LNP and delivered to Fah5981SB mice (FIG. 12D). The template RNA was designed 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. 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. 6 days post-dosing animals were sacrificed, and their liver collected for analyses. 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. Results showed that three of the four exemplary gene modifying polypeptides showed editing activity in vivo in murine liver (from about 1.2% to about 6%).

Taken together, FIGS. 12A-12D show that the RNA delivery of several exemplary gene modifying polypeptides can achieve significant editing activity across different target loci, in different cell types, and in vivo at a therapeutically relevant locus. Additionally, the results further demonstrate that exemplary gene modifying polypeptides comprising a AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA (SEQ ID NO: 11,041) linker, shown in Example 5 to be particularly effective in gene modifying polypeptides, can be used to achieve significant editing activity across different target loci, in different cell types, and in vivo at a therapeutically relevant locus. Additionally, the results further demonstrate that exemplary gene modifying polypeptides comprising RT domains from the SSFV, MMLV, AVIRE, or SSV RT families can achieve editing activity across different target loci, in different cell types, and in vivo at a therapeutically relevant locus.

Example 7: Characterizing the Editing Activity of 39 High Performing Exemplary Gene Modifying Polypeptides

This example describes characterization of the editing activity of a selection of 39 exemplary gene modifying polypeptides chosen from those identified in the preceding Examples based on their performance in the pooled RT family experiments. As described above, each gene modifying polypeptide contains Cas9 linked to a reverse transcriptase (RT). Specifically, this example describes the introduction of a gene modifying polypeptide to mammalian cells via lentiviral transduction, such that the RNA encoding the gene modifying polypeptide is reverse transcribed, integrated into the genome, and stably expressed in the mammalian cells, followed by transfection of a template guide RNA for in vitro editing, as a means of evaluating the editing activity of the individual gene modifying polypeptide.

In this example, exemplary gene modifying polypeptides comprised the following combinations of linkers and RT domains fused to a Cas9 domain:

Graph ID	Linker amino acid sequence	SEQ ID NO:	RT Variant Name
10373	PAPGGSGGG	11,051	MLVMS_P03355_PLV919
13642	GSSEAAAKGGG	11,052	MLVAV_P03356_3mutA
12793	EAAAKPAPGGS	11,053	MLVCB_P08361_3mutA
13522	GSSGGGEAAAK	11,054	MLVMS_P03355_3mutA_WS
16382	PAPGSSEAAAK	11,055	MLVMS_P03355_3mutA_WS
9438	GGGEAAAKGGS	11,056	XMRV6_A1Z651_3mutA
16661	AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	11,057	MLVMS_P03355_PLV919
5077	PAPAPAPAPAPAP	11,058	MLVFF_P26809_3mutA
14944	GGGEAAAKPAP	11,059	MLVFF_P26809_3mutA
15953	GSSPAPEAAAK	11,060	MLVMS_P03355_3mutA_WS
5082	PAPAPAPAPAPAP	11,061	MLVMS_P03355_PLV919
13233	GGGGSSEAAAK	11,062	MLVMS_P03355_PLV919
5071	PAPAPAPAPAPAP	11,063	MLVCB_P08361_3mutA
17380	SGGSSGGSSGSETPGTSESATPESSGGSSGGSS	11,064	MLVMS_P03355_PLV919
12507	GGSPAPEAAAK	11,065	MLVCB_P08361_3mutA
4213	EAAAKEAAAKEAAAKEAAAKEAAAKEAAAK	11,066	MLVCB_P08361_3mutA
12438	GGSEAAAKPAP	11,067	WMSV_P03359_3mutA
16591	AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	11,068	AVIRE_P03360_3mutA
3927	EAAAKEAAAKEAAAKEAAAK	11,069	MLVCB_P08361_3mutA
16664	AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	11,070	MLVMS_P03355_3mutA_WS
12807	EAAAKPAPGGS	11,071	MLVMS_P03355_3mutA_WS
1576	GGGGSGGGGSGGGGSGGGGSGGGGSGGGGS	11,072	AVIRE_P03360_3mutA
1646	GGGGSGGGGSGGGGSGGGGSGGGGSGGGGS	11,073	MLVMS_P03355_PLV919

14586	GSSPAPGGG	11,074	XMRV6_A1Z651_3mutA
14652	PAPGGGGSS	11,075	MLVCB_P08361_3mutA
1353	GGGGSGGGGSGGGGSGGGGS	11,076	MLVCB_P08361_3mutA
9370	GGGEAAAKGGS	11,077	MLVMS_P03355_3mut
6831	EAAAKGGG	11,078	PERV_Q4VFZ2_3mut
12513	GGSPAPEAAAK	11,079	MLVFF_P26809_3mutA
15021	GGGPAPEAAAK	11,080	BAEVM_P10272_3mutA
8576	GGGGSSGGS	11,081	WMSV_P03359_3mut
16609	AEAAAKEAAAKEAAAKEAAAKALEAEAAAK EAAAKEAAAKEAAAKA	11,082	FLV_P10273_3mutA
12691	EAAAKGGSPAP	11,083	PERV_Q4VFZ2_3mut
15894	GSSPAPEAAAK	11,084	FLV_P10273_3mutA
14924	GGGEAAAKPAP	11,085	KORV_Q9TTC1-Pro_3mutA
16704	AEAAAKEAAAKEAAAKEAAAKALEAEAAAKE AAAKEAAAKEAAAKA	11,086	SFV1_P23074_2mutA
4925	PAPAPAPAPAP	11,087	MLVBM_Q7SVK7_3mut
11771	GSSGGSPAP	11,088	HTLV2_P03363
707	GGSGGSGGSGGSGGS	11,089	WDSV_O92815

The exemplary gene modifying polypeptides were introduced to HEK293T cells carrying a BFP -expressing genomic landing pad by transfection of mRNA. To determine the editing activity of the gene modifying polypeptide, BFP-expressing cells containing the gene modifying polypeptide-are electroporated with a template RNA designed to convert BFP-to-GFP. Cells were analyzed using flow cytometry for expression of the color-converted fluorescent protein 3-4 days post electroporation.

