COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE PROTEINS OF THERAPEUTIC POTENTIAL

Field of the present Invention

A computational method for identifying adhesin and adhesin-like proteins; computer system for performing the method; and genes and proteins encoding adhesin and adhesin-like proteins

Background and prior art of the present invention

The progress in genome sequencing projects has generated a large number of inferred protein sequences from different organisms. It is expected that the availability of the information on the complete set of proteins from infectious human pathogens will enable us to develop novel molecular approaches to combat them. A necessary step in the successful colonization and subsequent manifestation of disease by microbial pathogens is the ability to adhere to host cells.

Microbial pathogens encode several proteins known as adhesins that mediate their adherence to host cell surface receptors, membranes, or extracellular matrix for successful colonization. Investigations in this primary event of host-pathogen interaction over the past decades have revealed a wide array of adhesins in a variety of pathogenic microbes. Presently, substantial information on the biogenesis of adhesins and the regulation of adhesin factors is available. One of the best understood mechanisms of bacterial adherence is attachment mediated by pili or fimbriae. Several afimbrial adhesins also have been reported. In addition, limited knowledge on the target host receptors also has been gained (Finlay, B.B. and Falkow, S 1997).

New approaches to vaccine development focus on targeting adhesins to abrogate the colonization process (Wizemann, *et al* 1999). However, the specific role of particular adhesins has been difficult to elucidate. Thus, prediction of adhesins or adhesin-like proteins and their functional characterization is likely to aid not only in deciphering the molecular mechanisms of host pathogen interaction but also in developing new vaccine formulations, which can be tested in suitable experimental model systems.

One of the best understood mechanisms of bacterial adherence is attachment mediated by pili or fimbriae. For example, FimH and PapG adhesins of *Escherichia coli* (Maurer, L., Orndorff, P.(1987), Bock, K., *et al.*(1985). Other examples of pili group adhesins include type IV pili in *Pseudomonas aeruginosa*, Neisseria species, Moraxella species, Enteropathogenic *Escherichia coli* and *Vibrio cholerae* (Sperandio V *et al* (1996).

Several afimbrial adhesins are HMW proteins of *Haemophilus influenzae* (van Schilfgaarde 2000), the filamentous hemagglutinin, pertactin, of *Bordetella pertussis* (Bassinet *et al* 2000), the BabA of *H. pylori* (Yu J *et al* 2002) and the YadA adhesin of *Yersinia enterocolitica* (Neubauer *et al* 2000). The intimin receptor protein (Tir) of Enteropathogenic *E. coli* (EPEC) is another type of adhesin (Ide T *et al* 2003). Other class of adhesins includes MrkD protein of *Kleibsella pneumoniae*, Hia of *H. influenzae* (St Geme *et al* 2000), Ag I/II of *Streptococcus mutans* and SspA, SspB of *Streptococcus gordonii* (Egland *et al* 2001), FnbA, FnbB of *Staphylococcus aureus* and SfbI, protein F of *Streptococcus pyogenes* , the PsaA of *Streptococcus pneumoniae* (De *et al* 2003).

A known example of adhesins approved as vaccine is the acellular pertussis vaccine containing FHA and pertactin against *B. pertussis* the causative agent of whooping cough (Halperin, S *et al* 2003). Immunization with FimH is being evaluated for protective immunity against pathogenic *E. coli* (Langermann S *et al* 2000), in *Streptococcus pneumoniae*, PsaA is being investigated as a potential vaccine candidate against pneumococcal disease (Rapola, S *et al* 2003). Immunization results with BabA adhesin showed promise for developing a vaccine against *H. pylori* (Prinz, C *et al* 2003). A synthetic peptide sequence anti-adhesin vaccine is being evaluated for protection against *Pseudomonas aeruginosa* infections.

Screening for adhesin and adhesin like proteins by conventional experimental method is laborious, time consuming and expensive. As an alternative, homology search is used to facilitate the identification of adhesins. Although, this procedure is useful in the analysis of genome organization (Wolf *et al* 2001) and of metabolic pathways (Peregrin-Alvarez *et al* 2003, Rison *et al* 2002), it is somewhat limited in allowing functional predictions when the homologues are not functionally characterized or the sequence divergence is high. Assignment of functional roles to proteins based on this technique has been possible for only about 60% of the predicted protein sequences (Fraser *et al* 2000). Thus, we explored the possibility of developing a non-homology method based on sequence composition properties combined with the power of the Artificial Neural Networks to identify adhesins and adhesin-like proteins in species belonging to wide phylogenetic spectrum.

Twenty years ago, Nishikawa *et al* carried out some of the early attempts to classify proteins into different groups based on compositional analysis (Nishikawa *et al* 1983).

More recently, the software PropSearch was developed for analyzing protein sequences where conventional alignment tools fail to identify significantly similar sequences (Hobohm, U. and Sander, C 1995). PropSearch uses 144 compositional properties of protein sequences to detect possible structural or functional relationships between a new sequence and sequences in the database. Recently the compositional attributes of proteins have been used to develop softwares for predicting secretory proteins in bacteria and apicoplast targeted proteins in *Plasmodium falciparum* by training Artificial Neural Networks (Zuegge *et al* 2001).

Zuegge et al have used the 20 amino acid compositional properties. Their objective was to extract features of apicoplast targeted proteins in *Plasmodium falciparum*. This is distinct from our software SPAAN that focuses on adhesins and adhesin-like proteins involved in host-pathogen interaction.

Hobohm and Sander have used 144 compositional properties including isoelectric point and amino acid and dipeptide composition to generate hypotheses on putative functional role of proteins that are refractory to analysis using other sequence alignment based approaches like BLAST and FASTA. Hobohm and Sander do not specifically address the issue of adhesins and adhesin-like proteins, which is the focus of SPAAN

Nishikawa et al had originally attempted to classify proteins into various functional groups. This was a curiosity driven exercise but eventually lead to the development of a software to discriminate extra-cellular proteins from intracellular proteins. This work did not address the issue of adhesins and adhesin-like proteins, which is the focus of SPAAN.

Thus, none of the aforementioned research groups have been able to envisage the methodology of the instant application. The inventive method of this application provides novel proteins and corresponding gene sequences.

Adhesins and adhesin-like proteins mediate host-pathogen interactions. This is the first step in colonization of a host by microbial pathogens. Attempts Worldwide are focused on designing vaccine formulations comprising adhesin proteins derived from pathogens. When immunized, host will have its immune system primed against adhesins for that pathogen. When a pathogen is actually encountered, the surveillance mechanism will recognize these adhesins, bind them through antigen-antibody interactions and neutralize the pathogen through complement mediate cascade and other related clearance mechanisms. This strategy has been successfully employed in

the case of Whooping cough and is being actively pursued in the case of Pneumonia, Gastric Ulcer and Urinary tract infections.

Objects of the present Invention

The main object of the present invention is to provide a computational method for identifying adhesin and adhesin-like proteins of therapeutic potential.

Another object of invention is to provide a method for screening the proteins with unique compositional characteristics as putative adhesins in different pathogens.

Yet, another object of the invention is providing the use of gene sequences encoding the putative adhesin proteins useful as preventive therapeutics.

Summary

In a first aspect, there is provided a computational method for identifying adhesin proteins, said method comprising steps of : a. computing the sequence-based attributes of protein sequences using five attribute modules of a neural network software, wherein the attributes are, (i) amino acid frequencies, (ii) multiplet frequency, (iii) dipeptide frequencies, (iv) charge composition, and (v) hydrophobic composition, b. training a artificial neural Network (ANN) for each of the computed five attributes, and c. identifying the adhesin and adhesin-like proteins having probability of being an adhesin (P_{ad}) as ≥ 0.51.

In a second aspect, there is provided a computer system for performing the method as described above, said system comprising a central processing unit, running SPAAN program, giving probabilities based on different attributes using Artificial Neural Network and in built other programs of assessing attributes, all stored in a memory device accessed by CPU, a display on which the central processing unit displays the screens of the above mentioned programs in response to user inputs; and a user interface device.

In a third aspect, there is provided a fully connected multilayer feed forward Artificial Neural Network based on the computational method as described above, comprising of an input layer, a hidden layer and an output layer which are connected in the said sequence, wherein each neuron is a binary digit number and is connected to each neuron of the subsequent layer for identifying adhesin or adhesin like proteins, wherein the program steps comprise: [a] feeding a protein sequence in FASTA format; [b] processing the sequence obtained in step [a] through the 5 modules named A, C, D, H and M, wherein attribute A represents an amino acid composition, attribute C represents a charge composition, attribute D represents a dipeptide composition of the 20 dipeptides [NG, RE, TN, NT, GT, TT, DE, ER, RR, RK, RI, AT, TS, IV, SG, GS, TG, GN, VI and HR], attribute H represents a hydrophobic composition and attribute M represents amino acid frequencies in multiplets to quantify 5 types of compositional attributes of the said protein sequence to obtain numerical input vectors respectively for each of the said attributes wherein the sum of numerical input vectors is 105; [c] processing of the numerical input vectors obtained in step [b] by the input neuron layer to obtain signals, wherein the number of neurons is equal to the number of numerical input vectors for each attribute; [d] processing of signals obtained from step

[c] by the hidden layer to obtain synaptic weighted signals, wherein the optimal number of neurons in the hidden layer was determined through experimentation for minimizing the error at the best epoch for each network individually; [e] delivering synaptic weighted signals obtained from step [d] to the output layer for assigning of a probability value for each protein sequence fed in step [a] as being an adhesin by each network module; and [f] using the individual probabilities obtained from step [e] for computing the final probability of a protein sequence being an adhesin denoted by the P_{ad} value, which is a weighted average of the individual probabilities obtained from step [e] and the associated fraction of correlation which is a measure of the strength of the prediction, wherein the input neuron layer consists of a total of 105 neurons corresponding to 105 compositional properties.

In a fourth aspect, there is provided a fully connected multilayer feed forward Artificial Neural Network based on the computational method as described above, comprising of an input layer, a hidden layer and an output layer which are connected in the said sequence, wherein each neuron is a binary digit number and is connected to each neuron of the subsequent layer for identifying adhesin or adhesin like proteins, wherein the program steps comprise: [a] feeding a protein sequence in FASTA format; [b] processing the sequence obtained in step [a] through the 5 modules named A, C, D, H and M, wherein attribute A represents an amino acid composition, attribute C represents a charge composition, attribute D represents a dipeptide composition of the 20 dipeptides [NG, RE, TN, NT, GT, TT, DE, ER, RR, RK, RI, AT, TS, IV, SG, GS, TG, GN, VI and HR], attribute H represents a hydrophobic composition and attribute M represents amino acid frequencies in multiplets to quantify 5 types of compositional attributes of the said protein sequence to obtain numerical input vectors respectively for each of the said attributes wherein the sum of numerical input vectors is 105; [c] processing of the numerical input vectors obtained in step [b] by the input neuron layer to obtain signals, wherein the number of neurons is equal to the number of numerical input vectors for each attribute; [d] processing of signals obtained from step [c] by the hidden layer to obtain synaptic weighted signals, wherein the optimal number of neurons in the hidden layer was determined through experimentation for minimizing the error at the best epoch for each network individually; [e] delivering synaptic weighted signals obtained from step [d] to the output layer for assigning of a probability value for each protein sequence fed in step [a] as being an adhesin by each network module; and [f] using the individual probabilities obtained from step [e] for computing the final probability of a protein sequence being an adhesin denoted by the P_{ad} value, which is a weighted average of the individual probabilities obtained from step [e] and the associated fraction of correlation which is a measure of the strength of the prediction, wherein the hidden layer comprises of neurons represented as 30 for amino acid frequencies, 28 for multiplet frequencies, 28 for dipeptide frequencies, 30 for charge composition and 30 for hydrophobic composition.

In a fifth aspect, there is provided a fully connected multilayer feed forward Artificial Neural Network based on the computational method as described above, comprising of an input layer, a hidden layer and an output layer which are connected in the said sequence, wherein each neuron is a binary digit number and is connected to each neuron of the subsequent layer for identifying adhesin or adhesin like proteins, wherein the program steps comprise: [a] feeding a protein sequence in FASTA format; [b] processing the sequence obtained in step [a] through the 5 modules named A, C, D, H and M, wherein attribute A represents an amino acid composition, attribute C represents a charge composition, attribute D represents a dipeptide composition of the 20 dipeptides [NG, RE, TN, NT, GT, TT, DE, ER, RR, RK, RI, AT, TS, IV, SG, GS, TG, GN, VI and HR], attribute H represents a hydrophobic composition and attribute M represents amino acid frequencies in multiplets to quantify 5 types of compositional attributes of the said protein sequence to obtain numerical input vectors respectively for each of the said attributes wherein the sum of numerical input vectors is 105; [c] processing of the numerical input vectors obtained in step [b] by the input neuron layer to obtain signals, wherein the number of neurons is equal to the number of numerical input vectors for each attribute; [d] processing of signals obtained from step [c] by the hidden layer to obtain synaptic weighted signals, wherein the optimal number of neurons in the hidden layer was determined through experimentation for minimizing the error at the best epoch for each network individually; [e] delivering synaptic weighted signals obtained from step [d] to the output layer for assigning of a probability value for each protein sequence fed in step [a] as being an adhesin by each network module; and [f] using the individual probabilities obtained from step [e] for computing the final probability of a protein sequence being an adhesin denoted by the P_{ad} value, which is a weighted average of the individual probabilities obtained from step [e] and the associated fraction of correlation which is a measure of the strength of the prediction, wherein the output layer comprises of neurons to deliver the output values as probability value for each protein sequence.

In one embodiment, there is provided a computational method for identifying adhesin and adhesin-like proteins, said method comprising steps of computing the sequence-based attributes of protein sequences using five attribute modules of software SPAAN, (i) amino acid frequencies, (ii) multiplet frequency, (iii) dipeptide frequencies, (iv) charge composition, and (v) hydrophobic composition, training the artificial neural Network (ANN) for each of the computed five attributes, and identifying the adhesin and adhesin-like proteins having probability of being an adhesin (P_{ad}) as ≥ 0.51; a computer system for performing the method; and genes and proteins encoding adhesin and adhesin-like proteins

Detailed description of the present Invention

Accordingly, the present invention relates to a computational method for identifying adhesin and adhesin-like proteins, said method comprising steps of computing the sequence-based attributes of protein sequences using five attribute modules of software SPAAN, (i) amino acid frequencies, (ii) multiplet frequency, (iii) dipeptide frequencies, (iv) charge composition, and (v) hydrophobic composition, training the artificial neural Network (ANN) for each of the computed five attributes, and identifying the adhesin and adhesin-like proteins having probability of being an adhesin (P_{ad}) as ≥ 0.51; a computer system for performing the method; and genes and proteins encoding adhesin and adhesin-like proteins

In an embodiment of the present invention, wherein the invention relates to a computational method for identifying adhesin and adhesin-like proteins, said method comprising steps of:

a. computing the sequence-based attributes of protein sequences using five attribute modules of a neural network software, wherein the attributes

are software, (i) amino acid frequencies, (ii) multiplet frequency, (iii) dipeptide frequencies, (iv) charge composition, and (v) hydrophobic composition,

b. training the artificial neural Network (ANN) for each of the computed five attributes, and

c. identifying the adhesin and adhesin-like proteins having probability of being an adhesin (P_{ad}) as ≥ 0.51.

In another embodiment of the present invention, wherein the invention relates to a method wherein the protein sequences is obtained from pathogens, eukaryotes, and multicellular organisms.

In an embodiment of the present invention, wherein the invention relates to a method, wherein the protein sequences are obtained from the pathogens selected from a group of organisms comprising *Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Mycoplasma pneumoniae, Mycobacterium tuberculosis, Rickettsiae prowazekii, Porphyromonas gingivalis, Shigella flexneri, Streptococcus mutans, Streptococcus pneumoniae, Neisseria meningitides, Streptococcus pyogenes, Treponema pallidum* and Severe Acute Respiratory Syndrome associated human coronavirus (SARS).

In yet another embodiment of the present invention, wherein the method of the invention is a non-homology method.

In still another embodiment of the present invention, wherein the invention relates to the method using 105 compositional properties of the sequences.

In still another embodiment of the present invention, wherein the invention relates to a method showing sensitivity of at least 90%.

In still another embodiment of the present invention, wherein the invention relates to the method showing specificity of 100%.

In still another embodiment of the present invention, wherein the invention relates to a method identifying adhesins from distantly related organisms.

In still another embodiment of the present invention, wherein the invention relates to the neural network has multi-layer feed forward topology, consisting of an input layer, one hidden layer, and an output layer.

In still another embodiment of the present invention, wherein the invention relates to the number of neurons in the input layer are equal to the number of input data points for each attribute.

In still another embodiment of the present invention, wherein the invention relates to the "P_{ad}" is a weighted linear sum of the probabilities from five computed attributes.

In still another embodiment of the present invention, wherein the invention relates to each trained network assigns a probability value of being an adhesin for the protein sequence.

In still another embodiment of the present invention, wherein the invention relates to a computer system for performing the method of claim 1, said system comprising a central processing unit, executing SPAAN program, giving probabilities based on different attributes using Artificial Neural Network and in built other programs of assessing attributes, all stored in a memory device accessed by CPU, a display on which the central processing unit displays the screens of the above mentioned programs in response to user inputs; and a user interface device.

In still another embodiment of the present invention, wherein the invention relates to a set of 274 annotated genes encoding adhesin and adhesin-like proteins, having SEQ ID Nos. 385 to 658.

In still another embodiment of the present invention, wherein the invention relates to a set of 105 hypothetical genes encoding adhesin and adhesin-like proteins, having SEQ ID Nos. 659 to 763.

In still another embodiment of the present invention, wherein the invention relates to a set of 279 annotated adhesin and adhesin-like proteins of SEQ ID Nos. 1 to 279.

In still another embodiment of the present invention, wherein the invention relates to a set of 105 hypothetical adhesin and adhesin-like proteins of SEQ ID Nos. 280 to 384.

One more embodiment of the present invention, wherein the invention also relates to a fully connected multilayer feed forward Artificial Neural Network based on the computational method as claimed in claim 1, comprising of an input layer, a hidden layer and an output layer which are connected in the said sequence, wherein each neuron is a binary digit number and is connected to each neuron of the subsequent layer for identifying adhesin or adhesin like proteins, wherein the program steps comprise:-

[a] feeding a protein sequence in FASTA format; [b] processing the sequence obtained in step [a] through the 5 modules named A, C, D, H and M, wherein attribute A represents an amino acid composition, attribute C represents a charge composition, attribute D represents a dipeptide composition of the 20 dipeptides [NG, RE, TN, NT, GT, TT, DE, ER, RR, RK, RI, AT, TS, IV, SG, GS, TG, GN, VI and HR], attribute H

represents a hydrophobic composition and attribute M represents amino acid frequencies in multiplets to quantify 5 types of compositional attributes of the said protein sequence to obtain numerical input vectors respectively for each of the said attributes wherein the sum of numerical input vectors is 105; [c] processing of the numerical input vectors obtained in step [b] by the input neuron layer to obtain signals, wherein the number of neurons is equal to the number of numerical input vectors for each attribute; [d] processing of signals obtained from step [c] by the hidden layer to obtain synaptic weighted signals, wherein the optimal number of neurons in the hidden layer was determined through experimentation for minimizing the error at the best epoch for each network individually; [e] delivering synaptic weighted signals obtained from step [d] to the output layer for assigning of a probability value for each protein sequence fed in step [a] as being an adhesin by each network module; [f] using the individual probabilities obtained from step [e] for computing the final probability of a protein sequence being an adhesin denoted by the P_{ad} value, which is a weighted average of the individual probabilities obtained from step [e] and the associated fraction of correlation which is a measure of the strength of the prediction.