FIG. 13 shows a graph of the editing activity for the 39 exemplary gene modifying polypeptides when delivered to HEK293T cells in DNA (plasmid) form or RNA (mRNA) form along with an exemplary template RNA. The results showed that a gene modifying polypeptide can be delivered to cells in the form of mRNA and achieve comparable editing activity as the same gene modifying polypeptide delivered to cells in the form of DNA. Additionally, these results demonstrate that the gene modifying systems described herein can be delivered entirely in RNA form (e.g., via mRNA encoding the gene modifying polypeptide and a template RNA).

Example 8: Arrayed Screening of Individual Gene Modifying Polypeptides in HEK293T and U2OS Cells

This example describes identification and characterization of several classes of gene modifying polypeptides capable of editing genomic DNA.

HEK293T cells or U2OS cells expressing BFP (as described in preceding Examples) were nucleofected with a plasmid expressing one of 373 gene modifying polypeptides and a plasmid expressing either exemplary tgRNA g4 or exemplary tgRNA g10 (each designed to convert BFP to GFP) on day 0, and then flow cytometry was used to analyze BFP and GFP expression on day 4 (FIG. 15). Cells having GFP signal were defined as having undergone a successful rewriting event, and the percent of cells that were GFP+ on day 4 was used to determined the performance of each gene modifying polypeptide.

The percent converted to GFP for each gene modifying polypeptide and condition, normalized to PL12162 were graphed in a box and whisker plot (FIG. 16). The results confirm that the tested gene modifying polypeptides have editing activity. The results further demonstrate that a number of gene modifying polypeptides exhibit higher editing activity across the four conditions tested than the benchmark gene modifying polypeptide (showing a normalized percent converted greater than 1). Gene modifying polypeptides exhibiting higher editing activity than the benchmark gene modifying polypeptide in at least one condition or in all four conditions are listed in the following Tables, along with controls.

Table D11: Gene Modifying Polypeptides Exhibiting Higher Editing Activity Than Benchmark in at Least One Condition

SEQ ID NOs				
36	1384	2326	2644	2877
39	1390	2327	2647	2878
43	1401	2328	2648	2879
49	1404	2329	2653	2883
140	1405	2335	2677	2894
193	1406	2338	2688	2943
300	1618	2346	2692	2950
307	1672	2363	2711	3036
309	1857	2364	2712	3042
317	1861	2365	2713	3042
324	1864	2370	2734	3044
480	1865	2371	2776	3045
590	1870	2449	2780	3047
647	1883	2503	2781	3055
715	1943	2505	2782	3056
801	2087	2506	2784	3057
871	2089	2507	2788	3061
873	2091	2510	2790	3062
901	2097	2511	2793	3063
912	2099	2514	2794	3064
958	2101	2515	2795	3080
1006	2106	2518	2798	3081
1012	2115	2519	2803	3084
1017	2120	2525	2804	3086
1018	2300	2526	2809	3093
1038	2301	2527	2812	3094
1049	2303	2528	2817	7735
1171	2304	2534	2831	
1197	2305	2542	2839	
1198	2308	2610	2845	
1225	2309	2611	2849	
1371	2311	2614	2852	

1372	2314	2615	2855	
1373	2315	2619	2860	
1374	2316	2623	2863	
1376	2317	2624	2868	
1377	2319	2633	2869	
1380	2322	2636	2872	
1382	2325	2641	2874	

Table D12: Gene Modifying Polypeptides Exhibiting Higher Editing Activity Than Benchmark in All Conditions

SEQ ID NOs
1018
1038
2309
2315
2325
2338
2611
2868
3084
7735

Table D13: Control sequences

Normal-ization Control	Positive Controls	Negative Controls
2892	2181	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSG ETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDE VAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYN QLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDA KLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQ DLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLL RKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTR KSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGM RKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDK DFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRD KQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQT VKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQL QNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPS EEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSR

		MNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLES EFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWD KGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYS VLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKR MLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVI LADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQ SITGLYETRIDLSQLGGDGGGGSGGSGGSGGSGGSGGSCQTKNTLNIDEYLLQFPDQLWASLPTDI GRMLVPPITIKIKDNASLPSIRQYPLPKDKTEGLRPLISSLENQGILIKCHSPCNTPIFPIKKAGRDEYRM IHDLRAINNIVAPLTAVVASPTTVLSNLAPSLHWFTVIDLSNAFFSVPIHKDSQYLFAFTFEGHQYTW TVLPQGFIHSPTLFSQALYQSLHKIKFKISSEICIYMDDVLIASKDRDTNLKDTAVMLQHLASEGHKVS KKKLQLCQQEVVYLGQLLTPEGRKILPDRKVTVSQFQQPTTIRQIRAFLGLVGYCRHWIPEFSIHSKFL EKQLKKDTAEPFQLDDQQVEAFNKLKHAITTAPVLVVPDPAKPFQLYTSHSEHASIAVLTQKHAGRT RPIAFLSSKFDAIESGLPPCLKACASIHRSLTQADSFILGAPLIIYTTHAICTLLQRDRSQLVTASRFSKWE ADLLRPELTFVACSAVSPAHLYMQSCENNIPPHDCVLLTHTISRPRPDLSDLPIPDPDMTLFSDGSYT TGRGGAAVVMHRPVTDDFIIIHQQPGGASAQTAELLALAAACHLATDKTVNIYTDSRYAYGVVHDF GHLWMHRGFVTSAGTPIKNHKEIEYLLKQIMKPKQVSVIKIEAHTKGVSMEVRGNAAADEAAKNA VFLVQRAGKRTADGSEFEKRTADGSEFESPKKKAKVE (SEQ ID NO: 15466)
	3143	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSG ETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDE VAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYN QLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDA KLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQ DLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLL RKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTR KSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGM RKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDK DFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRD KQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQT VKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQL QNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPS EEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSR MNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLES EFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWD KGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYS VLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKR MLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVI LADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQ SITGLYETRIDLSQLGGDGGGSSGGSEAAAKGGSCQTKNTLNIDEYLLQFPDQLWASLPTDIGRMLV PPITIKIKDNASLPSIRQYPLPKDKTEGLRPLISSLENQGILIKCHSPCNTPIFPIKKAGRDEYRMIHDLRA INNIVAPLTAVVASPTTVLSNLAPSLHWFTVIDLSNAFFSVPIHKDSQYLFAFTFEGHQYTWTVLPQG FIHSPTLFNQALYQSLHKIKFKISSEICIYMDDVLIASKDRDTNLKDTAVMLQHLASEGHKVSKKKLQL CQQEVVYLGQLLTPEGRKILPDRKVTVSQFQQPTTIRQIRAFLGKVGYCRHFIPEFSIHSKFLEKQLKP DTAEPFQLDDQQVEAFNKLKHAITTAPVLVVPDPAKPFQLYTSHSEHASIAVLTQKHAGRTRPIAFLS SKFDAIESGLPPCLKACASIHRSLTQADSFILGAPLIIYTTHAICTLLQRDRSQLVTASRFSKWEADLLRP ELTFVACSAVSPAHLYMQSCENNIPPHDCVLLTHTISRPRPDLSDLPIPDPDMTLFSDGSYTTGRGG AAVVMHRPVTDDFIIIHQQPGGASAQTAELLALAAACHLATDKTVNIYTDSRYAYGVVHDFGHLW MHRGFVTSAGTPIKNHKEIEYLLKQIMKPKQVSVIKIEAHTKGVSMEVRGNAAADEAAKNAVFLVQ RAGKRTADGSEFEKRTADGSEFESPKKKAKVE (SEQ ID NO: 15467)

		MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSG ETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDE VAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYN QLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDA KLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQ DLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLL RKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTR KSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGM RKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDK DFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRD KQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQT VKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQL QNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPS EEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSR MNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLES EFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWD KGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYS VLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKR MLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVI LADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQ SITGLYETRIDLSQLGGDGGGSSGGSPAPGGHLPPPPQVDQFPLNLPERLQALNDLVSKALEAGHIE PYSGPGNNPVFPVKKPNGKWRFIHDLRATNAITTTLTSPSPGPPDLTSLPTALPHLQTIDLTDAFFQI PLPKQYQPYFAFTIPQPCNYGPGTRYAWTVLPQGFKNSPTLFEQQLAAVLNPMRKMFPTSTIVQY MDDILLASPTNEELQQLSQLTLQALTTHGLPISQEKTQQTPGQIRFLGQVISPNHITYESTPTIPIKSQ WTLTELQVILGEIQWVSKGTPILRKHLQSLYSALHGYRDPRACITLTPQQLHALHAIQQALQHNCRG RLNPALPLLGLISLSTSGTTSVIFQPKQNWPLAWLHTPHPPTSLCPWGHLLACTILTLDKYTLQHYGQ LCQSFHHNMSKQALCDFLRNSPHPSVGILIHHMGRFHNLGSQPSGPWKTLLHLPTLLQEPRLLRPIF TLSPVVLDTAPCLFSDGSPQKAAYVLWDQTILQQDITPLPSHETHSAQKGELLALICGLRAAKPWPSL NIFLDSKYLIKYLHSLAIGAFLGTSAHQTLQAALPPLLQGKTIYLHHVRSHTNLPDPISTFNEYTDSLILA PLVPLAGKRTADGSEFEKRTADGSEFESPKKKAKVE (SEQ ID NO: 15468)
		MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSG ETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDE VAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYN QLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDA KLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQ DLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLL RKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTR KSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGM RKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDK DFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRD KQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQT VKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQL QNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPS EEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSR MNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLES EFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWD KGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYS VLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKR

		MLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVI LADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQ SITGLYETRIDLSQLGGDGGGSSGGSPAPGGSCQTKNTLNIDEYLLQFPDQLWASLPTDIGRMLVPPI TIKIKDNASLPSIRQYPLPKDKTEGLRPLISSLENQGILIKCHSPCNTPIFPIKKAGRDEYRMIHDLRAIN NIVAPLTAVVASPTTVLSNLAPSLHWFTVIDLSNAFFSVPIHKDSQYLFAFTFEGHQYTWTVLPQGFI HSPTLFNQALYQSLHKIKFKISSEICIYMDDVLIASKDRDTNLKDTAVMLQHLASEGHKVSKKKLQLC QQEVVYLGQLLTPEGRKILPDRKVTVSQFQQPTTIRQIRAFLGKVGYCRHFIPEFSIHSKFLEKQLKPD TAEPFQLDDQQVEAFNKLKHAITTAPVLVVPDPAKPFQLYTSHSEHASIAVLTQKHAGRTRPIAFLSS KFDAIESGLPPCLKACASIHRSLTQADSFILGAPLIIYTTHAICTLLQRDRSQLVTASRFSKWEADLLRPE LTFVACSAVSPAHLYMQSCENNIPPHDCVLLTHTISRPRPDLSDLPIPDPDMTLFSDGSYTTGRGGA AVVMHRPVTDDFIIIHQQPGGASAQTAELLALAAACHLATDKTVNIYTDSRYAYGVVHDFGHLWM HRGFVTSAGTPIKNHKEIEYLLKQIMKPKQVSVIKIEAHTKGVSMEVRGNAAADEAAKNAVFLVQR AGKRTADGSEFEKRTADGSEFESPKKKAKVE (SEQ ID NO: 15469)
		MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSG ETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDE VAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYN QLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDA KLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQ DLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLL RKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTR KSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGM RKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDK DFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRD KQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQT VKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQL QNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPS EEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSR MNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLES EFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWD KGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYS VLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKR MLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVI LADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQ SITGLYETRIDLSQLGGDGGGGGPAPGSSGGHLPPPPQVDQFPLNLPERLQALNDLVSKALEAGHIE PYSGPGNNPVFPVKKPNGKWRFIHDLRATNAITTTLTSPSPGPPDLTSLPTALPHLQTIDLTDAFFQI PLPKQYQPYFAFTIPQPCNYGPGTRYAWTVLPQGFKNSPTLFQQQLAAVLNPMRKMFPTSTIVQY MDDILLASPTNEELQQLSQLTLQALTTHGLPISQEKTQQTPGQIRFLGQVISPNHITYESTPTIPIKSQ WTLTELQVILGEIQWVSKGTPILRKHLQSLYSALHPYRDPRACITLTPQQLHALHAIQQALQHNCRG RLNPALPLLGLISLSTSGTTSVIFQPKQNWPLAWLHTPHPPTSLCPWGHLLACTILTLDKYTLQHYGQ LCQSFHHNMSKQALCDFLRNSPHPSVGILIHHMGRFHNLGSQPSGPWKTLLHLPTLLQEPRLLRPIF TLSPVVLDTAPCLFSDGSPQKAAYVLWDQTILQQDITPLPSHETHSAQKGELLALICGLRAAKPWPSL NIFLDSKYLIKYLHSLAIGAFLGTSAHQTLQAALPPLLQGKTIYLHHVRSHTNLPDPISTFNEYTDSLILA PLVPLAGKRTADGSEFEKRTADGSEFESPKKKAKVE (SEQ ID NO: 15470)

The data from each candidate tested within an RT family were grouped and compared to the data for the pooled RT families tested in the preceding Examples to verify that the trends seen in the pooled

experiments were replicated when the candidates were tested individually (FIG. 17). The results confirmed that the performance of exemplary gene modifying polypeptides when tested individually recapitulated the trends observed in the pooled experiments.

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.

CLAIMS

1. A gene modifying polypeptide comprising:

a Cas domain (e.g., a Cas nickase domain, e.g., a Cas9 nickase domain);

a reverse transcriptase (RT) domain of Table 1, 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 1 as the RT domain, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

2. The gene modifying polypeptide of claim 1, wherein the RT domain has a sequence with at least 90% identity to the RT domain of Table 1.

3. The gene modifying polypeptide of any of the preceding claims, wherein the RT domain has a sequence with at least 95% identity to the RT domain of Table 1.

4. The gene modifying polypeptide of any of the preceding claims, wherein the RT domain has a sequence with at least 98% identity to the RT domain of Table 1.

5. The gene modifying polypeptide of any of the preceding claims, wherein the RT domain has a sequence with at least 99% identity to the RT domain of Table 1.

6. The gene modifying polypeptide of any of the preceding claims, wherein the RT domain has a sequence with 100% identity to the RT domain of Table 1.

7. The gene modifying polypeptide of any of the preceding claims, wherein the linker has a sequence with at least 90% identity to the linker sequence from the same row of Table 1 as the RT domain.

8. The gene modifying polypeptide of any of the preceding claims, wherein the linker has a sequence with at least 95% identity to the linker sequence from the same row of Table 1 as the RT domain.

9. The gene modifying polypeptide of any of the preceding claims, wherein the linker has a sequence with at least 97% identity to the linker sequence from the same row of Table 1 as the RT domain.

10. The gene modifying polypeptide of any of the preceding claims, wherein the linker has a sequence with 100% identity to the linker sequence from the same row of Table 1 as the RT domain.

11. The gene modifying polypeptide of any of the preceding claims, wherein the RT domain comprises a mutation as listed in Table 2.

12. The gene modifying polypeptide of any of the preceding claims, wherein the Cas domain comprises a sequence of Table 7 or 8, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 98%, or 99% identity thereto.