In still another embodiment of the present invention, wherein the input neuron layer consists of a total of 105 neurons corresponding to 105 compositional properties.

In still another embodiment of the present invention, wherein the hidden layer comprises of neurons represented as 30 for amino acid frequencies, 28 for multiplet frequencies, 28 for dipeptide frequencies, 30 for charge composition and 30 for hydrophobic composition.

In still another embodiment of the present invention, wherein the output layer comprises of neurons to deliver the output values as probability value for each protein sequence.

Identification of novel adhesins and their characterization are important for studying host-pathogen interactions and testing new vaccine formulations. We have employed Artificial Neural Networks to develop an algorithm SPAAN (Software for Prediction of Adhesin and Adhesin-like proteins using Neural Networks) that can identify adhesin proteins using 105 compositional properties of a protein sequence. SPAAN could correctly predict well characterized adhesins from several bacterial species and strains. SPAAN showed 89% sensitivity and 100% specificity in a test data set that did not

contain proteins in the training set. Putative adhesins identified by the software can serve as potential preventive therapeutics.

The present invention provides a novel computational method for identifying adhesin and adhesin-like proteins of therapeutic potential. More particularly, the present invention relates to candidate genes for these adhesins. The invention further provides new leads for development of candidate genes, and their encoded proteins in their functional relevance to preventive approaches. This computational method involves calculation of several sequence attributes and their subsequent analyses lead to the identification of adhesin proteins in different pathogens. Thus, the present invention is useful for identification of the adhesin proteins in pathogenic organisms. The adhesin proteins from different genomes constitute a set of candidates for functional characterization through targeted gene disruption, microarrays and proteomics. Further, these proteins constitute a set of candidates for further testing in development of preventive therapeutics. Also, are provided the genes encoding the candidate adhesin proteins.

The present method offers novelty in the principles used and the power of Neural Networks to identify new adhesins compared to laborious and time consuming conventional methods. The present method is based on compositional properties of proteins instead of sequence alignments. Therefore this method has the ability to identify adhesin and adhesin like proteins from bacteria belonging to a wide phylogenetic spectrum. The predictions made from this method are readily verifiable through independent analysis and experimentation. The invention has the potential to accelerate the development of new preventive therapeutics, which currently requires high investment in terms of requirement of skilled labor and valuable time.

The present invention relates to a computational method for the identification of candidate adhesin proteins of therapeutic potential. The invention particularly describes a novel method to identify adhesin proteins in different genomes of pathogens. These adhesin proteins can be used for developing preventive therapeutics.

Accordingly, a computational method for identifying adhesin and adhesin-like proteins of therapeutic potential which comprises calculation of 105 compositional properties under the five sequence attributes, namely, Amino Acid frequency, Multiplet frequency, dipeptide frequency, charge composition and hydrophobic composition; and then training Artificial Neural Network (ANN, Feed Forward Error Back Propagation)

using these properties for differentiating between adhesin and non-adhesin class of proteins. This computational method involves quantifying 105 compositional attributes of query proteins and qualifying them as adhesins or non-adhesins by a P_{ad} value (Probability of being an adhesin). The present invention is useful for identification of adhesin and adhesin-like proteins in pathogenic organisms. These newly identified adhesin and adhesin-like proteins constitute a set of candidates for development of new preventive therapeutics that can be tested in suitable experimental model systems readily. In addition, the genes encoding the candidate adhesin and adhesin-like proteins are provided.

The invention provides a set of candidate adhesin and adhesin-like proteins and their coding genes for further evaluation as preventive therapeutics. The method of invention is based on the analysis of protein sequence attributes instead of sequence patterns classified to functional domains. Present method is less dependent on sequence relationships and therefore offers the potential power of identifying adhesins from distantly related organisms. The invention provides a computational method, which involves prediction of adhesin and adhesin-like proteins using Artificial Neural Networks. The proteins termed adhesin were found to be predicted with a high probability (P_{ad} 0.51) in various pathogens. Some adhesin sequences turned out to be identical or homologous to proteins that are antigenic or implicated in virulence. By this approach, proteins could be identified and short-listed for further testing in development of new vaccine formulations to eliminate diseases caused by various pathogenic organisms.

DESCRIPTION OF TABLES

Table 1: Output file format given by SPAAN.

Table 2: Organism Name, Accession number, Number of base pairs, Date of release and Total number of proteins.

Table 3. Prediction of well characterized adhesins from various bacterial pathogens using SPAAN.

Table 4. Analysis of predictions made by SPAAN on genome scans of a few selected pathogenic organisms.

Table 5: GI numbers and Gene IDs of new putative adhesins predicted by SPAAN in the genomes listed in Table 2.

Table 6: GI numbers and Gene IDs of hypothetical proteins predicted as putative adhesins by SPAAN in the genomes listed in Table 2.

Table 7: The list of 198 adhesins found in bacteria

Brief description of the accompanying drawings

Figure 1 shows the Neural Network architecture

Figure 2 shows assessment of SPAAN using defined test dataset.

Figure 3 (a) shows Histogram plots of the number of proteins in the various P_{ad} value ranges are shown. **(b)** Pairwise sequence relationships among the adhesins were determined using CLUSTAL W and plotted on X-axis. Higher scores indicate similar pairs. **(c)** plot for non-adhesins. Data are plotted in the 4 quadrant format for clear inspection.

Software program was written in C Language and operated on Red Hat Linux 8.0 operating system. The computer program accepts input protein sequences in FastA format and produces a tabulated output. The output Table contains one row for each protein listing the probability outputs of each of the five modules, a weighted average probability of these five modules (P_{ad}), and the function of the protein as described in the input sequence file. This software is called SPAAN (A Software for Prediction of Adhesins and Adhesin-like proteins using Neural Networks) and a software copyright has been filed. Although this software has multiple modules, the running of these modules have been integrated and automated. The user only needs to run one command.

AAcompo.c:

Input: File containing protein sequences in the fasta format.

Output: File containing frequencies of all 20 AAs for each protein in one row.

charge.c:

Input: File containing protein sequences in the fasta format.

Output: File containing frequency of charged amino acids (R, K, E and D) and moments (up to 18th order) of the positions of charged amino acids.

hdr.c:

Input: File containing protein sequences in the fasta format.

Output: File containing frequencies of 5 groups of amino acids formed on the basis their Hydrophobicity and moments of their positions up to 5th order.

multiplets.c:

Input: File containing protein sequences in the fasta format.

Output: File containing fractions of multiplets of each of the 20 amino acids.

querydipep.c:

Input: File.1 containing protein sequences in the fasta format.

File.2 containing list of the significant dipeptides in dipeptide analysis.

Output: File containing frequencies of the dipeptides listed in the input File.2 for each protein in the input File.1.

train.c:

Input: File containing following specifications –

1. Number of input and output parameters.
2. Number of nodes in the hidden layers.
3. Names of the training, validate and test data files.
4. Learning rate, coefficient of moment.
5. Maximum number of cycles for training.

Output: Outputs are as follows.

1. Output of the trained NN for the test data set.
2. Values of the weight connections in the trained NN.
3. Some extra information about training.

recognize.c:

Input: File containing following specifications –

1. Number of input and output parameters.
2. Number of nodes in the hidden layers.
3. Names of the query input file.
4. Name of the file containing values of the weight connections for trained NN.
5. Name of the output file.

Output: Outputs for the query entries calculated by the trained NN.

standard.c:

Input: File containing protein sequences in fasta format.

Output: File containing protein sequences in fasta format with all the new line characters removed lying within a sequence.

filter.c:

Input: File containing protein sequences in fasta format.

Output: File containing protein sequences from the input except those which are short in length (<50 AAs) and which contain any amino acid other than the 20 known amino acids.

The five attributes:

Amino Acid frequencies

Amino acid frequency f_i = (counts of ith amino acid in the sequence) / l ; i, = 1...20, l is the length of the protein.

Multiplet frequency

Multiplets are defined as homopolymeric stretches $(X)_n$ where X is any of the 20 amino acids and n is an integer > 2. After identifying all the multiplets, the frequencies of the amino acids in the multiplets were computed as

$f_i(m)$ = (counts of i^{th} amino acid occurring as multiplet) / l

Dipeptide frequencies

The frequency of a dipeptide (i, j) f_{ij} = (counts of ij^{th} dipeptide) / (total dipeptide counts); i, j ranges from 1 to 20.

It has been found that dipeptide repeats in proteins are important for functional expression of the clumping factor present on *Staphylococcus aureus* cell surface that binds to fibrinogen (Hartford *et al* 1999). Thus we included the dipeptide frequency module. The total number of dipeptides is 400. For optimal training of Neural Network, the ratio of total number of input vectors to the total number of weight connections must be around 2 to avoid over fitting (Andrea *et al*). Therefore, we identified the dipeptides whose frequencies in the adhesin data set (469 proteins, see database construction) were significantly different from that in the non-adhesin dataset (703 proteins) using *t-test*. The frequencies of top 20 dipeptides (when arranged in the descending order of the p-values of *t-test*), were fed to the Neural Network. These dipeptides were (using single letter IUPAC-IUB code) NG, RE, TN, NT, GT, TT, DE,

ER, RR, RK, RI, AT, TS, IV, SG, GS, TG, GN, VI, AND HR. With frequency inputs for 20 dipeptides and 28 neurons in the 2nd layer, the total number of weight connections is 588, and is in keeping with the criterion of avoiding over fitting.

Charge composition

The input frequency of charged amino acids (R, K, E and D considering the ionization properties of the side chains at pH 7.2) given by f_c = (counts of charged amino acids) / l

Further, information on the characteristics of the distribution of the charged amino acids in a given protein sequence was provided by computing the moments of the positions of the occurrences of the charged amino acids. Since moments characterize the patterns of distribution such as skewness and kurtosis (sharpness of the peak) we have used them to represent the distribution patterns of the charged residues in the sequence.

The general expression to compute moments of a given order; say 'i' is

M_r = r^{th} order moment of the positions of charged amino acids

$$= \sum \frac{(X_i - X_m)^r}{N}$$

Where, X_m = mean of all positions of charged amino acids

X_i = position of i^{th} charged amino acid

N = number of charged amino acids in the sequence

The moments 2^{nd} to 19^{th} order were used to train the ANN constituting a total 20 inputs in addition to frequency of charged amino acids and the length of the protein. The upper limit of 19^{th} order was set based on assessments of sensitivity and specificity on a small dataset of adhesins and non-adhesins. Moments of order greater than 19 were not useful in improvement of performance.

Hydrophobic composition

A given protein sequence was digitally transformed using the hydrophobic scores of the amino acids according to Brendel *et al.* (43). The scores for five groups of amino acids: (-8 for K, E, D, R), (-4 for S, T, N, Q), (-2 for P, H), (+1 for A, G, Y, C, W), (+2 for L, V, I, F, M).

Following inputs were given for each of the group

(a) f_i = (counts of i^{th} group) / (total counts in the protein); i ranges from 1 to 5

(b) m_{ji} = j^{th} order moment of positions of amino acids in i^{th} group; j ranges from 2 to 5.

A total of 25 inputs representing the hydrophobic composition of a protein were fed to the Neural Network. The rationale for using moments was same as described in the section on charge composition inputs.

Taken together a total of 105 compositional properties of a given protein sequence were used to predict their adhesin characteristics.

The software PropSearch uses 144 compositional properties of protein sequences to detect possible structural or functional relationships between a new sequence and sequences in the database (Hobohm and Sander 1995). The approach defines protein sequence dissimilarity (or distance) as a weighted sum of differences of compositional properties such as singlet and doublet amino acid composition, molecular weight, isoelectric point (protein property search or PropSearch). Compositional properties of proteins have also been used for predicting secretory proteins in bacteria and apicoplast targeted proteins in Plasmodium falciparum (Zuegge, et al. 2001). The properties used here are statistical methods, principal component analysis, self-organizing maps, and supervised neural networks. In SPAAN, we have used 105 compositional properties in the five modules viz. Amino Acid frequencies, Multiplet frequencies, Dipeptide frequencies, Charge composition, Hydrophobic composition. The total of 105 properties used in SPAAN are 20 for Amino acid frequencies, 20 for Multiplets frequencies, 20 for Dipeptide frequencies (Top 20 significant dipeptides are used, based on *t-test*), 20 for Charge composition (frequency of charged amino acids (R, K, E and D) and moments of 2nd to 19th order), and 25 for Hydrophobic composition (Amino acids were classified into five groups (-8 for K, E, D, R), (-4 for S, T, N, Q), (-2 for P, H), (+1 for A, G, Y, C, W), (+2 for L, V, I, F, M). A total of 25 inputs consisted of the following: Frequency of each group, Moments of positions of amino acids in each group from 2nd to 5th order.

Neural Network

A feed forward error back propagation Neural Network was used. The program is a kind gift from Charles W. Anderson, Department of Computer Science, Colorado State University, Fort Collins, CO 80523, anderson@cs.colostate.edu

Neural Network architecture

The Neural Network used here has a multi-layer feed-forward topology. It consists of an input layer, one hidden layer and an output layer. This is a 'fully-connected' Neural Network where each neuron *i* is connected to each unit *j* of the next layer (Figure 1).

The weight of each connection is denoted by w_{ij}. The state I_i of each neuron in the input layer is assigned directly from the input data, whereas the states of hidden layer neurons are computed by the sigmoid function,

$h_j = 1 / (1 + \exp -(w_{j0} + \quad w_{ij} I_i))$,

where, w_{j0} is the bias weight

The back propagation algorithm was used to minimize the differences between the computed output and the desired output. Ten thousand cycles (epochs) of iterations are performed. Subsequently, the best epoch with minimum error was identified. At this point the network produces approximate target values for a given input in the training set.

A network was trained optimally for each attribute. Thus five networks were prepared. The schematic diagram (Figure 1) shows the procedure adopted. The number of neurons in the input layer was equal to the number of input data points for each attribute (for example 20 neurons for 20 numerical input vectors of the amino acid composition attribute). The optimal number of neurons in the hidden layer was determined through experimentation for minimizing the error at the best epoch for each network individually. An upper limit for the total number of weight connections was set to half of the total number of input vectors to avoid over fitting as suggested previously (Andrea *et al*).

Computer programs to compute individual compositional attributes were written in C and executed on a PC under Red Hat Linux ver 7.3 or 8.0. The network was trained on the training set, checks error and optimizes using the validate set through back propagation. The validate set was different from the training set. Since, the number of well annotated adhesins were not many, we used the 'validate set' itself as test set for preliminary evaluation of the performance and to obtain the fraction of correlation to compute the weighted average probability (P_{ad} value) described in the next section. The training set had 367 adhesins and 580 non-adhesins. The validate set had 102 adhesins and 123 non-adhesins. The adhesins were qualified with a digit '1' and the non-adhesins were qualified with a digit '0'.

During predictions, the network is fed with new data from the sequences that were not part of training set. Each network assigns a probability value of being an adhesin to a given sequence. The final probability is computed as described in the next section.

Probability of being an adhesin, the P_{ad} value

Query proteins are processed modularly through network trained for each attribute. Thus, five probability outputs are obtained. Final prediction was computed using the following expression which is a weighted linear sum of the probabilities from five modules:

$$P_{ad} = \frac{(P_A * fc_A + P_C * fc_C + P_D * fc_D + P_H * fc_H + P_M * fc_M)}{(fc_A + fc_C + fc_D + fc_H + fc_M)}$$

P_i = Probability from i module,

fc_i = fraction of correlation of i module of the trained Neural Network,

Where i = A (Amino acid frequencies), C (Charge composition), D (Dipeptide frequencies), H (Hydrophobic composition), or M (Multiplet frequencies).

The fraction of correlation fc_i represents the fraction of total entries that were correctly predicted ($P_{i,adhesin} > 0.5$ and $P_{i,\ non\text{-}adhesin} < 0.5$) by the trained network on the test set used in preliminary evaluation (Charles Anderson).

Neural Network

A feed forward error back propagation Neural Network was used. The program was downloaded from the web site with permission from the author, Charles W. Anderson, Department of Computer Science, Colorado State University, Fort Collins, CO 80523, anderson@cs.colostate.edu

Statistical Analysis

All statistical procedures were carried out using Microsoft Excel (Microsoft Corporation Inc. USA).

Sequence analysis

Homology analysis was carried out using CLUSTAL W (Thompson *et al* 1994), BLAST (Altschul *et al* 1990), CDD (conserved domain database) search (Marchler-Bauer *et al* 2002).

The whole genome sequences of microbial pathogens present new opportunities for the development of clinical applications such as diagnostics and vaccines. The present invention provides new leads for the development of candidate genes, and their encoded proteins in their functional relevance to preventive therapeutics.

The protein sequences of both the classes, i.e. adhesin and non-adhesin, were downloaded from the existing database (National Centre for Biotechnology Information (NCBI), USA). A total of 105 compositional properties under the five sequence

attributes namely, amino acid composition, multiplet composition, dipeptide composition, charge composition and hydrophobic composition were computed by computer programs written in C language. The attributes were computed for all the proteins in both the databases. The sequence-based attributes were then used to train Artificial Neural Network for each of the protein attributes. Adhesins were qualified by the digit '1' and non-adhesins were qualified by the digit '0'. Finally each trained Artificial Neural Network was used to identify potential adhesins which can be envisaged to be useful for the development of preventive therapeutics against pathogenic infections. Accordingly, the invention provides a computational method for identifying adhesin and adhesin-like proteins of therapeutic potential, which comprises:

1. preparing two comprehensive data-sets of adhesin and non-adhesin proteins from publicly available information on protein sequences,

2. calculating computationally the sequence based attributes of the protein sequences in the publicly available protein datasets using specially developed Software for Prediction of Adhesins and Adhesin-like proteins using Neural Networks (SPAAN),

3. training the Artificial Neural Network (ANN) for the selected attributes,

4. assigning probability value suitable for an adhesin, "P_{ad}" to the query protein and identifying adhesin like property in the query proteins with the help of trained Artificial Neural Network implemented in SPAAN,

5. validating computationally the protein sequences as therapeutic potentials by comparing with the known protein sequences that are biochemically characterized in the pathogen genome.

In an embodiment of the invention the protein sequence data may be taken from an organism, specifically but not limited to organisms such as *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Mycoplasma pneumoniae*, *Mycobacterium tuberculosis*, *Rickettsiae prowazekii*, *Porphyromonas gingivalis*, *Shigella flexneri*, *Streptococcus mutans*, *Streptococcus pneumoniae*, *Neisseria meningitides*, *Streptococcus pyogenes*, *Treponema pallidum*, Severe Acute Respiratory Syndrome associated coronavirus.

In another embodiment to the present invention different sequence-based attributes used for identification of proteins of therapeutic potential, comprise amino acid composition, charge composition, hydrophobicity composition, multiplets frequencies, and dipeptide frequencies.

In an embodiment, the non-homologous adhesin protein sequence may be compared with that of known sequences of therapeutic applications in the selected pathogens.

In an embodiment of the invention, the sequences of adhesin or adhesin like proteins comprise sequences of sequences IDs listed in Tables 5 and 6 identified by the method of invention.

Another embodiment of the invention the computer system comprises a central processing unit, executing SPAAN program, giving probabilities based on different attributes using Artificial Neural Network and in built other programs of assessing attributes, all stored in a memory device accessed by CPU, a display on which the central processing unit displays the screens of the above mentioned programs in response to user inputs; and a user interface device.

In One embodiment of the present invention, the particulars of the organisms such as their name, strain, accession number in NCBI database and other details are given in Table 2:

The invention is further explained with the help of the following examples, which are given by illustration and should be construed to limit the scope of the present invention in any manner.

Example 1

Operating SPAAN:

The purpose of the program is to computationally calculate various sequence-based attributes of the protein sequences.

The program works as follows:

The internet downloaded FASTA format files obtained from http://www.ncbi.nlm.nih.gov were saved by the name <organism_name>.faa are converted in the standard format by C program and passed as input to another set of C programs which computes the 5 different attributes of protein sequences (a total of 105 compositional properties in all 5 modules).

The computed properties were fed as input to the 5 different Neural Networks. Each trained network assigns a probability value of being an adhesin for a query protein. The final probability (P_{ad}) was calculated as weighted average of these five individual probabilities. The weights were determined from a correlation value of correct prediction during test runs of each of the five modules.

Input/Output format:

Downloaded Files and their format:

<organism_name>.faa: file which stores the annotation and the protein sequence.

Input file Format: FASTA

">gi.vertline."<annotation>

For example,

>gi.vertline.2314605.vertline.gb.vertline.AAD08472.vertline.histidine and glutamine-rich protein

MAHHEQQQQQQANSQHHHHHHHHAHHHHYYGGEHHHHNAQQHAEQQAEQQ

AQQQQQQQAHQQQQQKAQQQNQQY

>gi.vertline.3261822.vertline.gn1.vertline.PID.vertline.e328405 PE_PGRS

MIGDGANGGPGQPGGPGGLLYGNGGHGGAGAAGQDRGAGNSAGLIGNGGAG

GAGGNGGIGGAGAPGGLGGDGGKGGFADEFTGGFAQGGRGGFGGNGNTGAS

GGMGGAGGAGGAGGAGGLLIGDGGAGGAGGIGGAGGVGGGGGAGGTGGGG

VASAFGGGNAFGGRGGDGGDGGDGGTGGAGGARGAGGAGGAGGWLSGHSG

AHGAMGSGGEGGAGGGGGARGEAGAGGGTSTGTNPGKAGAPGTQGDSGDP

GPPG

>gi.vertline.. . .

Table 1: Output file format given by SPAAN

<organism_name>.out

SN	P_A	P_C	P_D	P_H	P_M	P_{ad}-value	Protein Name
1	0.05683	0.290803	0.441338	0.50304	0.029503	0.260485	>gi.vertline.32454344.vertline.gb.vertline.AAP82966.1. vertline.orf1a polyprotein [SARS coronavirus Hong Kong ZY-2003]
2	0.639235	0.166721	0.054583	0.935385	0.453498	0.462452	>gi.vertline.32454345.vertline.gb.vertline.AAP82967.1. vertline.orf1ab polyprotein [SARS coronavirus Hong Kong ZY-2003]
3	0.651111	0.911504	0.438696	0.543944	0.924044	0.690247	>gi.vertline.32454346.vertline.gb.vertline.AAP82968.1. vertline.spike glycoprotein [SARS coronavirus Hong Kong ZY-2003]

4	0.464324	0.655003	0.179503	0.008700	0.241573	0.300970	>gi.vertline.32454347.vertline.gb.vertline.AAP82969.1. vertline.Orf3a [SARS coronavirus Hong Kong ZY-2003]

Where P_A, P_C, P_D, P_H, P_M are the outputs of the five Neural Networks.

Example 2 organisms and sequence numbers

Table 2: Organism Name, Accession number, Number of base pairs, Date of release and Total number of proteins analyzed

Organism Name	Accession Number	Number of base pairs	Date of release	Total no. of proteins
E. coli O157 H7	NC_002695	5498450	7-Mar-2001	5361
H. influenzae Rd	NC_000907	1830138	30-Sep-1996	1709
H. pylori J99	NC_000921	1643831	10-Sep-2001	1491
M. pneumoniae	NC_000912	816394	2-Apr-2001	689
M. tuberculosis H37Rv	NC_000962	4411529	7-Sep-2001	3927
R. prowazekii strain Madrid E	NC_000963	1111523	10-Sep-2001	835
P. gingivalis W83	NC_002950	2343476	9-Sep-2003	1909
S. flexneri 2a str. 2457T	NC_004741	4599354	23- Apr-2003	4072
S. mutans UA159	NC_004350	2030921	25-Oct-2002	1960
S. pneumoniae R6	NC_003098	2038615	6-Sep-2001	2043
N. meningitidis serogroup A strain Z2491	NC_003116	2184406	27-Sep-2001	2065
S. pyogenes MGAS8232	NC_003485	1895017	Jan 31, 2002	1845
T. pallidum subsp. pallidum str. Nichols	NC_000919	1138011	7-Sep-2001	1036
Severe Acute Respiratory Syndrome (SARS) associated coronavirus Frankfurt 1	AY291315	29727	11-JUN-2003	14
SARS coronavirus HSR 1	AY323977	29751	15-OCT-2003	14

SARS coronavirus ZJ01	AY297028	29715	19-MAY-2003	3
SARS coronavirus TW1	AY291451	29729	14-MAY-2003	11
SARS coronavirus CUHK-Su10	AY282752	29736	07-MAY-2003	4
SARS coronavirus Urbani	AY278741	29727	12-AUG-2003	12
SARS coronavirus	NC_004718	29751	9-Sep-2003	29
SARS coronavirus Tor2	AY274119	29751	16-MAY-2003	15
SARS coronavirus GD01	AY278489	29757	18-AUG-2003	12
SARS coronavirus CUHK-W1	AY278554	29736	31-JUL-2003	11
SARS coronavirus BJ01	AY278488	29725	01-MAY-2003	11

Example 3

The multi-layered feed forward Neural Network architecture implemented in SPAAN (figure 1). A given protein sequence in FASTA format is first processed through the 5 modules A, C, D, H, and M to quantify the five types of compositional attributes. A: Amino acid composition, C: Charge composition, D: dipeptide composition of the 20 dipeptides (NG, RE, TN, NT, GT, TT, DE, ER, RR, RK, RI, AT, TS, IV, SG, GS, TG, GN, VI, HR), H: Hydrophobic composition, M: Amino acid frequencies as Multiplets. The sequence shown is part of the FimH precursor (gi 5524634) of *E. coli*. Subsequently, these numerical data are input to the input neuron layer. The directions of arrows show data flow. The number of neurons chosen in the input layer was equal to the number of the numerical input vectors of each module. The network was optimally trained through minimization of error of detection based on validate set through back propagation. The details are described in the methods. Each network module assigns a probability value of the protein being an adhesin based on the corresponding attribute. The final probability of a protein sequence being an adhesin is the P_{ad} value a weighted average of the individual probabilities and the associated fraction of correlation which is a measure of the strength of the prediction.

Example 4

Performance of SPAAN assessed using a test set of 37 adhesins and 37 non-adhesins that were not part of the training set. Matthew's correlation coefficient (Mcc, plotted on

Y-axis) for all the proteins with P_{ad} values above a given threshold (plotted on X-axis) (figure 2). The Matthew's correlation is defined as:

$$Mcc = \frac{(TP*TN)-(FP*FN)}{\sqrt{(TN+FN)(IN+FP)(TP+FN)(TP+FP)}}$$

Where TP = True Positives, TN = True Negatives, FP = False Positives, FN = False Negatives.

Here TPs are adhesins, TNs are non-adhesins. In general, adhesins have high P_{ad} value, whereas non-adhesins have low P_{ad} value. Thus known adhesins with P_{ad} value above a given threshold are true positives whereas known non-adhesins with P_{ad} value below the given threshold are true negatives. The sensitivity, Sn is given by $\left(\frac{TP}{TP+FN}\right)$ and specificity, Sp is given by $\left(\frac{TP}{TP+FP}\right)$. False negatives are those cases, wherein a known adhesin had P_{ad} value lower than the chosen threshold. Similarly, a known non-adhesin with a P_{ad} value higher than the chosen threshold was taken as false positive. A theoretical polynomial curve of second order (dashed line) was fitted to the observed curve (smooth line) with a Karl-Pearson correlation coefficient R^2 = 0.9799. The maximum point of the theoretical curve (where first derivative vanishes and second derivative is negative) was chosen as reference (vertical dotted line) to identify the maximum Mcc = 0.94 on the observed curve (shown by arrow). The corresponding P_{ad} value threshold was 0.51. At this P_{ad} value threshold, Sn and Sp were 0.89 and 1.0 respectively. Note that the Mcc does not drop down to the x-axis because the highest P_{ad} value attained by adhesins was 0.939 in comparison to the theoretical attainable limit of 1.0.

Example 5

Assessment of SPAAN on well known adhesins from various bacterial pathogens.

Table 3. Prediction of well characterized adhesins from various bacterial pathogens using SPAAN.

Species	Disease caused	Adhesin[a]	Host ligand	P_{ad} value[b] (Range)
E. coli	Diarrhoea	PapG (27)	α-D-gal(1-4) β-D-Gal-containing receptors	0.84-0.76
		SfaS (5)	alpha-sialyl-beta-2,3-b-galactose	0.94-0.94
		FimH (63)	D-mannosides	0.96-0.23[c]

		Intimin (12)	tyrosine-phosphorylated form of host cell receptor Hp90	0.95-0.78
		PrsG (5)	Gal(alpha1-4)Gal	0.86-0.85
Nontypeable *H. influenzae*	Influenza	HMW1, HMW2	Human epithelial cells	0.97
		Hia (8)	human conjuctival cells	0.93-0.90
H. influenzae	bacterial meningitis[d]	HifE (18)	Sialylyganglioside-GM1	0.85-0.73
K. pneumoniae	Pneumonia	MrkD	type V collagen	0.82
B. pertussis	Whooping cough	FHA	Sulphated sugars on cell-surface glycoconjugates	0.85
		Pertactin	Integrins	0.43
Y. enterocolitica	Enterocolitis	YadA (5)	β_1 integrins	0.88-0.79
S. mutans	Dental Caries	SpaP (2) PAc	Salivary glycoprotein Salivary glycoprotein	0.88, 0.87 0.88
Streptococcus gordonii	Oral cavity	SspA (2)	Salivary glycoprotein	0.85, 0.84
		CshA	Fibronectin	0.78
		CshB	Fibronectin	0.63
		ScaA	Co-aggregation	0.71
		SspB (2)	Salivary glycoprotein	0.85,0.84
Streptococcus sobrinus	Tooth decay	SpaA PAg (2)	Salivary glycoprotein Salivary glycoprotein	0.89 0.89, 0.73
Streptococcus pyogenes	Scarlet Fever	Protein F	Fibronectin	0.49
Streptococcus pneumoniae	Bacterial Pneumonia	PsaA (5)	Human nasopharyngeal cells	0.82-0.78
		CbpA[e] / SpsA / PbcA/ PspC	phosphorylcholine of the teichoic acid.	0.81-0.49
Streptococcus parasanguis	Valve endocarditis	FimA	Salivary glycoprotein fibrin	0.76
Streptococcus sanguis	Tooth Decay	SsaB	Salivary glycoprotein	0.71
Enterococcus faecalis	Empyma in patients with liver disease	EfaA	Unknown	0.83
Staphylococcus aureus	Food Poisoning	FnbA FnbB (3)	Fibronectin Fibronectin	0.8 0.78, 0.77, 0.69
Helicobacter pylori	Peptic Ulcers	BabA (17)	difucosylated Lewis[b] blood group antigen	0.87-0.68

[a]: The number of sequences from different strains and homologs from related species analyzed are shown in parantheses.

[b]: Rounded off to the second decimal.

[c]: Out of 63 FimH proteins, 54 were from *E. coli*, 6 from *Shigella flexineri*, 2 from *Salmonella enterica* and 1 was from *Salmonella typhimurium*. Except 2 FimH proteins, the rest had P_{ad} 0.51. The 2 exceptions (gi numbers: 5524636, 1778448) were from *E. coli*. The gi:5524636 protein is annotated as a FimH precursor but is much shorter (129 amino acids) than other members of the family. The gi:1778448 protein is a *S. typhimurium* homolog in *E. coli*.

[d]: Other ailments include pneumonia, epiglottitis, osteomyelitis, septic arthritis and sepsis in infants and older children.

[e]: The adhesin CbpA is also known by alternative names SpsA, PbcA and PspC. A total of seven sequences were analyzed. Except 1 PspC sequence, the rest all had P_{ad} 0.51.

Example 6

Ability of SPAAN to discriminate adhesins from non-adhesins at Pad 0.51 (figure 3-a).

Example 7

The non-homology character of SPAAN assesses in both adhesins and non-adhesins (figure 3b and 3c).

Figure 3 (a – c). SPAAN is non-homology based software. A total of 130 adhesins and 130 non-adhesins were analyzed to assess whether the predictive power of SPAAN could be influenced by the sequence relationships. (a) Histogram plots of the number of proteins in the various P_{ad} value ranges are shown. Shaded bars represent adhesins whereas open bars represent non-adhesins. Note the SPAAN's ability to segregate adhesins and non-adhesins into two distinct cohesive groups. (b) Pairwise sequence relationships among the adhesins were determined using CLUSTAL W and plotted on X-axis. Higher scores indicate similar pairs. The corresponding differences in P_{ad} values in the same protein pair was plotted on the Y-axis. Each point in the diagram represents a pair. Arrow points to protein pairs of the FimH family with high ΔP_{ad} values in spite of high similarity: Since one of the FimH proteins (gi: 5524636) had very low P_{ad} value all pairs with this false negative protein show high ΔP_{ad} values. The protein (gi: 5524636) is of much shorter length compared with other members of the same family. (c) plot for non-adhesins. Data are plotted in the 4 quadrant format for clear inspection. Note that among protein pairs with CLUSTAL W score < 20 the majority (82% in adhesins and 86% in non-adhesins) have $\Delta P_{ad} < 0.2$. These data support the non-homology character of SPAAN.

Example 8

Genomescan of pathogens by SPAAN identifies well known adhesins and new adhesins and adhesin-like proteins

Table 4. Analysis of predictions made by SPAAN on genome scans of a few selected pathogenic organisms[a]

Species / Protein Class	*Escherichia coli* O157:H7	*Mycobacterium tuberculosis* H37Rv	SARS associated corona virus (11 strains)
Total number of proteins with P_{ad} 0.51	575	435	5
Known adhesins	17[b]	-	-
Putative proteins with adhesin like characteristics	92[c]	105[j]	-
Hypothetical proteins with adhesin-like characteristics	22[d]	-	-
Proteins likely to be extracytoplasmic or located at surface	190[e]	191[k]	5[m]
Phage proteins	30[f]	-	-
Others	13[g]	6[l]	-
Hypothetical proteins	157[h]	86[h]	-
Wrong predictions	54[i]	47[i]	-

[a]: SPAAN has general applicability. The three pathogens chosen here are those in which intense investigations are being conducted presently. *M. tuberculosis* is of special importance to developing countries.

[b]: Fimbrial adhesins, AidA-I, gamma intimin, curlin, translocated intimin receptor, putative adhesin and transport, Iha, prepilin peptidase dependent protein C.

[c]: These proteins have been annotated as proteins with a putative function. These sequences were analyzed using CDD (Conserved domain database, NCBI) and BLAST searches. Adhesin like domains were found in these proteins.

[d]: These proteins have been annotated as 'hypothetical'. These sequences were analyzed using CDD and BLAST searches. Adhesin like domains were found in these proteins.

[e]: These proteins are outer membrane, extracellular, transport, surface, exported, flagellar, periplasmic lipoprotein, and proteins annotated as 'hypothetical' but found to have similar functions listed here using BLAST and CDD searches.

[f]: The phage proteins were of the following functional roles – tail fiber, head decoration, DNA injection, tail, major capsid, host specificity, endolysin.

[g]: Proteins predicted by SPAAN but not readily classifiable into the classes listed here have been collectively grouped as 'Others'. However, some of these proteins are known to participate in host-pathogen interactions. The annotated functional roles are typeIII secretion, antibiotic resistance, heat shock, acid shock, structural, tellurium resistance, terminase, Hcp-like, Sec-independent translocase, uncharacterized nucleoprotein, HicB-like.

[h]: These proteins have been annotated as hypothetical. Re-analyses of these proteins using BLAST and CDD failed identify any function for these proteins.

[i]: These proteins have been annotated with functional roles that are very likely to occur within the cell. Hence these proteins may have remote possibility of functioning as adhesins or adhesin-like proteins. Therefore this set of proteins have been incorrectly predicted as adhesins or adhesin-like by SPAAN.

[j]: These proteins are PE_PGRS, PE proteins. Several reports (for example Brennan *et al.*) indicate that PE_PGRS proteins may be localized to cell surface and aid in host-pathogen interaction.

[k]: Lipoproteins (lpp, lpq, lpr), PPE, outer membrane, surface, transport, secreted, periplasmic, extracellular, ESAT-6, peptidoglycan binding, exported, mpt (with extracellular domains), and proteins annotated as 'hypothetical' but found to have similar functions listed here using BLAST and CDD searches.

[l]: These proteins were of the following functions - glutaredoxin-like thioltransferase, putative involvement in molybdate uptake, ATP synthase chain, sulphotransferases, S.erythraea rhodanese-like protein M29612|SERCYSA_5, unknown function.

[m]: These proteins were the spike glycoprotein with antigenic properties, and nsp2, nsp5, nsp6 and nsp7.