13. The gene modifying polypeptide of any of the preceding claims, wherein the Cas domain is a Cas nickase domain.

14. The gene modifying polypeptide of any of the preceding claims, wherein the Cas domain is a Cas9 nickase domain.

15. The gene modifying polypeptide of any of the preceding claims, wherein the Cas domain comprises an N863A mutation.

16. The gene modifying polypeptide of any of the preceding claims, which comprises an NLS, e.g., wherein the gene modifying polypeptide comprises two NLSs.

17. The gene modifying polypeptide of any of the preceding claims, which comprises an NLS N-terminal of the Cas9 domain.

18. The gene modifying polypeptide of any of the preceding claims, which comprises an NLS C-terminal of the RT domain.

19. The gene modifying polypeptide of any of the preceding claims, which comprises a first NLS which is N-terminal of the Cas9 domain and a second NLS which is C-terminal of the RT domain.

20. The gene modifying polypeptide of any of the preceding claims, which 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.

21. The gene modifying polypeptide of any of the preceding claims, which 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.

22. The gene modifying polypeptide of any of the preceding claims, which comprises a GG amino acid sequence between the Cas domain and the linker.

23. The gene modifying polypeptide of any of the preceding claims, which comprises an AG amino acid sequence between the RT domain and the second NLS.

24. The gene modifying polypeptide of any of the preceding claims, which comprises a GG amino acid sequence between the linker and the RT domain.

25. The gene modifying polypeptide of any of the preceding claims, which 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.

26. The gene modifying polypeptide of any of the preceding claims, which comprises an amino acid sequence with at least 90% identity to any of SEQ ID Nos: 1-3332 in the sequence listing.

27. The gene modifying polypeptide of any of the preceding claims, which comprises an amino acid sequence with at least 95% identity to any of SEQ ID Nos: 1-3332 in the sequence listing.

28. The gene modifying polypeptide of any of the preceding claims, which comprises an amino acid sequence with at least 98% identity to any of SEQ ID Nos: 1-3332 in the sequence listing.

29. The gene modifying polypeptide of any of the preceding claims, which comprises an amino acid sequence with at least 99% identity to any of SEQ ID Nos: 1-3332 in the sequence listing.

30. The gene modifying polypeptide of any of the preceding claims, which comprises an amino acid sequence with 100% identity to any of SEQ ID Nos: 1-3332 in the sequence listing.

31. The gene modifying polypeptide of any of the preceding claims, which produces an increase in converted GFP+ of at least 10%, 20%, 30%, 40%, 50%, 60%, 70%, 75%, 80%, 85%, 90%, 95%, 100%, 125%, 150%, 175%, 200%, 250%, 300%, 400%, 500%, 600%, 700%, 800%, 900%, 1000%, 1500%, 2000%, or 2500% relative to unsorted input cells in an assay of Example 2 using HEK cells and g4 guide RNA.

32. The gene modifying polypeptide of any of the preceding claims, which has an activity that is at least 50%, 60%, 70%, 80%, or 90% of the activity of a gene modifying polypeptide comprising, in an N-terminal to C-terminal direction:
a) an NLS and Cas domain sequence of SEQ ID NO: 4000;
b) a linker having the sequence EAAAKGSS (SEQ ID NO: 5152);
c) an RT domain having the sequence of PERV_Q4VFZ2_3mutA_WS; and
d) an NLS sequence of SEQ ID NO: 4001,
in an assay of Example 1 using HEK cells and g4 guide RNA.

33. The gene modifying polypeptide of any of the preceding claims, which has an activity that is at least 10%, 20%, 30%, 40%, 50%, 60%, 70%, 75%, 80%, 85%, 90%, 95%, 100%, 125%, 150%, 175%, 200%, 250%, 300%, 400%, 500%, 600%, 700%, 800%, 900%, 1000%, 1500%, 2000%, or 2500% greater than the activity of a gene modifying polypeptide comprising a sequence of SEQ ID NO: 4002, e.g., in an assay of Example 1 using HEK cells and g4 guide RNA.

34. A nucleic acid (e.g., DNA or RNA, e.g., mRNA) encoding the gene modifying polypeptide of any of the preceding claims.

35. A cell comprising the gene modifying polypeptide of any of claims 1-33 or the nucleic acid of claim 34.

36. A system comprising:
i) the gene modifying polypeptide of any of claims 1-33, and
ii) a template RNA that comprises:
a) a gRNA spacer that is complementary to a portion a target nucleic acid sequence;

b) a gRNA scaffold that binds the Cas domain of the gene modifying polypeptide;

c) a heterologous object sequence; and

d) a primer binding site sequence (PBS sequence).

37. A method for modifying a target nucleic acid in a cell (e.g., a human cell), the method comprising contacting the cell with the system of claim 36, or nucleic acid encoding the same, thereby modifying the target nucleic acid.