Table 5: New putative adhesins predicted by SPAAN in the genomes listed in table 2 –

(Total number = 279)

Protein GI Number	Gene ID	Protein name
Escherichia coli O157:H7		
13360742	912619	hemagglutinin/hemolysin-related protein
13362986	914770	putative ATP-binding component of a transport system
13361114	913228	putative tail fiber protein
13364757	913676	minor fimbrial subunit/D-mannose specific adhesin
13362687	915687	putative fimbrial-like protein
13360856	912599	AidA-I adhesin-like protein
13364140	915374	putative fimbrial protein
13359793	914435	putative invasin
13364768	913650	putative invasin
13364034	915471	Gamma intimin
13362703	915668	putative DNA transfer protein precursor
13364141	915376	putative fimbrial protein
13359819	914463	AidA-I adhesin-like protein
13360480	917768	putative fimbrial-like protein
13362692	915681	putative fimbrial-like protein
13362585	916824	putative ATP-binding component of a transport system
13359881	914526	putative flagellin structural protein
13361579	917311	putative type 1 fimbrial protein precursor
13360880	913991	curlin major subunit CsgA
13364036	915465	translocated intimin receptor Tir
13360740	912615	putative major pilin protein
13361582	917317	putative ATP-binding component of a transport system and adhesin protein
13364754	913683	export and assembly outer membrane protein of type 1 fimbriae
13360484	917767	homolog of Salmonella FimH protein

13364751	913688	major type 1 subunit fimbrin
13359597	913742	putative fimbrial protein
13362550	916787	putative ATP-binding component of a transport system
13359595	913739	putative fimbrial protein
13359599	913748	probable outer membrane porin protein involved in fimbrial assembly
13363900	915704	putative fimbrial protein precursor
13361575	917307	putative fimbrial-like protein
13364756	913678	fimbrial morphology
13363496	916142	truncated putative fimbrial protein
13359601	913761	putative fimbrial-like protein
13364145	915368	putative type 1 fimbrial protein
13363902	915708	putative outer membrane usher protein precursor
13361576	917309	putative outer membrane protein
13361013	913353	putative major tail subunit
13364755	913682	fimbrial morphology
13360738	912793	putative outer membrane usher protein
13363928	915608	alpha-amylase
13363495	916144	putative outer membrane protein
13362383	916617	putative type-1 fimbrial protein
13364373	914972	outer membrane vitamin B12 receptor protein BtuB
13360879	912479	minor curlin subunit precursor CsgB
13360739	912756	putative chaperone protein
13361574	917314	putative fimbrial-like protein
13361127	913212	outer membrane protease precursor
13363210	916442	putative lipoprotein
13361104	913238	major tail protein
13361709	917446	putative major tail subunit
13359725	914366	outer membrane pore protein PhoE
13360875	913765	curli production assembly/transport component CsgF
13362170	913927	putative outer membrane protein
13361473	917203	putative BigB-like protein

13364025	915286	EspF protein
13360081	916982	outer membrane receptor for ferric enterobactin (enterochelin) and colicins B and D
13362977	914779	hypothetical lipoprotein
13360351	917632	outer membrane protein X
13360696	914208	putative outer membrane precursor
13361456	917206	putative outer membrane protein
13361626	917374	putative outer host membrane protein precursor
13361698	917449	putative outer membrane protein
13362186	913421	putative outer membrane protein precursor
13362697	915676	long-chain fatty acid transport protein FadL
13360918	914188	flagellar hook protein FlgE
13360737	912506	putative outer membrane protein
13360342	917629	putative outer membrane receptor for iron transport
13363396	916248	outer membrane channel TolC
13361958	912705	putative scaffolding protein in the formation of a murein-synthesizing holoenzyme
13359921	914566	nucleoside-specific channel-forming protein TSX
13360944	913890	outer membrane receptor for ferric iron uptake
13359998	914644	putative outer membrane transport protein
13363390	916251	putative ferrichrome iron receptor precursor
13364227	915153	outer membrane phospholipase A
13361982	912846	putative outer membrane protein
13360129	917032	a minor lipoprotein
13361817	912692	putative outer membrane protein
13360233	917507	membrane spanning protein TolA
13362837	915218	putative outer membrane lipoprotein
13362328	912985	putative colanic acid biosynthesis glycosyl transferase
Haemophilus influenzae Rd		
16272254	949521	prepilin peptidase-dependent protein D
16272928	950762	immunoglobin A1 protease
16272129	951072	lipoprotein

16273251	950616	hemoglobin-binding protein
30995429	950130	opacity protein
16272854	949634	protective surface antigen D15
16272283	950648	opacity associated protein
16272604	949701	hemoglobin-binding protein
Helicobacter pylori J99		
4155101	889167	putative vacuolating cytotoxin (VacA) paralog
4154798	890022	putative vacuolating cytotoxin (VacA) paralog
4155426	890036	putative vacuolating cytotoxin (VacA) paralog
4155390	890075	vacuolating cytotoxin
4155400	890058	outer membrane protein - adhesin
4155681	889718	putative Outer membrane protein
4155420	890042	Outer membrane protein/porin
4155775	889799	outer membrane protein - adhesin
4155419	890044	Outer membrane protein/porin
4154526	889066	putative Outer membrane protein
4154724	889419	putative Outer membrane protein
4155862	890404	putative Outer membrane protein
4156048	889958	putative IRON(III) DICITRATE TRANSPORT PROTEIN
4154510	889297	putative Outer membrane protein
4155432	889515	putative outer membrane protein
4155623	889671	putative Outer membrane protein
4155700	889739	putative Outer membrane function
4154740	889426	Outer membrane protein/porin
4155692	889743	putative Outer membrane protein
4155594	889648	putative outer membrane protein
4155680	889719	putative Outer membrane protein
4155217	890243	putative Outer membrane protein
4155958	889905	putative Outer membrane protein
4155201	890259	putative Outer membrane protein
4155013	889232	cag island protein
4154974	889032	putative Outer membrane protein

4155214	890244	putative Outer membrane protein
4154973	889042	Outer membrane protein
4155344	890115	putative Outer membrane protein
4155099	889160	FLAGELLIN A
4155023	888978	cag island protein
4155035	889201	cag island protein, CYTOTOXICITY ASSOCIATED IMMUNODOMINANT ANTIGEN
4155289	890164	NEURAMINYLLACTOSE-BINDING HEMAGGLUTININ PRECURSOR
Mycoplasma pneumoniae		
13507881	877207	involved in cytadherence
13507880	877268	ADP1_MYCPN adhesin P1
13508228	877211	species specific lipoprotein
13508181	877124	species specific lipoprotein
13508179	877071	Mollicute specific lipoprotein, MG307 homolog, from M. genitalium
13508178	877118	Mollicute specific lipoprotein, MG307 homolog, from M. genitalium,
13508176	876797	Mollicute specific lipoprotein, MG307 homolog, from M. genitalium
13508175	876848	Mollicute specific lipoprotein, MG307 homolog, from M. genitalium
13508106	876953	involved in cytadherence
13508350	877112	similar to phosphate binding protein Psts
Mycobacterium tuberculosis H37 Rv		
15607496	886491	PPE
15607445	886592	PPE
15610644	888270	PE_PGRS
15608588	886605	PE_PGRS
15609627	887941	PE_PGRS
15610643	888256	PE_PGRS
15607718	887725	PE_PGRS

15609054	885362	PPE
15610486	888113	PPE
15610483	888120	PPE
15610479	888033	PPE
15609771	888573	PE_PGRS
15610648	888306	PE_PGRS
15610481	888114	PE_PGRS
15608117	885264	PE_PGRS
15607973	885391	PE_PGRS
15608231	885258	PE_PGRS
15608906	885429	PE_PGRS
15608891	885544	PPE
15609990	888171	PE_PGRS
15609055	885506	PPE
15608227	887094	PE_PGRS
15610524	888151	PE_PGRS
15609490	886003	PPE
15607886	888664	PE_PGRS
15609624	887909	PE_PGRS
15607420	886621	PE_PGRS
15608897	885325	PE_PGRS(wag22)
15608590	886595	PE_PGRS
15609728	887992	PE_PGRS
15608012	885742	PE_PGRS
15608534	886745	PE_PGRS
15608940	885730	PE_PGRS
15607887	888662	PE_PGRS
15609235	888312	PE_PGRS
15610694	887822	PPE
15609533	885517	PE_PGRS
15610480		PE_PGRS

Rickettsia prowazekii strain Madrid E

15604316	883411	CELL SURFACE ANTIGEN (sca3)
15604546	883694	CELL SURFACE ANTIGEN (sca5)

Porphyromonas gingivalis W83

34541453	2551934	hemagglutinin protein HagA
34540040	2551409	lipoprotein, putative
34540364	2552375	extracellular protease, putative
34541613	2552074	hemagglutinin protein HagE
34540183	2551891	internalin-related protein

Shigella flexneri 2a str. 2457T

30065424	1080663	minor fimbrial subunit, D-mannose specific adhesin
30062726	1077662	putative adhesion and penetration protein
30063758	1078834	putative fimbrial-like protein
30065431	1080671	major type 1 subunit fimbrin (pilin)
30063366	1078379	flagellar protein FliD
30064308	1079668	outer membrane fluffing protein
30062613	1077555	flagellar hook protein FlgE
30061954	1076843	conserved hypothetical lipoprotein
30065173	1080393	putative lipase
30065425	1080664	minor fimbrial subunit, precursor polypeptide
30064485	1079637	putative fimbrial protein
30062615	1077558	flagellar basal body L-ring protein FlgH
30064307	1079452	outer membrane fluffing protein
30065601	1080859	putative glycoprotein/receptor
30062118	1077025	putative fimbrial-like protein
30064099	1079223	lipoprotein
30062616	1077559	flagellar basal body P-ring protein FlgI
30063546	1078596	putative fimbrial-like protein
30062940	1077910	putative outer membrane protein
30065426	1080665	minor fimbrial subunit, precursor polypeptide
30062779	1077721	putative outer membrane protein
30064194	1079329	putative lipoprotein
30063365	1078378	flagellin

30062298	1077222	outer membrane protein X
30064968	1080175	putative major fimbrial subunit
30061858	1076740	outer membrane pore protein E (E,Ic,NmpAB)
30062178	1080410	minor lipoprotein
30062479	1077412	putative fimbrial-like protein
30062565	1077506	minor curlin subunit precursor
30063880	1078972	putative outer membrane lipoprotein
30064531	1079686	cytoplasmic membrane protein
30065033	1080243	putative receptor protein
Streptococcus mutans UA159		
24378550	1029610	putative secreted antigen GbpB/SagA; putative peptidoglycan hydrolase
24379087	1028055	cell surface antigen SpaP
24380463	1029310	putative membrane protein
24379075	1028046	penicillin-binding protein 2b
24378955	1027967	penicillin-binding protein 1a; membrane carboxypeptidase
24379801	1028662	glucan-binding protein C, GbpC
24379528	1029536	hypothetical protein; possible cell wall protein, WapE
24379231	1028158	putative glucan-binding protein D; BglB-like protein
24380488	1029325	conserved hypothetical protein; possible transmembrane protein
24380291	1029139	putative amino acid binding protein
24379342	1028247	putative penicillin-binding protein, class C; fmt-like protein
24380047	1028904	putative ABC transporter, branched chain amino acid-binding protein
24378698	1029755	putative ABC transporter, metal binding lipoprotein; surface adhesin precursor; saliva-binding protein; lipoprotein receptor LraI (LraI family)
24378708	1029768	putative transfer protein
24379427	1028331	cell wall-associated protein precursor WapA
24379272	1028196	putative amino acid transporter, amino acid-binding protein
24379641	1028511	putative ABC transporter, amino acid binding protein

Streptococcus pneumoniae R6

15902395	934801	Choline-binding protein
15902381	934810	Choline-binding protein F
15902165	932894	Surface protein pspA precursor
15904047	934859	Choline binding protein D
15904036	933487	Choline binding protein A
15903986	933069	Choline-binding protein
15903796	933669	Autolysin (N-acetylmuramoyl-L-alanine amidase)

Neisseria meningitidis Z2491

15794121	907145	putative membrane protein
15794144	907168	putative surface fibril protein
15793284	906275	truncated pilin
15793460	906456	IgA-specific serine endopeptidase
15793282	906273	fimbrial protein precursor (pilin)
15793337	906332	adhesin
15793253	906243	putative lipoprotein
15794356	907848	putative lipoprotein
15793684	906699	putative membrane protein
15793290	906281	truncated pilin
15793283	906274	truncated pilin
15793475	906471	haemoglobin-haptoglobin-utilization protein
15793406	906401	porin, major outer membrane protein P.I
15794985	907333	adhesin MafA2
15794344	907836	putative lipoprotein
15794622	908118	hypothetical outer membrane protein
15793599	906604	pilus-associated protein
15793763	906779	putative periplasmic binding protein

Streptococcus pyogenes MGAS8232

19745214	995235	putative secreted protein
19746570	994224	putative penicillin-binding protein 1a
19745593	994771	putative 42 kDa protein
19745813	993958	putative adhesion protein

19745225	994839	putative choline binding protein
19745828	995250	streptolysin S associated protein
19746229	995021	putative minor tail protein
19746909	994105	putative laminin adhesion
19745560	995061	putative cell envelope proteinase
Treponema pallidum subsp. pallidum str. Nichols		
15639714	2611034	flagellar hook protein (flgE)
15639609	2611657	tpr protein J (tprJ)
15639111	2610909	tpr protein C (tprC)
15639125	2610968	tpr protein D (tprD)
SARS coronavirus		
31581505		spike protein S [SARS coronavirus Frankfurt 1]
32187357		spike protein S [SARS coronavirus HSR 1]
32187342		spike glycoprotein [SARS coronavirus ZJ01]
30698329		putative spike glycoprotein S [SARS coronavirus TW1]
30421454		putative spike glycoprotein [SARS coronavirus CUHK-Su10]
30027620		S protein [SARS coronavirus Urbani]
29836496	1489668	E2 glycoprotein precursor; putative spike glycoprotein [SARS coronavirus]
30795145		spike glycoprotein [SARS coronavirus Tor2]
31416295		spike glycoprotein S [SARS coronavirus GD01]
30023954		putative E2 glycoprotein precursor [SARS coronavirus CUHK-W1]
30275669		spike glycoprotein S [SARS coronavirus BJ01]
29837498		3C-like proteinase nsp5-pp1a/pp1ab (3CL-PRO) [SARS coronavirus]
29837501		putative nsp8-pp1a/pp1ab [SARS coronavirus]
29837503		putative nsp10-pp1a/pp1ab; formerly known as growth-factor-like protein [SARS coronavirus]
29837502		putative nsp9-pp1a/pp1ab [SARS coronavirus]

Table 6: Hypothetical proteins predicted as putative adhesins by SPAAN in the genomes listed in table 2 –

(Total number of proteins = 105)

Protein GI number	Gene ID
Escherichia coli O157:H7	
13363955	915578
13360000	914929
13362244	912369
13359999	914888
13361583	917316
13361172	913156
13361131	913207
13359780	914422
13360571	912499
13362197	912893
13362260	912399
13360947	913505
13361464	917196
13361635	917367
13362421	916655
13361463	917195
Haemophilus influenzae Rd	
16272115	951058
30995442	950581
Helicobacter pylori J99	
4155526	889586
4155712	889748
4155632	889684
4156035	889468
4155499	

Mycoplasma pneumoniae

13507870	877230
13508239	877245
13508109	876868
13508025	877084
13507838	876784
13507883	877183
13507871	877239
13507944	877056
13508241	876750
13507942	877055
13507840	877387
13507867	877242
13508201	877044
13507941	876985
13508114	877397

Mycobacterium tuberculosis H37Rv

15611014	886198
15610173	887320
15609513	885515
15608094	885411
15610958	886155
15607528	886436
15607678	887473
15609587	885760
15610708	887227
15609526	885246
15611033	886225
15609028	885094
15607730	887771
15609121	885813
15608255	885951

15608409 887039

15609124 885815

15607734 887797

Rickettsia prowazekii strain Madrid E

15604649 883964

15604322 883472

15604659 883996

15604417 883217

Porphyromonas gingivalis W83

34540233 2551594

Shigella flexneri 2a str. 2457T

30062687 1077638

30062956 1080449

30063681 1078754

30065435 1080675

30063891 1078983

30063211 1078195

30065233 1080463

30064387 1079531

30062638 1077590

30065236 1080466

30061839 1076721

Streptococcus mutans UA159

24378864 1029452

24380475 1029319

24380237 1029088

24379203 1028139

24380480 1029320

24379275 1029489

24379291 1028216

24379295 1028215

24379804 1028663

24379162 1029417

24378987 1029363

24379179 1028118

24379166 1028107

24378827 1029444

24380216 1029067

Streptococcus pneumoniae R6

15902140 932867

15903446 934616

15903916 934001

15903848 933609

15902832 934332

15902372 934804

15902152 932889

Neisseria meningitidis Z2491

15793668 906680

15794714 907603

Streptococcus pyogenes MGAS8232

19747011 993608

19747024 994165

19747012 994373

19746396 995057

19746651 993824

19745883 995045

19745912 994077

Treponema pallidum subsp. pallidum str. Nichols

15639844 2611061

15639720 2611059

Table 7: The list of 198 adhesins found in bacteria

PapG (E. coli)

12837502

7407201

7407207
7407205
147096
4240529
7407203
42308
7443327
78746
18265934
26111419
26250987
26109826
26249418
13506767
42301
78745
129622
147092
13506906
7407209
147080
281926
7407199
147100
78744

SfaS (E.coli)

477910
264035
42959
134449
96425

FimH (E.coli)

26251208
26111640
5524634
29422425
5524630
29422435
29422415
10946257
29422419
11120564
29422457
11120562
29422459
5524632
29422455
29422453
29422451
29422449
29422447
29422445
29422443
29422437
29422433
29422431
29422429
29422427
29422423
29422421
29422417
729494
1361011
1790775

3599571
29422441
12620398
29422439
5524628
1787779
1742472
1742463
15801636
25321294
12515169
11120566
24051859
24112911
13360484
15800801
15830279
25392018
25500156
12514120
1787173
16128908
16501811
16759519
24051219
24112354
30040724
30062478
6650093
5524636
1778448

Intimin (E.coli)

17384659
4388530
1389879
15723931
4323336
4323338
4323340
4323342
4323344
4323346
4323348
4689314

PrsG (E.coli)

42523
42529
7443328
7443329
1172645

HMW1 (Nontypeable *H. influenzae)*

282097

HMW2 (Nontypeable H. influenzae)

5929966

Hia (Nontypeable H. influenzae)

25359682
25359489
25359709
25359628
25359414
25359389
21536216
25359445

HifE (H. influenzae)

13506868
13506870
13506872
13506874
13506876
3688787
3688790
3688793
2126301
1170264
1170265
533127
535169
3025668
3025670
3025672
3025674
642038

MrkD (K. pneumoniae)

127307

FHA (B. pertussis)

17154501

Pertactin (B. pertussis)

33571840

YadA (Y. enterocolitica)

10955604
4324391
28372996
23630568
32470319

SpaP (S. mutans)

26007028

47267

PAc (S. mutans)

129552

SspA (Streptococcus gordonii)

25990270

1100971

CshA (Streptococcus gordonii)

457707

CshB (Streptococcus gordonii)

18389220

ScaA (Streptococcus gordonii)

310633

SspB (Streptococcus gordonii)

25055226

3220006

SpaA (Streptococcus sobrinus)

546643

PAg (Streptococcus sobrinus)

217036

47561

Protein F (Streptococcus pyogenes)

19224134

PsaA (Streptococcus pneumoniae)

18252614

7920456

7920458

7920460

7920462

CbpA[e] / SpsA / PbcA/ PspC
(Streptococcus pneumoniae)

14718654

2425109

2576331

2576333

3153898

9845483

19548141

FimA (Streptococcus parasanguis)

97883

SsaB (Streptococcus sanguis)

97882

EfaA (Enterococcus faecalis)

493017

FnbA (Staphylococcus aureus)

120457

FnbB (Staphylococcus aureus)

581562

21205592

13702452

BabA (Helicobacter pylori)

13309962

13309964

13309966

13309968

13309970

13309972

13309974

13309976

13309978

13309980

13309982

13309984

13309986

13309988

13309990

13309992

13309994

Advantages:

1. The method helps in discovering putative adhesins, which are of great importance in drug discoveries and preventive therapeutics.
2. The method is useful in predicting the adhesive nature of even unique proteins, because it is independent of the homology of the query proteins with other proteins.
3. This method is easy to use. For calculating the output, only the amino acid sequence is required as input. No other information is required to get the information about its adhesive nature.