38. A gene modifying polypeptide comprising:

a Cas domain (e.g., a Cas nickase domain, e.g., a Cas9 nickase domain);

a reverse transcriptase (RT) domain comprising the RT domain of a reference gene modifying polypeptide having the sequence of any one of SEQ ID NOs: 1-7743, 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 comprises the linker of said reference gene modifying polypeptide, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

39. A gene modifying polypeptide comprising:

a Cas domain (e.g., a Cas nickase domain, e.g., a Cas9 nickase domain);

a reverse transcriptase (RT) domain of Table 1, 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 1 as the RT domain, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

40. A gene modifying polypeptide comprising:

a Cas domain (e.g., a Cas nickase domain, e.g., a Cas9 nickase domain);

a reverse transcriptase (RT) domain of Table A1, 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 comprises a sequence from the same row of Table A1 as the RT domain, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

41. A gene modifying polypeptide comprising:

a Cas domain (e.g., a Cas nickase domain, e.g., a Cas9 nickase domain);

a reverse transcriptase (RT) domain of Table A5, 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 comprises a sequence from the same row of Table D1 as the RT domain, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

42. A gene modifying polypeptide comprising:

a Cas domain (e.g., a Cas nickase domain, e.g., a Cas9 nickase domain);

a reverse transcriptase (RT) domain of Table T1, 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 comprises a sequence from the same row of Table D1 as the RT domain, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

43. A gene modifying polypeptide comprising:

a Cas domain (e.g., a Cas nickase domain, e.g., a Cas9 nickase domain);

a reverse transcriptase (RT) domain of Table T2, 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 comprises a sequence from the same row of Table D1 as the RT domain, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

44. A gene modifying polypeptide comprising:

a Cas domain (e.g., a Cas nickase domain, e.g., a Cas9 nickase domain);

a reverse transcriptase (RT) domain of Table D1, 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 comprises a sequence from the same row of Table D1 as the RT domain, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

45. A gene modifying polypeptide comprising:

a Cas domain (e.g., a Cas nickase domain, e.g., a Cas9 nickase domain);

a reverse transcriptase (RT) domain of Table D2, 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 comprises a sequence from the same row of Table D2 as the RT domain, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

46. A gene modifying polypeptide comprising:

a Cas domain (e.g., a Cas nickase domain, e.g., a Cas9 nickase domain);

a reverse transcriptase (RT) domain of Table D3, 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 comprises a sequence from the same row of Table D3 as the RT domain, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

47. A gene modifying polypeptide comprising:

a Cas domain (e.g., a Cas nickase domain, e.g., a Cas9 nickase domain);

a reverse transcriptase (RT) domain of Table D4, 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 comprises a sequence from the same row of Table D4 as the RT domain, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

48. A gene modifying polypeptide comprising:

a Cas domain (e.g., a Cas nickase domain, e.g., a Cas9 nickase domain);

a reverse transcriptase (RT) domain of Table D5, 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 comprises a sequence from the same row of Table D5 as the RT domain, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

49. A gene modifying polypeptide comprising:

a Cas domain (e.g., a Cas nickase domain, e.g., a Cas9 nickase domain);

a reverse transcriptase (RT) domain of Table D6, 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 comprises a sequence from the same row of Table D6 as the RT domain, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

50. A gene modifying polypeptide comprising:

a Cas domain (e.g., a Cas nickase domain, e.g., a Cas9 nickase domain);

a reverse transcriptase (RT) domain of Table D7, 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 comprises a sequence from the same row of Table D7 as the RT domain, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

51. A gene modifying polypeptide comprising:

a Cas domain (e.g., a Cas nickase domain, e.g., a Cas9 nickase domain);

a reverse transcriptase (RT) domain of Table D8, 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 comprises a sequence from the same row of Table D8 as the RT domain, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

52. A gene modifying polypeptide comprising:

a Cas domain (e.g., a Cas nickase domain, e.g., a Cas9 nickase domain);

a reverse transcriptase (RT) domain of Table D9, 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 comprises a sequence from the same row of Table D9 as the RT domain, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

53. A gene modifying polypeptide comprising:

a Cas domain (e.g., a Cas nickase domain, e.g., a Cas9 nickase domain);

a reverse transcriptase (RT) domain of Table D10, 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 comprises a sequence from the same row of Table D10 as the RT domain, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

54. A gene modifying polypeptide comprising:

a Cas domain (e.g., a Cas nickase domain, e.g., a Cas9 nickase domain);

a reverse transcriptase (RT) domain of Table D11, 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 comprises a sequence from the same row of Table D11 as the RT domain, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

55. A gene modifying polypeptide comprising:

a Cas domain (e.g., a Cas nickase domain, e.g., a Cas9 nickase domain);

a reverse transcriptase (RT) domain of Table D12, 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 comprises a sequence from the same row of Table D12 as the RT domain, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

56. A gene modifying polypeptide comprising:

a Cas domain (e.g., a Cas nickase domain, e.g., a Cas9 nickase domain);

a reverse transcriptase (RT) domain of Table T1, 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 comprises a sequence from the same row of Table T1 as the RT domain, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

57. A gene modifying polypeptide comprising:

a Cas domain (e.g., a Cas nickase domain, e.g., a Cas9 nickase domain);

a reverse transcriptase (RT) domain of Table T2, 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 comprises a sequence from the same row of Table T2 as the RT domain, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

58. A gene modifying polypeptide comprising:

a Cas domain (e.g., a Cas nickase domain, e.g., a Cas9 nickase domain);

an AVIRE reverse transcriptase (RT) domain (e.g., as described herein), 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 comprises a sequence as listed in Figure 11, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

59. A gene modifying polypeptide comprising:

a Cas domain (e.g., a Cas nickase domain, e.g., a Cas9 nickase domain);

a reverse transcriptase (RT) domain comprising an amino acid sequence of an RT domain provided in any one of SEQ ID NOs: 1-7743, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto; and

a linker disposed between the RT domain and the Cas domain comprising an amino acid sequence of a linker as listed in Table 10, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto,

wherein the amino acid sequences of the RT domain and the linker are provided in the same amino acid sequence of any one of SEQ ID NOs: 1-7743,

which produces an increase in converted GFP+ of at least 10%, 20%, 30%, 40%, 50%, 60%, 70%, 75%, 80%, 85%, 90%, 95%, 100%, 125%, 150%, 175%, 200%, 250%, 300%, 400%, 500%, 600%, 700%, 800%, 900%, 1000%, 1500%, 2000%, or 2500% relative to unsorted input cells in an assay of Example 2 using HEK cells and g4 guide RNA.