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Claims

1. A computational method for identifying adhesin proteins, said method comprising steps of :
   a. computing the sequence-based attributes of protein sequences using five attribute modules of a neural network software, wherein the attributes are, (i) amino acid frequencies, (ii) multiplet frequency, (iii) dipeptide frequencies, (iv) charge composition, and (v) hydrophobic composition,
   b. training a artificial neural Network (ANN) for each of the computed five attributes, and
   c. identifying the adhesin and adhesin-like proteins having probability of being an adhesin (P_{ad}) as ≥ 0.51.
2. A method as claimed in claim 1, wherein the protein sequences are obtained from pathogens, eukaryotes, and multicellular organisms.
3. A method as claimed in claim 1, wherein the protein sequences are obtained from the pathogens selected from a group of organisms comprising *Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Mycoplasma pneumoniae, Mycobacterium tuberculosis, Rickettsiae prowazekii, Porphyromonas gingivalis, Shigella flexneri, Streptococcas mutans, Streptococcus pneumoniae, Neisseria meningitides, Streptococcus pyrogenes, Treponema pallidum* and Severe Acute Respiratory Syndrome associated human coronavirus (SARS).
4. A method as claimed in claim 1, wherein the method is a non-homology method.
5. A method as claimed in claim 1, wherein the method uses 105 compositional properties of the sequences.
6. A method as claimed in claim 1, wherein the method shows sensitivity of at least 90%.
7. A method as claimed in claim 1, wherein the method shows specificity of 100%.
8. A method as claimed in claim 1, wherein the method helps identifies adhesins from distantly related organisms.
9. A method as claimed in claim 1, wherein the neural network has multi-layer feed forward topology, consisting of an input layer, one hidden layer, and an output layer.

10. A method as claimed in claim 9, wherein the number of neurons in the input layer are equal to the number of input data points for each attribute.

11. A method as claimed in claim 1, wherein the "P_{ad}" is a weighted linear sum of the probabilities from five computed attributes.

12. A method as claimed in claim 1, wherein each trained network assigns a probability value of being an adhesin for the protein sequence.

13. A computer system for performing the method of claim 1, said system comprising a central processing unit, running SPAAN program, giving probabilities based on different attributes using Artificial Neural Network and in built other programs of assessing attributes, all stored in a memory device accessed by CPU, a display on which the central processing unit displays the screens of the above mentioned programs in response to user inputs; and a user interface device.

14. A fully connected multilayer feed forward Artificial Neural Network based on the computational method as claimed in claim 1, comprising of an input layer, a hidden layer and an output layer which are connected in the said sequence, wherein each neuron is a binary digit number and is connected to each neuron of the subsequent layer for identifying adhesin or adhesin like proteins, wherein the program steps comprise:-

[a] feeding a protein sequence in FASTA format ;

[b] processing the sequence obtained in step [a] through the 5 modules named A, C, D, H and M, wherein attribute A represents an amino acid composition, attribute C represents a charge composition, attribute D represents a dipeptide composition of the 20 dipeptides [NG, RE, TN, NT, GT, TT, DE, ER, RR, RK, RI, AT, TS, IV, SG, GS, TG, GN, VI

and HR], attribute H represents a hydrophobic composition and attribute M represents amino acid frequencies in multiplets to quantify 5 types of compositional attributes of the said protein sequence to obtain numerical input vectors respectively for each of the said attributes wherein the sum of numerical input vectors is 105;

[c] processing of the numerical input vectors obtained in step [b] by the input neuron layer to obtain signals, wherein the number of neurons is equal to the number of numerical input vectors for each attribute;

[d] processing of signals obtained from step [c] by the hidden layer to obtain synaptic weighted signals, wherein the optimal number of neurons in the hidden layer was determined through experimentation for minimizing the error at the best epoch for each network individually;

[e] delivering synaptic weighted signals obtained from step [d] to the output layer for assigning of a probability value for each protein sequence fed in step [a] as being an adhesin by each network module; and

[f] using the individual probabilities obtained from step [e] for computing the final probability of a protein sequence being an adhesin denoted by the P_{ad} value, which is a weighted average of the individual probabilities obtained from step [e] and the associated fraction of correlation which is a measure of the strength of the prediction,

wherein the input neuron layer consists of a total of 105 neurons corresponding to 105 compositional properties.

15. A fully connected multilayer feed forward Artificial Neural Network based on the computational method as claimed in claim 1, comprising of an input layer, a hidden layer and an output layer which are connected in the said sequence, wherein each neuron is a binary digit number and is connected to each neuron of the subsequent layer for identifying adhesin or adhesin like proteins, wherein the program steps comprise:-

[a] feeding a protein sequence in FASTA format ;

[b] processing the sequence obtained in step [a] through the 5 modules named A, C, D, H and M, wherein attribute A represents an amino acid composition, attribute C represents a charge composition, attribute D represents a dipeptide

composition of the 20 dipeptides [NG, RE, TN, NT, GT, TT, DE, ER, RR, RK, RI, AT, TS, IV, SG, GS, TG, GN, VI and HR], attribute H represents a hydrophobic composition and attribute M represents amino acid frequencies in multiplets to quantify 5 types of compositional attributes of the said protein sequence to obtain numerical input vectors respectively for each of the said attributes wherein the sum of numerical input vectors is 105;

[c] processing of the numerical input vectors obtained in step [b] by the input neuron layer to obtain signals, wherein the number of neurons is equal to the number of numerical input vectors for each attribute;

[d] processing of signals obtained from step [c] by the hidden layer to obtain synaptic weighted signals, wherein the optimal number of neurons in the hidden layer was determined through experimentation for minimizing the error at the best epoch for each network individually;

[e] delivering synaptic weighted signals obtained from step [d] to the output layer for assigning of a probability value for each protein sequence fed in step [a] as being an adhesin by each network module; and

[f] using the individual probabilities obtained from step [e] for computing the final probability of a protein sequence being an adhesin denoted by the P_{ad} value, which is a weighted average of the individual probabilities obtained from step [e] and the associated fraction of correlation which is a measure of the strength of the prediction,

wherein the hidden layer comprises of neurons represented as 30 for amino acid frequencies, 28 for multiplet frequencies, 28 for dipeptide frequencies, 30 for charge composition and 30 for hydrophobic composition.

16. A fully connected multilayer feed forward Artificial Neural Network based on the computational method as claimed in claim 1, comprising of an input layer, a hidden layer and an output layer which are connected in the said sequence, wherein each neuron is a binary digit number and is connected to each neuron of the subsequent layer for identifying adhesin or adhesin like proteins, wherein the program steps comprise:-

[a] feeding a protein sequence in FASTA format ;

[b] processing the sequence obtained in step [a] through the 5 modules named A, C, D, H and M, wherein attribute A represents an amino acid composition, attribute C represents a charge composition, attribute D represents a dipeptide composition of the 20 dipeptides [NG, RE, TN, NT, GT, TT, DE, ER, RR, RK, RI, AT, TS, IV, SG, GS, TG, GN, VI and HR], attribute H represents a hydrophobic composition and attribute M represents amino acid frequencies in multiplets to quantify 5 types of compositional attributes of the said protein sequence to obtain numerical input vectors respectively for each of the said attributes wherein the sum of numerical input vectors is 105;

[c] processing of the numerical input vectors obtained in step [b] by the input neuron layer to obtain signals, wherein the number of neurons is equal to the number of numerical input vectors for each attribute;

[d] processing of signals obtained from step [c] by the hidden layer to obtain synaptic weighted signals, wherein the optimal number of neurons in the hidden layer was determined through experimentation for minimizing the error at the best epoch for each network individually;

[e] delivering synaptic weighted signals obtained from step [d] to the output layer for assigning of a probability value for each protein sequence fed in step [a] as being an adhesin by each network module; and

[f] using the individual probabilities obtained from step [e] for computing the final probability of a protein sequence being an adhesin denoted by the P_{ad} value, which is a weighted average of the individual probabilities obtained from step [e] and the associated fraction of correlation which is a measure of the strength of the prediction,

wherein the output layer comprises of neurons to deliver the output values as probability value for each protein sequence.

Application Project

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<130> AppFileReference :
<140> CurrentAppNumber :
<141> CurrentFilingDate :

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LDNASPTEIL SRNVVVNGKV SADELNVVAG NNYVNAAGQV TGSVSATGSR NGYSVDVAKL 240
GGMYANKISL VSTEKGVGVR NLGVIAGGVN GVSIDSKGNL LNSNAQIQSA STINLTTNGT 300
LDNTTGTVTS VGTISLNTNK NTIVNTRAGN ISTMGDIYVN SGTIDNTNGK LAAAGMLAVD 360
TNNATLINSG KGSSVGIEAG LVALKTGTLN NSNGQIRGGY VGLESAALNN NNGDIQTTGD 420
IAIISNGNVD NNKGLIRSST GHIVIGAAGS VNNGSTKTAD TGSSDSLGII ADTGVEIGAN 480
NINNNGGQIA SNGNVSLSSY STIDDVAGKI LSNSKVIIKG SSLRNDTGGI SGKQGIEVAV 540
GGSLTNNIGV ISSEEGDISL LANSVDNHGG FMMGQNITME SMSGVNNNTA LIVASKKLKI 600
NARGSIENRD GNNFGNAYGL YFGMPQQTGG MVGKEGIELS GQNIYNNNSR LIAEDGPLTL 660
QAQNTFDNTR ALVTSGADAS IQVGGTYYNN YATTWSAGNL DIDATTLQNS SSGTMIDNNA 720
TGFIASDKNL SLEVVNSLTN YGWISGKGDV DVTVNNGNLY NRNTIAAEKG LDIAALNGIE 780
NWKDISAGGD LTMNTNRHVT NNSNSNMVGQ NIVINAVNDI NNRGNIVSDA DLNVTTKGNL 840
YNYLYMVGYG DIALSANSVA NNNATIEATG DLIIDSKGNV GNNRGNLHAL NGVLSVKGNN 900
LNNDNGEIRG YGDVTLALTG NYDSYKGSLT SETGDVTLTA NIVDNAYGLI AGENVSVDAK 960
STIYNNTALI AANKKLVINA GGNLENRDGN NFLRNNGALF GITDNVGGIV GKEGVTLSAQ 1020
NVYNNNSSII AENGPLNLLS RGTLDNTRAL LSSGADAIIR AAGTFYNNYA TTYSAGNLDV 1080
YAASLNNASD GRLEDNTATG VIASDKNLDL SVDNSVTNYG WISGKGDVHF NVLKGTLYNR 1140
NAIAADNALT INALNGVENF KDIVAGTALT IDTQKYVINN SNSNMLGQTI AINAVNDINN 1200
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LIESGGYQDV GRHNNYVGQS NNTTINGGRQ SIHDGGISTG TIIESGNQDV YKGGISNGTT 180
IKGGASRVEG GSANGTLIDG GSQIVKVQGH ADGTTINKSG SQDVVQGSLA TNTTINGGRQ 240
YVEQSTVETT TIKNGGEQRV YESRALDTTI EGGTQSLNSK STAKNTQIYS GGTQIIDNTS 300
SSDVIEVYSG GVLDVSGGTA TNVTQHDGAI LKTNTNGTTV SGTNSEGAFS IHNHVADNVL 360
LENGGHLDIN AYGSANKTII KDKGTMSVLT NAKADATRID NGGVMDVAGN ATNTIINGGT 420
QNINNYGIAT GTNINSGTQN IKSGGKADTT IISSGSRQVV EKDGTAIGSN ISAGGSLIVY 480
TGGIAHGVNQ ETGSALVANT GAGTDIEGYN KLSHFTITGG EANYVVLENT GELTVVAKTS 540
AKNTTIDAGG KLIVQKEAKT DSTRLNNGGV LEVQDGGEAK HVEQQSGGAL IASTTSGTLI 600
EGTNSYGDAF YIRNSEAKNV VLENAGSLTV VTGSRAVDTI INANGKMDVY GKDVGTVLNS 660
AGTQTIYASA TSDKANIKGG KQTVYGLATE ANIESGEQIV DGGSTEKTHI NGGTQTVQNY 720
GKAINTDIVS GLQQIMANGT AEGSIINGGS QIVNEGGLAE NSVLNDGGTL DVREKGSATG 780
IQQSSQGALV ATTRATRVTG TRADGVAFSI EQGAANNILL ANGGVLTVES DTSSDKTQVN 840
TGGREIVKTK ATATGTTLTG GEQIVEGVAN ETTINDGGIQ TVSANGEAIK TTINEGGTLT 900
VNDNGKATDI VQNSGAALQT STANGIEISG THQYGTFSIS GNLATNMLLE NGGNLLVLAG 960
TEARDSTVGK GGAMQNQGQD SATKVNSGGQ YTLGRSKDEF QALARAEDLQ VAGGTAIVYA 1020
GTLADASVSG ATGSLSLMTP RDNVTPVKLE GAIRITDSAT LTIGNGVDTT LADLTAASRG 1080
SVWLNSNNSC AGTSNCEYRV NSLLLNDGNV YLSAQTAAPA TTNGIYNTLT TNELSGSGNF 1140
YLHTNVAGSR GDQLVVNNNA TGNFKIFVQD TGVSPQSDDA MTLVKTGGGD ASFSLGNTGG 1200
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PTPVPEKRIT PSTAAVLNMA ATLPLVFDAE LNSIRERLNI MKASPHNNNV WGATYNTRNN 1320
VTTDAGAGFE QTLTGMTVGI DSPNDIPEGI ATLGAFMGYS HSHIGFDRGG HGSVGSYSLG 1380
GYASWEHESG FYLDGVVKLN RFESNVAGKM SSGGAANGSY HSNGLGGHIE TGMRFTDGNW 1440
NLTPYASLTG FTADNPEYHL SNGMESKSVD TRSIYRELGA TLSYNMRLGN GMEIEPWLKA 1500

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AQNTAA[illegible] 130
TEASKSAAAA ESSKSAAATS AGAAKTSETN AAVSQQSAAT SASTATTKAS EAASSARDAS 240
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AAALSASAAS TSAGQASASA TAAGKSAESA ASSASTATTK AGEATEQASA AASSASAAKT 360
SETNAKASET SAESSKTAAA SSASSAASSA SSASASKDEA TRQASAAKSS ATTASTKATE 420
AAGSATAAAQ SKSTAESAAT RAETAAKRAE DIASAVALED ASTTKKGIVQ LSSATNSTSE 480
SLAATPKAVK AAYELANGKY TAQDATTAQK GIVQLSNATN STSEMLAATP KSVKAAYDLA 540
NGKYTAQDAT TAQKGIVQLS SATNSASETL AATPKAVKAA NDNANGRVPS ARKVNGKALS 600
SDITLTPKDI GTLNSTTMSF SGGAGWFKLA TVTMPQASSV VSITLIGGAG FNVGSPQQAG 660
ISELVLRAGN GNPKGITGAL WQRTSTGFTN FAWVNTSGDT YDIYVAIGNY ATGVNIQWDY 720
TSNASVTIHT SPAYSANKPE GLTDGTVYSL YTPSEQFYPP GAPIPWPSDT VPSGYALMQG 780
QTFDKSAYPK LAAAYPSGVI PDMRGWTIKG KPASGRAVLS QEQDGIKSET HSASASSTDL 840
GTKTTSSFDY GTKSTNNTGA HTHSVSGTAA SAGNHTHSVT GASAVSQWSQ NGSVHKVVSA 900
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GCDVSARDVT VTLPDYPGSV PIPLTVYCAK SQNLGYYLSG TTADAGNSIF TNTASFSPAQ 240
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QVVLEGGTAS DTVIRDGGGQ SLNGLAVNTT LNNRGEQWVH EGGVATGTII NRDGYQSVKS 180
GGLATGTIIN TGAEGGPDSD NSYTGQKVQG TABSTTINKN GRQIILFSGL ARDTLIYAGG 240
DQSVHGRALN TTLNGGYQYV HRDGLALNTV INEGGWQVVK AGGAAGNTTI NQNGELRVHA 300
GGEATAVTQN TGGALVTSTA ATVIGTNRLG NFTVENGKAD GVVLESGGRL DVLESHSAQN 360
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GGQATGKTWL AFTNVGNSNL GVATTGQGIR VVDAQNGATT EEGAFALSRP LQAGAFNYTL 600
NRDSDEDWYL RSENAYRAEV PLYTSMLTQA MDYDRILAGS RSHQTGVNGE NNSVRLSIQG 660
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DGSRAGTVRD DAGSLGGYLN LVHTSSGLWA DIVAQGTRHS MKASSDNNDF RARGWGWLGS 780
LETGLPFSIT DNLMLEPQLQ YTWQGLSLDD GQDNAGYVKF GHGSAQHVRA GFRLGSHNDM 840
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ISVLNAGYTA VPFEHVSNQA TTTDHTCQGN KTTAVGVSLK TGADAKISFR IKRSINGTVV 180
IPITDIALLY ANISSTTTRG EAIAKVRISG SLTAPQSCQI NAGQVIYFDF DTIPASEFSS 240
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KLNVDKDFSL KDSSLEMLYP IYDTPTNMLF TQGAIHRTDD RTQSNIGFGW RHFSGNDWMA 180
GVNTFIDHDL SRSHTRIGVG AEYWRDYLKL SANGYIRASG WKKSPDIEDY QERPANGWDI 240
RAEGYLPAWP QLGASLMYEQ YYGDEVGLFG KDKRQKDPHA ISAEVTYTPV PLLTLSAGHK 300
QGKSGENDTR FGLEVNYRIG EPLAKQLDTD SIRERRVLAG SRYDLVERNN NIVLEYRKSE 360
VIRIALPERI EGKGGQTLSL GLVVSKATHG LKNVQWEAPS LLAEGGKITG QGSQWQVTLP 420
AYRPGKDNYY AISAVAYDNK GNTSKRVQTE VVITGAGMSA DRTALTLDGQ SRIQMLANGN 480
EQKPLVLSLR DAEGQPVTGM KDQIKTELTF KPAGNIVTRS LKATKSQAKP TLGEFTETEA 540
GVYQSVFTTG TQSGEATITV SVDGMSKTVT AELRATMMDV ANSTLSANEP SGDVVADGQQ 600
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RAFSEQYQLG TLQQTLKFVA GPLDAAHSSI TLNPDKPVVG GTVTAIWTVK DAYDNPVTSL 720
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VVADALSSNQ SKVSVAEDHV KAGESTTVTL VAKDAHGNAI SGLALSASLT GTASEGATVS 840
SWTEKGNGSY VATLTTGGKT GELRVMPLFN GQPAATEAAQ LTVIAGEMSS ANSTLVADNK 900
APTVKTTTEL TFTVKDAYGN PVTGLKPDAP VFSGAASTGS ERPSAGNWTE KGNGVYVSTL 960
TLGSAAGQLS VMPRVNGQNA VAQPLVLNVA GDASKAEIRD MTVKVNNQLA NGQSANQITL 1020
TVVDTYGNPL QGQEVTLTLP QGVTSKTGNT VTTNAAGKAD IELMSTVAGE HNISASVNGA 1080
QKTVTVKFNA DASTGQANLQ VDAAAQKVAN GKDAFTLTAN VEDKNGNPVP GSLVTFNLPR 1140
GVKPLTGDNV WVKANDEGKA ELQVVSVTAG TYEITASAGN SQPSNTQTIT FVADKATATV 1200
SGIEVIGNYA LADGNAKQTY KVTVTDANNN LLKDSEVTLT ASPANLVLTP NGTAKTNEQG 1260
QAIFTATTTV AAKYTLTAKV SQADGQESTK TAESKFVADD TNAVLTASSD VTSLVADGIS 1320
TAKLEVTLMS ANNPVGGNMW VDIKTPEGVT EKDYQFLPSK NDHFVSGKIT RTFSTSKPGV 1380
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IGLTGWRSAP ELDNDFEARP ANGWDLRAEG WLPAWFQLGG KLVYEQYYGD EVALFDKNDR 180
QSNPHAITAG LNYTPFPLLT LSAEQRQGKQ GENDTRFAVD LTWQPSSSMQ KQLNPDEVAG 240
RRSLAGSRYD LIDRNNNIVL EYRKKELIRL SLLDPVKGKS GEIKPLVSSL QTKYALKGYN 300
IEAAALEAAG GKVSTSGKDI TVTLPGYRFT NTPETDNTWS IDVTAEDVKG NLSRHEQSMV 360
VIQAPTLSQK DSLLSVNPLT VAADKKSTTT LTVTAHDSDG TPVPGLALQT RSEGVQDITL 420
SDWTDNGDGS YTQILTAGTT SGSVTLTPQI NGESAVKESI VVNIVPVVSS RDHSSITIDN 480
VSYYAGDDIK VRVELKDDSN QPVAYQKEEL VKAVTVENSK PGATIVWHEE QPGVYAANYP 540
AYKQGTALRA QLSLHNWNAP LQSHIYNIEA NQNKARVATL SATNNDVYAD KKTFNTLTIN 600
VTDESDNPLT NHQVTFKNEK GSAEFVEPPQ QNTDAYGVAT INMVSQVAEE NTISATLPNG 660
FSQRIIAKFV SDSSTPKFKQ LVADPDTIIA GNSQGSTLTA IITDFHNNPL KDMKVNFVAP 720
GGSQLDNTTA TTDQSGIVRV HLTSSKAGSY SVDASLEVDK NIHQSVTITV VPNREQSVMT 780
LNAGSGSAIA NNTNIVTLTA SVKDVYGHPL PDEDVKFTLP ASMTGNFTLS SETARTDANG 840
DAVVTLRGTK AGEFTVTATL TRNNTVAYQQ VTFIGDTNSA QLQPLTASLN SIVAGNSTGS 900
TLTATILDAY QNPLKDQLVT FQSNDVTLSE TEVTTNTLGQ ATVIMTSNIA GQHNVVVSRK 960
AQASDNKTFS LSVLPDESSA KVISITGAEK TITVGENITL RILVQDAFNN VIAGQRVRLS 1020
AQPTTNITIG DTAYTDNNGY AYVNLLSTQP GVYQVTATLD NNSSSKVDVN VANGKLELTS 1080
SKPETTVHNS EGITLTATAR NARGELMPGQ IITFSVTPEG ATLSNTGEVL TDQSGQAKVT 1140
LTSDKVNVYT VTAIMGKDVP VQSQVTVAVK ADAKTAHVVS VVASPDTITA DGIDSSTITS 1200
RVEDDYGFPV EGVDISHGLD TKGSPVVNIP TTRTDQSGQV TATITSTLAE TLTVNVQVPG 1260
TANQSATITL VAGTADESKS ILKSDVDTLK ADYQQSAKLT LTLQDKYGNP IVTSDHLEFV 1320
QSGPFVNFLK LSDIDYSQRN YGEYTVTVTG GKEGTATLIP MLNGVHQANL SISLNLIQSI 1380
KEMSGHVTAN NHTFSTAKFP SEGFAGAYYT LNNDNFEAGK TVDDYMFSSS QGWVSVDASG 1440
KVSFANIGDQ TSVTISAVPR QGGTTYQTLI KLKGWWVNNG NHTNIWLAAN ALCHAKNDGY 1500
NLPGITHLTS GENKRTQGSL YGEWGNVGAF SSNSQFTPGA YWTSESDDYS RHYYVQMLTG 1560
MTGSDADSSP QLTACRKSL 1579
<212> Type : PRT
<211> Length : 1579
SequenceName : SEQ ID 9
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MITHGCYTRT RHKHKLKKTL IMLSAGLGLF FYVNQNSFAN GENYFKLGSD SKLLTHDSYQ 60
NRLFYTLKTG ETVADLSKSQ DINLSTIWSL NKHLYSSESE MMKAAPGQQI ILPLKKLPFE 120
YSALPLLGSA PLVAAGGVAG HTNKLTKMSP DVTKSNMTDD KALNYAAQQA ASLGSQLQSR 180
SLNGDYAKDT ALGIAGNQAS SQLQAWLQHY GTAEVNLQSG NNFDGSSLDF LLPFYDSEKM 240
LAFGQVGARY IDSRFTANLG AGQRFFLPAN MLGYNVFIDQ DFSGDNTRLG IGGEYWRDYF 300
KSSVNGYFRM SGWHESYNKK DYDERPANGF DIRFNGYLPS YPALGAKLIY EQYYGDNVAL 360
FNSDKLQSNP GAATVGVNYT PIPLVTMGID YRHGTGNEND LLYSMQFRYQ FDKSWSQQIE 420
PQYVNELRTL SGSRYDLVQR NNNIILEYKK QDILSLNIPH DINGTEHSTQ KIQLIVKSKY 480
GLDRIVWDDS ALRSQGGQIQ HSGSQSAQDY QAILPAYVQG GSNIYKVTAR AYDRNGNSSN 540
NVQLTITVLS NGQVVDQVGV TDFTADKTSA KADNADTITY TATVKKNGVA QANVPVSFNI 600
VSGTATLGAN SAKTDANGKA TVTLKSSTPG QVVVSAKTAE MTSALNASAV IFFDQTKASI 660
TEIKADKTTA VANGKDAIKY TVKVMKNGQP VNNQSVTFST NFGMFNGKSQ TQATTGNDGR 720
ATITLTSSSA GKATVSATVS DGAEVKATEV TFFDELKIDN KVDIIGNNVR GELPNIWLQY 780
GQFKLKASGG DGTYSWYSEN TSIATVDASG KVTLNGKGSV VIKATSGDKQ TVSYTIKAPS 840
YMIKVDKQAY YADAMSICKN LLPSTQTVLS DIYDSWGAAN KYSHYSSMNS ITAWIKQTSS 900
EQRSGVSSTY NLITQNPLPG VNVNTPNVYA VCVE 934
<212> Type : PRT
<211> Length : 934
SequenceName : SEQ ID 10
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MLVLSESFKN KLLPMNGYMK GGSDSGSKAQ ARATEKGIEL QREMWQTNMQ NLAPFTPLAQ 60