60. A nucleic acid (e.g., DNA or RNA, e.g., mRNA) encoding the gene modifying polypeptide of any of the claims 38-59.

61. A cell comprising the gene modifying polypeptide of any of claims 38-59 or the nucleic acid of claim 60.

62. A system comprising:

i) the gene modifying polypeptide of any of claims 38-59, and

ii) a template RNA that comprises:

a) a gRNA spacer that is complementary to a portion a target nucleic acid sequence;

b) a gRNA scaffold that binds the Cas domain of the gene modifying polypeptide;

c) a heterologous object sequence; and

d) a primer binding site sequence (PBS sequence).

63. A method for modifying a target nucleic acid in a cell (e.g., a human cell), the method comprising contacting the cell with the system of claim 62, or nucleic acid encoding the same, thereby modifying the target nucleic acid.

64. A gene modifying polypeptide comprising:

a reverse transcriptase (RT) domain of an AVIRE RT, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto;

a Cas nickase domain, wherein the RT domain is C-terminal of the Cas domain; and

a linker disposed between the Cas nickase domain and the RT domain, wherein the linker comprises an amino acid sequence as listed in Table 10, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto.

65. A gene modifying polypeptide comprising:

a reverse transcriptase (RT) domain comprising the RT domain of a reference gene modifying polypeptide having sequence of any one of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 9, 10, 12, 13, 14, 6076, 6143, 6200, 6254, 6274, 6315, 6328, 6337, 6403, 6420, 6440, 6513, 6552, 6613, 6671, 6822, 6840, 6884, 6907, 6970, 7025, 7052, 7078, 7243, 7253, 7318, 7379, 7486, 7524, 7668, 7680, 7720, 1137, 1138, 1139, 1140, 1141, 1142, 1143, 1144, 1145, 1146, 1147, 1148, 1149, 1150, 1151, 1152, 1153, 1154, 1155, 1156, 1157, 1158, 1159, 1160, 1161, 1162, 1163, 1164, 1165, 1166, 1167, 6015, 6029, 6045, 6077, 6129, 6144, 6164, 6201, 6227, 6244, 6250, 6264, 6289, 6304, 6316, 6384, 6421, 6441, 6492, 6514, 6530, 6569, 6584, 6621, 6651, 6659, 6683, 6703, 6727, 6732, 6745, 6755, 6784, 6817, 6823, 6841, 6871, 6885, 6898, 6908, 6933, 6971, 7009, 7018, 7045, 7053, 7068, 7079, 7096, 7104, 7122, 7151, 7163, 7181, 7244, 7273, 7319, 7336, 7380, 7402, 7462, 7487, 7525, 7569, 7626, 7689, 7707, 7721, 1371, 1372, 1373, 1374, 1375, 1376, 1377, 1378, 1379, 1380, 1381, 1382, 1383, 1384, 1385, 1386, 1387, 1388, 1389, 1390, 1391, 1392, 1393, 1394, 1395, 1396, 1397, 1398, 1399, 1400, 1401, 1402, 1403, 1404, 1405, 1406, 1407, 1408, 1409, 1410, 1411, 1412, 1413, 1414, 1415, 1416, 1417, 1418, 1419, 1420, 1421, 1422, 1423, 1424, 1425, 1426, 1427, 1428, 1429, 1430, 1431, 1432, 1433, 1434, 1435, 1436, 1437, 1439, 1440, 1441, 1442, 1443, 1444, 1445, 1446, 1447, 6001, 6030, 6078, 6108, 6130, 6165, 6265, 6275, 6305, 6329, 6370, 6385, 6404, 6531, 6585, 6622, 6652, 6733, 6756, 6765, 6798, 6824, 6972, 7046, 7054, 7069, 7080, 7105, 7123, 7143, 7152, 7204, 7320, 7351, 7381, 7403, 7438, 7488, 7500, 7526, 7588, 7612, 7627 or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto;

a Cas nickase domain, wherein the RT domain is C-terminal of the Cas domain; and

a linker disposed between the Cas nickase domain and the RT domain, wherein the linker comprises the linker of said reference gene modifying polypeptide, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

66. A gene modifying polypeptide comprising:

a reverse transcriptase (RT) domain having the sequence of SEQ ID NO: 8001, 8002, or 8003, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto;

a Cas nickase domain, wherein the RT domain is C-terminal of the Cas nickase domain; and

a linker disposed between the RT domain and the Cas nickase domain, wherein the linker comprises an amino acid sequence of the linker of any of SEQ ID NOS: a reference gene modifying polypeptide having sequence of any one of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 9, 10, 12, 13, 14, 6076, 6143, 6200, 6254, 6274, 6315, 6328, 6337, 6403, 6420, 6440, 6513, 6552, 6613, 6671, 6822, 6840, 6884, 6907, 6970, 7025, 7052, 7078, 7243, 7253, 7318, 7379, 7486, 7524, 7668, 7680, 7720, 1137, 1138, 1139, 1140, 1141, 1142, 1143, 1144, 1145, 1146, 1147, 1148, 1149, 1150, 1151, 1152, 1153, 1154, 1155, 1156, 1157, 1158, 1159, 1160, 1161, 1162, 1163, 1164, 1165, 1166, 1167, 6015, 6029, 6045, 6077, 6129, 6144, 6164, 6201, 6227, 6244, 6250, 6264, 6289, 6304, 6316, 6384, 6421, 6441, 6492, 6514, 6530, 6569, 6584, 6621, 6651, 6659, 6683, 6703, 6727, 6732, 6745, 6755, 6784, 6817, 6823, 6841, 6871, 6885, 6898, 6908, 6933, 6971, 7009, 7018, 7045, 7053, 7068, 7079, 7096, 7104, 7122, 7151, 7163, 7181, 7244, 7273, 7319, 7336, 7380, 7402, 7462, 7487, 7525, 7569, 7626, 7689, 7707, 7721, 1371, 1372, 1373, 1374, 1375, 1376, 1377, 1378, 1379, 1380, 1381, 1382, 1383, 1384, 1385, 1386, 1387, 1388, 1389, 1390, 1391, 1392, 1393, 1394, 1395, 1396, 1397, 1398, 1399, 1400, 1401, 1402, 1403, 1404, 1405, 1406, 1407, 1408, 1409, 1410, 1411, 1412, 1413, 1414, 1415, 1416, 1417, 1418, 1419, 1420, 1421, 1422, 1423, 1424, 1425, 1426, 1427, 1428, 1429, 1430, 1431, 1432, 1433, 1434, 1435, 1436, 1437, 1439, 1440, 1441, 1442, 1443, 1444, 1445, 1446, 1447, 6001, 6030, 6078, 6108, 6130, 6165, 6265, 6275, 6305, 6329, 6370, 6385, 6404, 6531, 6585, 6622, 6652, 6733, 6756, 6765, 6798, 6824, 6972, 7046, 7054, 7069, 7080, 7105, 7123, 7143, 7152, 7204, 7320, 7351, 7381, 7403, 7438, 7488, 7500, 7526, 7588, 7612, 7627, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

67. A gene modifying polypeptide comprising:

a reverse transcriptase (RT) domain having the sequence of SEQ ID NO: 8,003, or a sequence having at least 95% identity thereto;

a Cas nickase domain, wherein the RT domain is C-terminal of the Cas nickase domain; and

a linker disposed between the RT domain and the Cas nickase domain, wherein the linker comprises an amino acid sequence according to SEQ ID NO: 5217 or 15,401.

68. A gene modifying polypeptide comprising:

a reverse transcriptase (RT) domain having the sequence of SEQ ID NO: 8,020, or a sequence having at least 95% identity thereto;

a Cas nickase domain, wherein the RT domain is C-terminal of the Cas nickase domain; and

a linker disposed between the RT domain and the Cas nickase domain, wherein the linker comprises an amino acid sequence according to SEQ ID NO: 5217 or 15,402.

69. A gene modifying polypeptide comprising:

a reverse transcriptase (RT) domain having the sequence of SEQ ID NO: 8,074, or a sequence having at least 95% identity thereto;

a Cas nickase domain, wherein the RT domain is C-terminal of the Cas nickase domain; and

a linker disposed between the RT domain and the Cas nickase domain, wherein the linker comprises an amino acid sequence according to SEQ ID NO: 15,403.

70. A gene modifying polypeptide comprising:

a reverse transcriptase (RT) domain having the sequence of SEQ ID NO: 8,113, or a sequence having at least 95% identity thereto;

a Cas nickase domain, wherein the RT domain is C-terminal of the Cas nickase domain; and

a linker disposed between the RT domain and the Cas nickase domain, wherein the linker comprises an amino acid sequence according to SEQ ID NO: 15,404.

71. A gene modifying polypeptide comprising:

a reverse transcriptase (RT) domain comprising the RT domain of a reference gene modifying polypeptide having the sequence of any one of SEQ ID NOs: 1-7743,; and

a Cas nickase domain, wherein the RT domain is C-terminal of the Cas nickase domain; and

a linker disposed between the RT domain and the Cas nickase domain, wherein the linker comprises the linker of said reference gene modifying polypeptide.

72. A nucleic acid molecule encoding the gene modifying polypeptide of any of claims 64-71.

73. A cell comprising the gene modifying polypeptide of any of claims 64-71.

74. A cell comprising the nucleic acid molecule of claim 72.

75. A system comprising:

i) the gene modifying polypeptide of any of claims 64-71, or a nucleic acid molecule encoding the gene modifying polypeptide of claim 72, and

ii) a template RNA that comprises:

a) a gRNA spacer that is complementary to a portion a target nucleic acid sequence;

b) a gRNA scaffold that binds the Cas nickase domain of the gene modifying polypeptide;

c) a heterologous object sequence; and

d) a primer binding site sequence.

76. A lipid nanoparticle formulation comprising the gene modifying polypeptide of any of claims 64-71, the nucleic acid of claim 72, or the system of claim 75.

77. A method for modifying a target nucleic acid molecule in a cell, the method comprising contacting the cell with the system of claim 75, thereby modifying the target nucleic acid molecule.

78. A method of using a gene modifying polypeptide according to any of claims 64-71, or a nucleic acid of claim 72, or a system of claim 75, to modify a target genome by target-primed reverse transcription, the method comprising contacting the target genome with the gene modifying polypeptide, nucleic acid, or system, thereby modifying the target nucleic acid molecule.