QYVSQLQNLS SLQGQGQALN QYYNSQQYKD LAGQARYQSL AAAEATGGLG STATGNQLAA 120
IAPTLGQNWL SGQMNNYNNL ANIGLGALTG QANAGQNYAN NVSQLYQQQA AASAANANKP 180
SGLQSFATGA IGGAASGAMI GSAVPVIGTG IGALAGGVIG GLGSLF 226

<212> Type : PRT
<211> Length : 226
SequenceName : SEQ ID 11
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MKKILSGLIL LLCCPYGFAA NGDGATHMSN LSFGPLTVAA ANNHSGYNIF EALSNTTGTY 60
PVRCHCDDTH GGPGQQTAFF PIFYTGDAAP GLVLERTLNG LNYYALNDYL SVGVTIFIIN 120
NQYAAIPFEH LSNQSTSPQH TCGAGNNGST VNLDSGRSAK LSFYVRHSIT GTVTIPTTEV 180
AWLYAGMSDH FPKTTPVSKV TIRGQLTAPQ NCELTPNQSI DVDFQKINSA EFSSTAGSII 240
AERKIKTEVT VSCTGMEDVR STEVVSASMI AANRSADATM IVTSNPDVGI KIFDKNDRPV 300
NVDGGNLPAD MGAISRLGKT DGSVTFYSAP ASLTGAKPAP DNGFTATATL VIEFTN 356

<212> Type : PRT
<211> Length : 356
SequenceName : SEQ ID 12
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MNKIYRLKWN RSRNCWSVCS ELGSRVKGKK SRAVLISAIS LYSSLVFADD VIVNQDKTID 60
FGKENQSIDY RITVTDNANL VINATDTSRP RLTLASGGGL DITGGKVTIN GPLNFLLKGT 120
GFLNVSNAGS ELYADDLYES NSGMRHDRGY FNVSNGGKIH VKGTSRLTYL QGNVSGEGSQ 180
VNSETFFMGV YGSYGGNQYL SVNNGGEVNA RKQISLGYYD QVSDTTLAVS EGGKISAPTI 240
SLSTNSELAL GAQEGSAAKA AGIIDAEKIE FVWAKTSEKK ITLNHTDKDA TISADIVSGS 300
EGLGYINALN GTTYLTGDNS AFSGKVKIEQ NGALGTTQNI GTAEINNRGK LHLKADDSMT 360
FANKISGNGT ISIDSGTVEL TGNNYAFSGY IDVASGAVAV ISEDKNIGRA ELDVDGKLQI 420
NANKDWVFDN DLEGRGIVEI NMGNHEFSFD EFAYTDWFQG SLAFQNTTFN LEKNAEFLQK 480
GGITAGQGSL VTVGKGAHSI STLGFSGGTV DFGALTAGAQ MTEGTVNVSK TLDLRGEGVI 540
QVSDSDVVRS VSRDIDSALS LTEVDDGNST IKLVDAQGAE VLGDAGNLQL QDKNGQILSS 600
SAQRDIQQNG QKAAVGTYDY RLTSGVNNDG LYIGYGLTQL DLHATDSDAL VLSSNGKSEN 660
AADLSAKITG SGDLAFSSQK GQTVSLSNKD NDYTGVTDLR SGTLLLNNDN VLGNTHELRL 720
AAETELDMNG HSQTVGTLNG SADSLLSLNG GSLTVTNGGT STGSLTGSGE LNIQGGTLDI 780
AGDNSNLTAN VNIANSANVL VSHAQGLGSA NVENNGTLAL NNSAEKRAAA SVNYALGGNL 840
TNNGTLMTGM SGQQAGNVLV VKGNYHGNNG QLVMNTVLNG DDSVTDKLVV EGDTSGTTAV 900
TVNNAGGTGA KTLNGIELIH VDGKSEGEFV QAGRIVAGAY DYTLARGQGA NSGNWYLTSG 960
SDSPELQPEP DPMPNPEPNP NPEPNPNPTP TPGPDLNVDN DLRPEAGSYI ANLAAANTMF 1020
TTRLHERLGN TYYTDMVTGE QKQTTMWMRH EGGHNKWRDG SGQLKTQSNR YVLQLGGDVA 1080
QWSQNGSDRW HVGVMAGYGN SDSKTISSRT GYRAKASVNG YSTGLYATWY ADDESRNGAY 1140
LDSWAQYSWF DNTVKGDDLQ SESYKSKGFT ASLEAGYKHK LAEFNGSQGT RNEWYVQPQA 1200
QVTWMGVKAD KHRESNGTLV HSNGDGNVQT RLGVKTWLKS HHKMDDGKSR EFQPFVEVNW 1260
LHNSKDFSTS MDGVSVTQDG ARNIAEIKTG VEGQLNANLN VWGNVGVQVA DRGYNDTSAM 1320
VGIKWQF 1327

<212> Type : PRT
<211> Length : 1327
SequenceName : SEQ ID 13
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MITMKKSVLT AFITVVCATS SVMAADDNAI TDGSVTFNGK VIAPACTLVA ATKDSVVTLP 60
DVSATKLQTN GQVSGVQTDV PIELKDCDTT VTKNATFTFN GTADTTQITA FANQASSDAA 120
TNVALQMYMN DGTTAIKPDT ETGNILLQDG DQTLTFKVDY IATGKATSGN VNAVTNFHIN 180
YY 182

<212> Type : PRT
<211> Length : 182
SequenceName : SEQ ID 14

SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :

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MSKFVKTAIA ATMVMGAPAS TSTIAAGNNG TARFYGTIED SPCSIVPDDH KLEVDMGDIG      60
SGILKNNGTS TPKAFQIHLQ DCVFDTQTTM TTTFTGNASS TNSGNYYTIY NTDTGAAFNN     120
VSLAIGDAQG TSYKSGAGIE QKIVNDTATN KGKAKQTLDF KAWLVGAADA PDLGNFEANT     180
TFQITYL                                                               187
```

<212> Type : PRT
<211> Length : 187
SequenceName : SEQ ID 15
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :

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MRVIFLRKEY LSLLPSMIAS LFSANGVAAA IDLCQGYDIK ASCHASRQSL SGITQVWSIA      60
DGQWLVFSDM TNNASGGAVF LQQGAEFTLS PENETGMTLF ANNTVSGEYN NGGAIFAKEN     120
STLNLTDVIF SGNVAGGYGG AIYSSGTNDT GAIDLRVTNA VFRNNIANDG KGGAIYTINN     180
DIYLSDDVFN NNQAYTSTSY SDGDGGAIDV TDNNSDSKHP SGYTIINNTA FTNNTAEGYG     240
GAIYTNSATA PYLIDISVDD SYSQNGGVLV DENNSAAGYG DGPSSAAGGF MYLGLSEVTF     300
DIADGKTLVI GNTENDGAVD SIAGTGLITK TGSGDLVLNA DNNDFTGEMQ IENGEVTLGR     360
SNSLMNVGDT HCQDDPQDCY GLTIGSIDKY QNQAELNVGS TQQTFAHSLT GFQNGTLNID     420
AGGNVTVNQG SFAGTIEGAG QLTIAQNGSY VLAGAQSMAL TGDIVVDAGA VLSLEGDAAD     480
LAALQDDPQS IVLNGGMLDL SDFSTWQSGT SYKDGLEVSG SSGTVIGSQD VVDLAGGNDM     540
HIGGDGKDGV YVVIDAGDGQ VSLANDNQYL GTTQIASGTL MVSDNSQLGY THYNRQVIFT     600
DKPQESVMEI TANVDTRSTT TEHGRDIEMR ADGEVAVDAG VDTQWGALMA DSSGQHQDEG     660
STLTKTGAGT LELTASGTTQ SAVRVEEGTL QGDVADIFPY ASSLWVGDGA TFVTGADQDI     720
QSIDATSSGT IDISDGTVLR LTGQDTSVAL NASLFNCDGT LVNATDGVTL TGELNTNLET     780
DSLTYLSNVT VNGNLTNTSG AVSLQNGVAG DTLTVNGDYT GGGTLLLDSE LNGDDSVSDQ     840
LVMNGNTAGN TTVVVNSITG IGEPTSTGIK VVDFAADPTQ FQNNAQFSLA GSGYVNMGAY     900
DYTLVEDNND WYLRSQEVTP PSPPDPDPTP DPDPTQDPDP TPDPEPTPAY QPVLNAKVGG     960
YLNNLRAANQ AFMMERRDHA GGDGQTLNLR VIGGDYHYTA AGQLAQHEDT STVQLSGDLF    1020
SGRWGTDGEW MLGIVGGYSD NQGDSRSSMT GTRADNQNHG YAVGLTSSWF QHGKQKQGAW    1080
LDNWLQYAWF SNDVSEHEDG VDHYHSSGII ASLEAGYQWL PGRGVVIEPQ AQVIYQGVQQ    1140
DDFTAANRAR VSQSQGDDIQ TRLGLHSEWR TAVHVIPTLD LNYYHDPHST EIEEDASTIS    1200
DDAVKQRGEI KVGVTGNISQ RVSLRGSVAW QKGSDDFAQT AGFLSMTVKW               1250
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<212> Type : PRT
<211> Length : 1250
SequenceName : SEQ ID 16
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :

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MHSWKKKLIV SQLALACTLA ITSQANAATN DISGQTYNTF HHYNDATYAD DVYYDGYVGW      60
NNYAADSYYN GDIYPVINNA TVNGVISTYY LDDGISTNTN ANSLTIKNST IHGMITSECM     120
TTDCADDRAT GYVYDRLTLS VDNSTIDDNY EHYTYNGTYN NAADTHVVDV YDMGTAITLD     180
QEVDLSITNN SHVAGITLTQ GYEWEDIDDN TVSTGVNSSE VFNNTITVKD STVTSGSWTD     240
EGTTGWFGHT GNASNYSNTL TADDVAIAAI ANPYADNAMQ TTVTLDNSTL MGDVVFSSNF     300
DENFFPQGAN SYRDADGDVD TNGWDGTDRM DVTLNNGSKW VGAAMSVHMV DEDGDGSYDG     360
YAVGTEATAT LLDIAANSLW PSSTVGVDNI NTQYDENGHI VGNEVYQSGL FNVTLNGGSE     420
WDTTKSSLID TLSINSGSQV NVADSRLISD TVSLTGGSNL NIGEDGHVAT NTLTIDNSTV     480
KMSDDVSAGW GLEDAALYAN TITVTNDGLL DINVDQFDAN PFQADTLNLT STTDTNGNIH     540
AGVFDIHSSD YVMDTDLVND RTNDTTKSNY GYGLIAMNSD GHLTINGNGD NDNTASIEAG     600
QNEVDNNGDH VAAATGNYKV RIDNATGAGS IADYNGNELI YVNDKNSNAT FSAANKADLG     660
AYTYQAEQRG NTVVLQQMEL TDYANMALSI PSANTNIWNL EQDTVGTRLT NSRHGLADNG     720
GAWVSYFGGN FNGDNGTINY DQDVNGIMVG VDTKIDGNNA KWIVGAAAGF AKGDMNDRSG     780
QVDQDSQTAY IYSSAHFANN VFVDGSLSYS HFNNDLSATM SNGTYVDGST NSDAWGFGLK     840
AGYDFKLGDA GYVTPYGSIS GLFQSGDDYQ LSNDMKVDGQ SYDSMRYELG VDAGYTFTYS     900
EDQALTPYFK LAYVYDDSNN DNDVNGDSID NGTEGSAVRV GLGTQFSFTK NFSAYTDANY     960
LGGGDVDQDW SANVGVKYTW                                                 980
```

<212> Type : PRT

<211> Length : 980
SequenceName : SEQ ID 17
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MKLKHVGMIV VSVLAMSSAA VSAAEGDESV TTTVNGGVIH FKGEVVNAAC AIDSESMNQT 60
VELGQVRSSR LAKAGDLSSA VGFNIKLNDC DTNVSSNAAV AFLGTTVTSN DDTLALQSSA 120
AGSAQNVGIQ ILDRTGEVLI LDGATFSAKT DLIDGTNILP FQARYIALGQ SVAGTANADA 180
TFKVQYL 187
<212> Type : PRT
<211> Length : 187
SequenceName : SEQ ID 18
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MKLLKVAAIA AIVFSGSALA GVVPQYGGGG GNHGGGGNNS GPNSELNIYQ YGGGNSALAL 60
QADARNSDLT ITQHGGGNGA DVGQGSDDSS IDLTQRGFGN SATLDQWNGK DSHMTVKQFG 120
GGNGAAVDQT ASNSTVNVTQ VGFGNNATAH QY 152
<212> Type : PRT
<211> Length : 152
SequenceName : SEQ ID 19
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MPIGNLGHNP NVNNSIPPAP PLPSQTDGAG GRGQLINSTG PLGSRALFTP VRNSMADSGD 60
NRASDVPGLP VNPMRLAASE ITLNDGFEVL HDHGPLDTLN RQIGSSVFRV ETQEDGKHIA 120
VGQRNGVETS VVLSDQEYAR LQSIDPEGKD KFVFTGGRGG AGHAMVTVAS DITEARQRIL 180
ELLEPKGTGE SKGAGESKGV GELRESNSGA ENTTETQTST STSSLRSDPK LWLALGTVAT 240
GLIGLAATGI VQALALTPEP DSPTTTDPDA AASATETATR DQLTKEAFQN PDNQKVNIDE 300
LGNAIPSGVL KDDVVANIEE QAKAAGEEAK QQAIENNAQA QKKYDEQQAK RQEELKVSSG 360
AGYGLSGALI LGGGIGVAVT AALHRKNQPV EQTTTTTTTT TTTSARTVEN KPANNTPAQG 420
NVDTPGSEDT MESRRSSMAS TSSTFFDTSS IGTVQNPYAD VKTSLHDSQV PTSNSNTSVQ 480
NMGNTDSVVY STIQHPPRDT TDNGARLLGN PSAGIQSTYA RLALSGGLRH DMGGLTGGSN 540
SAVNTSNNPP APGSHRFV 558
<212> Type : PRT
<211> Length : 558
SequenceName : SEQ ID 20
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MFSTFKKAAL LAAIALPFST MAAPTVTPQG EVTDQTCSVN INGQTNSVVL MPTVAMADFG 60
ATLADGQSAG QTPFTVSVSN CQAPTGADQA INTTFLGYDV DASTGVMGNR DTSSDAAKGF 120
GIQLMDSSTS GNPVTLAGAT NVPGLTLKVG DTEASYDFGA RYFVIDSAAA TAGKITAVAE 180
YTLSYL 186
<212> Type : PRT
<211> Length : 186
SequenceName : SEQ ID 21
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MNSEGGKPGN VLTVNGNYTG NNGLMTFNAT LGGDNSPTDK MNVKGDTQGN TRVRVDNIGG 60
VGAQTVNGIE LIEVGGNSAG NFALTTGTVE AGAYVYTLAK GKGNDEKNWY LTSKWDGVTP 120

ADTPDPINNP PVVDPEGPSV YRPEAGSYIS NIAAANSLFS HRLHDRLGEP QYTDSLHSQD 180
SASSMWMREV GGHERSSAGD GQLNTQANRY VLQLGGDLAQ WSSNAQDRWH LGVMAGYANQ 240
HSNTQSNRVG YKSDGRISGY SAGLYATWYQ NDANKTGAYV DSWALYNWFD NSVSSDNRSA 300
DDYDSRGVTA SVEGGYTFEA GTCSGSEGTL NTWYVQPQAQ ITWMGVKDSD HARKDGTRIE 360
TEGDGNVQTR LGVKTYLNSH HQRDDGKQRE FQPYIEANWI NNSKVYAVKM NGQTVSRDGA 420
RNLGEVRTGV EAKVNNNLSL WGNVGVQLGD KGYSDTQGML GVKYSW 466
<212> Type : PRT
<211> Length : 466
SequenceName : SEQ ID 22
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MSYLNLRLYQ RNTQCLHIRK HRLAGFFVRL FVACAFAVQA PLSSAELYFN PRFLADDPQA 60
VADLSRFENG QELPPGTYRV DIYLNNGYMA TRDVTFNTGD SEQGIVPCLT RAQLASMGLN 120
TASVAGMNLL ADDACVPLTT MVQDATAHLD VGQQRLNLTI PQAFMSNRAR GYIPPELWDP 180
GINAGLLNYN FSGNSVQNRI GGNSHYAYLN LQSGLNIGAW RLRDNTTWSY NSSDRSSGSK 240
NKWQHINTWL ERDIIPLRSR LTLGDGYTQG DIFDGINFRG AQLASDDNML PDSQRGFAPV 300
IHGIARGTAQ VTIKQNGYDI YNSTVPPGPF TINDIYAAGN SGDLQVTIKE ADGSTQIFTV 360
PYSSVPLLQR EGHTRYSITA GEYRSGNAQQ EKPRFFQSTL LHGLPAGWTI YGGTQLADRY 420
RAFNFGIGKN MGALGALSVD MTQANSTLPD DSQHDGQSVR FLYNKSLNES GTNIQLVGYR 480
YSTSGYFNFA DTTYSRMNGY NIETQDGVIQ VKPKFTDYYN LAYNKRGKLQ LTVTQQLGRS 540
STLYLSGSHQ TYWGTSNVDE QFQAGLNTAF EDINWTLSYS LTKNAWQKGR DQMLARNVNI 600
PFSHWLRSDS KSQWRHASAS YSMSHDLNGR MTNLAGVYGT LLEDNNLSYS VQTGYAGGGD 660
GNSGSTGYAT LNYRGGYGNA NIGYSHSDDI KQLYYGVSGG VLAHANGVTL GQPLNDTVVL 720
VKAPGAKDAK VENQTGVRTD WRGYAVLPYA TEYRENRVAL DTNTLADNVD LDNAVANVVP 780
TRGAIVRAEF KARVGIKLLM TLTHNNKPLP FGAMVTSESS QSSGIVADNG QVYLSGMPLA 840
GKVQVKWGEE ENAHCVANYQ LPPESQQQLL TQLSAECR 878
<212> Type : PRT
<211> Length : 878
SequenceName : SEQ ID 23
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MQIIFGEKCV SLLRLFFAAV LMLWCAQTAA YSGQCHTTQG NPYIGVNFGV KTLEEEENTT 60
GVVKDKFYQW NESNDYYVSC DCDKDNVRSG RWAFAADSPL VYLGDNWYKI NDYLAAKVLL 120
QVKGSSPTAV PFENVGTGAD TRWHICDPGG QRLGGQGASG NSGSFSLKIL QPFVGSVVIP 180
PMALARLFEC YNIPAGDSCT TTGTPVLVYY LSGTINSLGS CSVNAGETIE VDLGDVFAAN 240
FRVVGHKPLG ARTAELAIPV RCNTGNAGLV NVNLSLTATT DPSYPQAIKT SRPGVGVVVT 300
DSQNNIISPA GGTLPLSIPD DADSIA 326
<212> Type : PRT
<211> Length : 326
SequenceName : SEQ ID 24
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MKIKTLAIVV LSALSLSSTA ALAAAATTVNG GTVHFKGEVV NAACAVDAGS VDQTVQLGQV 60
RTASLAQDGA TSSAVGFNIQ LNDCDTNVAS KAAVAFLGTV IDAGHTNVLA LQSSAAGSAT 120
NVGVQILDRT GAALTLDGAT FSEQTTLNNG TNTIPFQARY YAIGEATPGA ANADATFKVQ 180
YQ 182
<212> Type : PRT
<211> Length : 182
SequenceName : SEQ ID 25
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :

MKLKVIATLI ATVAVGVSFN SNFASASTTS ASLTVNSNLT MGTCSAQIMD NSNKVINEVV 60
FGNVYISELG AKSKVQQFKI RFSNCSGLPQ NSAQIVLAPN GISCAGSQSS SAGFSNKFTD 120
ASAATRTAVE VWTTDTPESN GSTQFHCAQK IPVPVTLPAD TTTQPYDYPL SARMTVAEGR 180
LVTDVRPGNF RSPTTFTITY Q 201

<212> Type : PRT
<211> Length : 201
SequenceName : SEQ ID 26
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MASTVEYGET VDGVVLEKDI QLVYGTANNT KINPGGEQHI KEFGISSNTE INGGYQYIEM 60
NGTAEYSVLN DGYQIVQMGG AANQTTLNNG VLQVYGAAND PTIKGGRLIV EKDGITVLAA 120
IEKGGLLEVK EGGLAIAVDQ KAGGAIKAST RVMEVFGTNR LGQFEIKNGI ANNMLLENGG 180
SLRVEENDFA YNTTVDSGGL LEVMDGGTAT GVDKKAGGKL IVSTNALEVS GTNSKGQFSI 240
KDGVSKNYEL DDGSGLIVME DTQAIDTILD EHATMQSLGK DTGTRVQANA VYDLGRSDQN 300
GSITYSSKAI SENMVINNGR ANVWAGTMVN VSVRGNDGIL EVMKPQINYA PAMLVGKVVV 360
SEGASLRTHG AVDTSKADVS LENSAWTIIA DITTTNQNTR LNLANLAMSG ANVIMMDESV 420
TRSSVTASAE NFTTLTTNTL SGNGNFYMRT DMANHQSDQL NVTGQATGDF KIFVTDTGAS 480
PAAGDSLTLV TTGGGDAAFT LGNAGGVVDI GTYEYTLLDN GNHSWSLAEN RAQITPSTTD 540
VLNMAAAQPL VFDAELDTVR ERLGSVKGVS YDTAMWSSAI NTRNNVTTDA GAGFEQTLTG 600
LTLGIDSRFS REESSTIRGL FFGYSHSDIG FDRGGKGNVD SYTLGAYAGW EHQNGAYVDG 660
VVKVDRFANT IHGKMSNGAT AFGDYNSNGA GAHVESGFRW VDGLWSVRPY LAFTGFTTDG 720
QDYTLSNGMR ADVGNTRILR AEAGTAVSYH MDLQNGTTLE PWLKAAVRQE YADSNQVKVN 780
DDGKFNNDVA GTRGVYQAGI RSSFTPTLSG HLSVSYGNGA GVESPWNTQA GVVWTF 836

<212> Type : PRT
<211> Length : 836
SequenceName : SEQ ID 27
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MQRKGNKLLI QLCSVTLLFF TTSWYALANE CYIERNAEGD YHMKLSSTQL SLASQMVEVP 60
TEIAEATWDV NIQLRGDAIG CKSLGDSKAV HFLNTADPSL ISTYTTTNGA ALLKTTVPGI 120
VYSVELLCLS CGAADELDLW LPAQSGADNF IPSTQTKWAY EYSDQSWYLR FRLFITPEFK 180
PKNGVSSGTT IAGKIASWYI GTNDQPWINF YIDNDSLKFF VDEPTCATVA LAQDQGNVSG 240
NQVTLGNSYV SEVKNGLTRE IPFSIRAEYC YASKITVKLK AANKPSDATL VGKTTGSASG 300
VAVKVNSTYD NSKVLLKADG SNTVDYNFAA WSNNLLFLPF TAQLVPDGSG NAVGVGTPSG 360
NATFSFTYE 369

<212> Type : PRT
<211> Length : 369
SequenceName : SEQ ID 28
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MYQFTHQKSR IPKKTLLAAC CALFYSSNGA AADTVEYDSS FLMGTGASTI DVKRYAQGNP 60
TPPGLYNVRV FVNGQATSSL EIPFVDIGEN SAAACLTHKN LAQLHIKQPE QPVTLLAREG 120
EEEDCLDLAK SYEKADVCFD GSDQFLDLTI PQAYVLKSYG GYVDPSLWES GINAATLAYT 180
LNAYHTSSDN DNSDSVYGAF NSGINLGAWH FRARGNYNWT TDNGSDFDFQ DRYLQRDIPA 240
IRSQIIMGDA YTTGETFDSV NVRGVRLYSD SRMLPSALAS YAPTIRGVAN SNAKVTVTQS 300
GYKIYETTVP PGEFVIDDIS PSGFGSELVV TIEEADGSKR TFTQPFSSVV QMQRPGVGRW 360
DFSAGKVIDD SLRSEPNMGQ ASYYYGLNNL FTGYTGIQFT DNNYLAGLLG VGINTSIGAF 420
AVDVTHSRAE IPDDKTYQGQ SYRVTWNKLF QDTGTSFNLA AYRYSTQDYL GLHDALVLID 480
DAKHLSADED KNTMQTYSRM KNQFTVSINQ PLNIAYEDYG SLFISGSWTY YWAANNSRTE 540
YNVGYSKSVS WGSFSVNLQR SWNEDGEKDD AMYVSVSVPI ENILGGKRKS SGFRNLNTQL 600
NTDFDGSHQL NVNSSGNTEN NLVNYSVNAG YSLDKNAGDL ASVGGYLNYE SGLGGISASA 660
SATSDNSQQY SISTDGGFVL HSGGLTFTNN SFSSNDTLVL INALGAKGAR INNSNNEIDR 720
WGYAVTSSVS PYRENRVGLN IETLENDVEL KSTSATTVPR SGSVVLTRFE TDEGRSAVLN 780
ITAANGKSIP FAAEVYQGEV MIGSMGQGGQ AFVRGINDSG ELIVRWYENN QTIDCKLHYQ 840

FPAQPQTQGS TNTLLLNNLT CQVANH 866
<212> Type : PRT
<211> Length : 866
SequenceName : SEQ ID 29
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MKFKRLLHSG IASLSLVACG VNAATDLGPA GDIHFSITIT TKACEMEKSD LEVDMGTMTL 60
QKPAAVGTVL SKKDFTIELK ECDGISKATV EMDSQSDSDD DSMFALEAGG ATGVALKIED 120
DKGTQQVPKG SSGTPIEWAI DGETTSLHYQ ASYVVVNTQA TGGTANALVN FSITYE 176

<212> Type : PRT
<211> Length : 176
SequenceName : SEQ ID 30
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MKYNNIIFLG LCLGLTTYSA LSADSVIKIS GRVLDYGCTV SSDSLNFTVD LQKNSARQFP 60
TTGSTSPAVP FQITLSECSK GTTGVRVAFN GIEDAENNTL LKLDEGSNTA SGLGIEILDG 120
NMRPVKLNDL HAGMQWIPLV PEQNNILPYS ARLKSTQKSV NPGLVRASAT FTLEFQ 176

<212> Type : PRT
<211> Length : 176
SequenceName : SEQ ID 31
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MKWRKRGYLL AAILALASAT IQAADVTITV NGKVVAKPCT VSTTNATVDL GDLYSFSLMS 60
AGAASAWHDV ALELTNCPVG TSRVTASFSG AADSTGYYKN QGTAQNIQLE LQDDSGNTLN 120
TGATKTVQVD DSSQSAHFPL QVRALTVNGG ATQGTIQAVI SITYTYS 167
<212> Type : PRT
<211> Length : 167
SequenceName : SEQ ID 32
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MKRAPLITGL LLISTSCAYA SSEGCGADST SGATNYSSVV DDVTVNQTDN VTGREFTSAT 60
LSSTNWQYAC SCSAGKAVKL VYMVSPVLTT TGHQTGYYKL NDSLDIKTMN RPGNPGD 117

<212> Type : PRT
<211> Length : 117
SequenceName : SEQ ID 33
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MKKALLAAAL VMASGSALAV DGGHIDFNGM VQSGTCKVGV VDTGMHSVTT DGVVTLDTAN 60
VTDTFAEVSA TAVGLLPKEF MISVECDPGA PKNAELTMGS ASYANTSGTL NNNMNITVNG 120
IAPAQNVNIA VHNMKNKAGA AEIKQVEMNN SSEVQELTLD AEGKGQYVFN ASYVKAPNSP 180
AVTAGHVTTN ALYTVAYK 198
<212> Type : PRT
<211> Length : 198
SequenceName : SEQ ID 34

SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MKPNMIVGAL ALTSVFMAGH LQAADGTVHF RGEIIDSTCE VTPETKDQVV DLGKVNRTAF 60
SGVDDVAAPT AFSIDLTQCP ETFKSAAIRF DGNEDAHGNG NLAIGTPLDN SNDAAAGISP 120
SDNSGDYTGA GAVSAAKGVA IRLYNRADNT QVKLYENSAS TPISNGNASM KFMARYIATE 180
TTIDPGTANA DSQFTVEYIK 200
<212> Type : PRT
<211> Length : 200
SequenceName : SEQ ID 35
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MPIFQREGHL KYSFAAGEYQ AGNYDSASPR FGQLDLIYGL PWGMTAYGGV LISNNYNAFT 60
LGIGKNFGYI GAISIDVTQA KSELNNDRDS QGQSYRFLYS KSFESGTDFR LAGYRYSTSG 120
FYTFQEATDV RSDADSDYNR YHKRSEIQGN LTQQLGAYGS VYLNLTQQDY WNDAGKQNTV 180
SAGYNGRIGK VSYSIAYSWN KSPEWDESDR LWSFNISVPL GRAWSNYRVT TDQDGRTNQQ 240
VGVSGTLLED RNLSYSVQEG YASNGVGNSG NANVGYQGGS GNVNVGYSYG KDYRQLNYSV 300
RGGVIVHSEG VTLSQPLGET MTLISVPGAR NARVVNNGGV QVDWMGNAIV PYAMPYRENE 360
ISLRSDSLGD DVDVENAPQK VVPTRGAIVR ARFDTRVGYR VLMTLLRSAG SPVPFGATAT 420
LITDKQNEVS SIVGEEGQLY ISGMPEEGRV LIKWGNDASQ QCVAPYKLSL ELKQGGIIPV 480
SANCQ 485
<212> Type : PRT
<211> Length : 485
SequenceName : SEQ ID 36
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MSGYTVKPPT GDSNEQTQFI DYFNLFYSKR DQEQISISQQ LGNYGATFFS ASRQSYWNTS 60
RSDQQISFGL NVPFGDITTS LNYSYSNNIW QNDRDHLLAF TLNVPFSHWM RTDSQSAFRN 120
SNASYSMSND LKGGMTNLSG VYGTLLPDNN LNYSVQVGNT HGGNTSSGTS GYSTLNYRGA 180
YGNTNVGYSR SGDSSQIYYG MSGGIIAHAD GITFGQPLGD TMVLVKAPGA DNVKIENQTG 240
IHTDWRGYAI LPFATEYREN RVALNANSLA DNVELDETVV TVIPTHGAIA RATFNAQIGG 300
KVLMTLKYGN KSVPFGAIVT HGENKNGSIV AENGQVYLTG LPQSGKLQVS WGNDKNSNCI 360
VDYKLPEVSP GTLLNQQTAI CR 382
<212> Type : PRT
<211> Length : 382
SequenceName : SEQ ID 37
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MSALYERSQL TQVMISSAPA TAETMEKAEY LRLDCTIKEV QFTAGQKQDI DVTTLCSTEQ 60
ENINGLGASS EISMSGNFYL NQAQNALRDA YDNDTVYAFK VQFPSGKGFK FLAEVRQHTW 120
SSGTNGVVAA TFSLRLKGKP VSYVVPLAFV KNLDKTLTVN TGALLTMSVS VNGGTPPYKH 180
AWKKDGQPVE GQTTDTFSKP GAQSGDKGAY TCEVTDSAEQ PQSITSDACT VTVNGAGG 238

<212> Type : PRT
<211> Length : 238
SequenceName : SEQ ID 38
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :

MRNKPFYLLC AFLWLAVSHA LAADSTITIR GYVRDNGCSV AAESTNFTVD LMENAAKQFN 60
NIGATTPVVP FRILLSPCGN AVSAVKVGFT GVADSHNANL LALENTVSAA SGLGIQLLNE 120
QQNQIPLNAP SSAISWTTLT PGKPNTLNFY ARLMATQVPV TAGHINATAT FTLEYQ 176

<212> Type : PRT
<211> Length : 176
SequenceName : SEQ ID 39
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MNKSVVSISA AMLVLLCQPV MGSEISPATP SDEDNYTFDP QLFRGSRFSQ SSLAKLTTRE 60
SVAPGNYKMD IYTNNKLSGS WNVTFKEAAD GRVLPCLTPE VADAIGLKTG EDKGEKDPVC 120
TFAKELAPGI TSQTQLSQLR LDLSVPQSQL ISRPRGYVPP SELDTGASLA FMNYIANYYN 180
VAYSGQNAHS QRSLWASFNG GINLGAWQYR QLSNMTWDND KGNQWNNIRS YLQRPLPAIN 240
SQLMMGQLIT SGRFFSGLSY HGVSLATDER MLPDSMRGYA PTIRGVAATN ARVSVMQNGH 300
EIYQTTVAPG PFEINDLYPT SYSGDLDVTV TEANGAVSRF SVPFSAVPES MRPGTSRYNV 360
EVGKTQDSGD DSMFGDLTWQ HGMTNTLTFN SGSRIADGYQ ALMLGGVYGS SLGAFGANLT 420
WSHARVPESE AQSGWMSQLT WSKTFQPTST TVSLAGYRYS TSGYRDLADV LGERHAASNK 480
QSWDSSQWRQ QSRFDLTLSQ SLANYGNLFV SGSTQNYRGG KSRDTQLQLG YSNSFSHGIS 540
MNLSVGRQRM GGYKDNSDDM QTVTSLSFSF PLGGNGPRVP SLSNSWTHST DGSSQLQSSL 600
TGMLDEAQTT NYSLNVMRDQ QYKQTTLSGN MQKRFSQTTV GLNASKGQDY WQASGNVQGA 660
MAVHGGGITF GPYLGETFAL VEAKGAEGAK VYNSSQLEIN DSGYALVPAV TPYRYNRISL 720
DPQGMDGDAE LVDSERQVAP VAGAAVKVIF RTRPGKALLI KSRMADGSEL PMGADVLDEN 780
NTVVGIAGQG GQIYLRTEQT KGHLSVRWGE GANDSCQLPF DISGKDSNSP IIRLNETCQS 840

<212> Type : PRT
<211> Length : 840
SequenceName : SEQ ID 40
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MKLAACFLTL LPGFAVAASW TSPGFPAFSE QGTGTFVSHA QLPKGTRPLT LNFDQQCWQP 60
ADAIKLNQML SLQPCSNTPP QWRLFRDGKY TLQIDTRSGT PTLMISIQNA AEPVANLVRE 120
CPKWDGLPLT LDVSATFPEG AAVRDYYSQQ IAIVKNGQIT LQPAATSNGL LLLERAETDA 180
SAPFDWHNAT VYFVLTDRFE NGDPSNDQSY GRHKDGMAEI GTFHGGDLRG LTNKLDYLQQ 240
LGVNALWISA PFEQIHGWVG GGTKGDFPHY AYHGYYTQDW TNLDANMGNE ADLRTLVDSA 300
HQRGIRILFD VVMNHTGYAT LADMQEYQFG ALYLSGDEVK KTLGERWSDW KPAAGQTWHS 360
FNDYINFSDK TGWDKWNGKN WIRTDIGDYD NPGFDDLTMS LAFLPDIKTE STTASGLPVF 420
YKNKTDTHAK AIDGFTPRDY LTHWLSQWVR DYGIDGFRVD TAKHVELPAW QQLKTEASAA 480
LREWKKANPD KALDDKPFWM TGEAWGHGVM QSDYYRHGFD AMINFDYQEQ AAKAVDCIAQ 540
MDTTWQQMAE KLQGFNVLSY LSSHDTRLFR EGGDKAAELL LLAPGAVQIF YGDESSRPFG 600
PTGSDPLQGT RSDMNWQDVS GKSAANVAHW QKISQFRARH PAIGAGKQTT LSLKQGYGFV 660
REHGDDKVLV IWAGQQ 676

<212> Type : PRT
<211> Length : 676
SequenceName : SEQ ID 41
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MPQRHHQGHK RTPKQLALII KRCLPMVLTG SGMLCTTANA EEYYFDPIML ETTKSGMQTT 60
DLSRFSKKYA QLPGTYQVDI WLNKKKVSQK KITFTANAEQ LLQPQFTVEQ LRELGIKVDE 120
IPALAEKDDD SVINSLEQII PGTAAEFDFN HQRLNLSIPQ IALYRDARGY VSPSRWDDGI 180
PTLFTNYSFT GSDNRYRQGN RSQRQYLNMQ NGANFGPWRL RNYSTWTRND QASSWNTISS 240
YLQRDIKALK SQLLLGESAT SGSIFSSYNF TGVQLASDDN MLPNSQRGFA PTVRGIANSS 300
AIVTIRQNGY VIYQSNVPAG AFEINDLYPS SNSGDLEVTI EESDGTQRRF IQPYSSLPMM 360
QRPGHLKYSA TAGRYRADAN SDSKEPEFAE ATAIYGLNNT FTLYGGLLGS EDYYALGIGI 420
GGTLGALGAL SMDINRADTQ FDNQHSFHGY QWRTQYIKDI PETNTNIAVS YYRYTNDGYF 480
SFDEANTRNW DYNSRQKSEI QFNISQTIFD GVSLYASGSQ QDYWGNNEKN RNISVGVSGQ 540

QWGIGYSLNY QYSRYTDQNN DRALSLNLSI PLERWLPRSR VSYQMTSQKD RPTQHEMRLD 600
GSLLDDGRLS YSLEQSLDDD NNHNSSVNAS YRSPYGTFSA GYSYGNDSSQ YNYGVTGGVV 660
IHPHGVTLSQ YLGNAFALID ANGASGVRIQ NYPGIATDPF GYAVVPYLTT YQENRLSVDT 720
TQLPDNVDLE QTTQFVVPNR GAMVAARFNA NIGYRVLVTV SDRNGKPLPF GALASNDDTG 780
QQSIVDEGGI LYLSGISSKS QSWTVRWGNQ ADQQCQFAFS TPDSEPTTSV LQGTAQCH 838

<212> Type : PRT
<211> Length : 838
SequenceName : SEQ ID 42
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MMFRNRILLI FILWANFTWA GCRTTASLNI TDGINVGEIL ANETSFSKSV VFTGISCDTS 60
TDKIVYKNIQ SDWVEVGPFG NGEKLKVKIE SLGKTSDTIG KSSNAQAVLP YVVKIARGTP 120
DFTGERKSTW FISDTVIANI GGESSSSIDF WLGICKALKF NWCVNYLTSK LAGDTFTLGL 180
NISYYPKNTT CKPENTVIKV DDIALFQLRN QGKIAANSKE GTITLKCDNL FGDKKQASRN 240
MVVYLSSSDL VKGSNTILRG KTDNGVGFVL DLTEPPKGTE AAIKISANGD QGAATSLWKT 300
DKPGVSLNSN IINIPVMASY YVYDEKKVKS GALEATALIN VKYD 344
<212> Type : PRT
<211> Length : 344
SequenceName : SEQ ID 43
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MIKKASLLTA CSVTAFSAWA QDTSPDTLVV TANRFEQPRS TVLAPTTVVT RQDIDRWQST 60
SVNDVLRRLP GVDITQNGGS GQLSSIFIRG TNASHVLVLI DGVRLNLAGG SGSADLSQFP 120
IALVQRVEYI RGPRSAVYGS DAIGGVVNII TTRDEPGTEI SAGWGSNSYQ NYDVSTQQQL 180
GDKTRVTLLG DYAHTHGYDV VAYGNTGTQA QPDNDGFLSK TLYGALEHNF TDAWSGFVRG 240
YGYDNRTNYD AYYSPGSPLV DTRKLYSQSW DAGLRYNGEL IKSQLITSYS HSKDYNYDPH 300
YGRYDSSATL DEMKQYTVQW ANNIIIGHGN VGAGVDWQKQ STAPGTAYVK DGYDQRNTGI 360
YLTGLQQVGD FTFEGAARSD DNSQFGREGT WQTSAGWEFI EGYRFIASYG TSYKAPNLGQ 420
LYGFYGNPNL DPEKSKQWEG AFEGLTAGVN WRISGYRNDV SDLIDYDDHT LKYYNEGKAR 480
IKGVEATANF DTGPLTHTVS YDYVDARNAI TDTPLLRRAK QQVKYQLDWQ LYDFDWGITY 540
QYLGTRYDKD YSSYPYQTVK MGGVSLWDLA VAYPVTSHLT VRGKIANLFD KDYETVYGYQ 600
TAGREYTLSG SYTF 614
<212> Type : PRT
<211> Length : 614
SequenceName : SEQ ID 44
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MKNKLLFMML TILGAPGIAA AAGYDLANSE YNFAVNELSK SSFNQAAIIG QAGTNNSAQL 60
RQGGSKLLAV VAQEGSSNRA KIDQTGDYNL AYIDQAGSAN DASISQGAYG NTAMIIQKGS 120
GNKANITQYG TQKTAIVVQR QSQMAIRVTQ R 151
<212> Type : PRT
<211> Length : 151
SequenceName : SEQ ID 45
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MNIFAYLLVL VFSMSMSSSA FASVVMTGTR IIFPGDAKEK TIQLRNTSDQ PYIINIHVED 60
ERGSDKNVPF MPTPQTFRME AAAGQALRLL YTGNNLPQDR ESVFWFSFSQ LPYLNKNDKS 120
QNQLILALTN RVKIFYRPSS IVGKSSDAPK NLTYQVKQNR IEVTNPTGYY VTIRAAELLN 180
NGKKVPLANS VMIAPQSTTE WTLPSGISVA PGAQIHLVTV NDYGVNVTSE HAL 233

<212> Type : PRT
<211> Length : 233
SequenceName : SEQ ID 46
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MKRLHKRFLL ATFCALLTAT LQAADVTITV NGRVVAKPCT IQTKEANVNL GDLYTRNLQQ 60
PGSASGWHNI TLSLTDCPAE TSAVTAIVTG STDNTGYYKN EGTAENIQIE LRDDQDATLK 120
NGDSKTVIVD EITRNAQFPL KARAITVNGN ASQGTIEALI NVIYTWQ 167
<212> Type : PRT
<211> Length : 167
SequenceName : SEQ ID 47
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MRAKLLGIVL TTPIAISSFA STETLSFTPD NINADISLGT LSGKTKERVY LAEEGGRKVS 60
QLDWKFNNAA IIKGAINWDL MPQISIGAAG WTTLGSRGGN MVDQDWMDSS NPGTWTDESR 120
HPDTQLNYAN EFDLNIKGWL LNEPNYRLGL MAGYQESRYS FTARGGSYIY SSEEGFRDDI 180
GSFPNGERAI GYKQRFKMPY IGLTGSYRYE DFELGGTFKY SGWVEASDND EHYDPGKRIT 240
YRSKVKDQNY YSVSVNAGYY VTPNAKVYVE GTWNRVTNKK GNTSLYDHND NTSDYSKNGA 300
GIENYNFITT AGLKYTF 317
<212> Type : PRT
<211> Length : 317
SequenceName : SEQ ID 48
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MFFKRGKILS AGRLNKKSLG IVMLLSVGLL LAGCSGSKSS DTGTYSGSVY TVKRGDTLYR 60
ISRTTGTSVK ELARLNGISP PYTIEVGQKL KLGGAKSSSS TRKSTAKSTT KTASVTPSSA 120
VPKSSWPPVG QRCWLWPTTG KVIMPYSTAD GGNKGIDISA PRGTPIYAAG AGKVVYVGNQ 180
LRGYGNLIMI KHSEDYITAY AHNDTMLVNN GQSVKAGQKI ATMGSTDAAS VRLHFQIRYR 240
ATAIDPLRYL PPQGSKPKC 259
<212> Type : PRT
<211> Length : 259
SequenceName : SEQ ID 49
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MPTPNPLAPV KGAGTTLWVY NGNGDPYANP LSDNDWSRLA KVKDLTPGEL TAESYDDSYL 60
DDEDADWAAT GQGQKSAGDT SFTLAWMPGE QGQQALLAWF NEGDTRAYKI RFPNGTVDVF 120
RGWVSSIGKA VTAKEVITRT VKVTNVGRPS MAEDRSTVTA ATGMTVTPAS TSVVKGQSTT 180
LTVAFQPEGA TDKSFRAVSA DKTKATVSVS GMTITVKGVA AGKVNIPVVS GNGEFAAVAE 240
INVTAS 246
<212> Type : PRT
<211> Length : 246
SequenceName : SEQ ID 50
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MSALYERSQL TQVMISSAPA TAETMDKAEY LRLDCTIKEV QFTAGQKQDI DVTTLCSTEQ 60
ENINGLGASS EISMSGNFYL NQAQNALRDA YDNDALYAFK VLFPSGKGFK FLAEVRQHTW 120
SSGTNGVVAA TFSLRLKGKP VSFVVPLAFV KNLDKTLTVN TGALLTMSVS ANGGTPPYKY 180

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AWKKDGQPVD GQTTDTFSKP GAQSADAGKY TCVVTDSAEK AQSVTSVECT VTVSAAAG      238

<212> Type : PRT
<211> Length : 238
      SequenceName : SEQ ID 51
      SequenceDescription :

Sequence
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<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MKKSTLALVV MGIVASASVQ AAEIYNKDGN KLDVYGKVKA MHYMSDNDSK DGDQSYIRFG      60
FKGETQINDQ LTGYGRWEAE FAGNKAESDT AQQKTRLAFA GLKYKDLGSF DYGRNLGALY     120
DVEAWTDMFP EFGGDSSAQT DNFMTKRASG LATYRNTDFF GVIDGLNLTL QYQGENENRD     180
VKKQNGDGFG TSLTYDFGGS DFAISGAYTN SDRTNEQNLQ SRGTGKRAEA WATGLKYDAN     240
NIYLATFYSE TRKMTPITGG FANKTQNFEA VAQYQFDFGL RPSLGYVLSK GKDIEGIGDE     300
DLVNYIDVGA TYYFNKNMSA FVDYKINQLD SDNKLNINND DIVAVGMTYQ F               351

<212> Type : PRT
<211> Length : 351
      SequenceName : SEQ ID 52
      SequenceDescription :

Sequence
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<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MRVKHAVVLL MLISPLSWAG TMTFQFRNPN FGGNPNNGAF LLNSAQAQNS YKDPSYNDDF      60
GIETPSALDN FTQAIQSQIL GGLLSNINTG KPGRMVTNDY IVDIANRDGQ LQLNVTDRKT     120
GQTSTIQVSG LQNNSTDF                                                   138
<212> Type : PRT
<211> Length : 138
      SequenceName : SEQ ID 53
      SequenceDescription :

Sequence
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<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MKRKVLAMLV PALLVAGAAN AAEIYNKDGN KLDLYGKVAG LHYFSDDASS DGDMSYARIG      60
FKGETQIADQ FTGYGQWEFN IGANGPESDK GNTATRLAFA GFGFGQNGTF DYGRNYGVVY     120
DVEAWTDMLP EFGGDTYAGA DNFMNGRANS VATYRNNGFF GQVDGLNFAL QYQGNNEKSG     180
LFDQEGSGNG NGRKLAKENG DGSVCPLPMT LTLV                                 214
<212> Type : PRT
<211> Length : 214
      SequenceName : SEQ ID 54
      SequenceDescription :

Sequence
--------
<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MNTVTLEGGT FNNNGTLNDV VKIEKNSNAV INNTGSLSTL QLHDGTVNNS GIASARVNAQ      60
GDAVFNNLAG GEARKGAILY NSAVVNNAGT WKMGYQDENN NAGTLDIDDK STFNNSGKLI     120
LDNSKNAIRF QGSNANATLY NTGEMTLDAA LGAGAILYDD GASEFINKGV VDAKVTVAVS     180
TAGATESDAF LWNQDGGVIN FDKDNASAVK FTHNNYVALN DGVMNISGNN AVAMEGDKNA     240
QLVNNGVINL GTEGTTDTGL TGMQLDANAT ADAVIENNGT INIFANDSFA FSVLGTEGHI     300
VNNGTVVIAD GVTGSGLIKQ GDSVNVEGVN GNSGNNTEVH YTDYTLPDMP NTYTTSPFSE     360
TTDSGSSDGS SNNLNGYIVG TNVDGSAGKL KVNNASMNGV GINTGFAAGT ADTTVSFDNV     420
VEGINLTDAD AITSTSVVWT AKGSTDASGN VDVIMSKNAY TDVATDASVN DVAKALDAGY     480
TNNELYTSLN VGTTAELNSA LKQVSGSQAT TVFREARVLS NRFSMLADAA PKVGNGLAFN     540
VVAKGDPRAE LGNNTEYDML ALRKTVDLSE SQSMSLEYGI ARLDGDGAQK AGDNGVTGGY     600
SQFFGLKHQM SFDNGMRWNN ALRYDVHNLD SSRSVAYGDV SKTADTDVKQ QYLELRSEGA     660
KTFEPREGLK ITPYAGVKLR HSLEGGYQER NAGDFNLSMN SGSETAVDSI VGLKLDYAGK     720
GGWSANATLE GGPNLSYSKS QRTASLAGAG SQHFNVDDGQ KGGGINSLAS VGVKYSSKES     780
SLNLDAYHWK EDGISDKGVM LNFKKTF                                         807
<212> Type : PRT
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<211> Length : 807
SequenceName : SEQ ID 55
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MLNGISNAAS TLGRQLVGIA SRVSSAGGTG FSVAPQAVRL TPVKVHSPFS PGSSNVNART 60
IFNVSSQVTS FTPSRPAPPP PTSGQASGAS RPLPPIAQAL KEHLAAYEKS KGPEALGFKP 120
ARQAPPPPTS GQASGASRPL PPIAQALKEH LAAYEKSKGP EALGFKPARQ APPPPTSGQA 180
SGASRPLPPI AQALKEHLAA YEKSKGPEAL GFKPARQAPP PPTGPSGLPP LAQALKDHLA 240
AYEQSKKG 248
<212> Type : PRT
<211> Length : 248
SequenceName : SEQ ID 56
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MNKKIHSLAL LVNLGIYGVA QAQEPTDTPV SHDDTIVVTA AEQNLQAPGV STITADEIRK 60
NPVARDVSEI IRTMPGVNLT GNSTSGQRGN NRQIDIRGMG PENTLILIDG KPVSSRNSVR 120
QGWRGERDTR GDTSWVPPEM IERIEVLRGP AAARYGNGAA GGVVNIITKK GSGEWHGSWD 180
AYFNAPEHKE EGATKRTNFS LTGPLGDEFS FRLYGNLDKT QADAWDINQG HQSARAGTYA 240
TTLPAGREGV INKDINGVVR WDFAPLQSLE LEAGYSRQGN LYAGDTQNTN SDAYTRSKYG 300
DETNRLYRQN YSLTWNGGWD NGVTTSNWVQ YEHTRNSRIP EGLAGGTEGK FNEKATQDFV 360
DNDLDDVMLH SEVNLPIDFL VNQTLTLGTE WNQQRMKDLS SNTQALTGIN TGGAIDGVSA 420
TDRSPYSKAE IFSLFAENNM ELTDSTIVTP GLRFDHHSIV GNNWSPALNI SQGLGDDFTL 480
KMGIARAYKA PSLYQTNPNY ILYSKGQGCY ASAGGCYLQG NDDLKAETSI NKEIGLEFKR 540
DGWLAGITWF RNDYRNKIEA GYVAVGQNAV GTDLYQWDNV PKAVVEGLEG SLNVPVSETV 600
MWTNNITYML KSENKTTGDR LSIIPEYTLN STLSWQARED LSMQTTFTWY GKQQPKKYNY 660
KGQPAVGPET KEISPYSIVG LSATWDVTKN VSLTGGVDNL FDKRLWRAGN AQTTGDLAGA 720
NYIAGAGAYT YNEPGRTWYM SVNTHF 746
<212> Type : PRT
<211> Length : 746
SequenceName : SEQ ID 57
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MGGRFSLRYK KLSYRFVFLT LAGCSSVGNQ SLKNETQESV KTKIVKGKTT KQDVLASFGE 60
PDSRSLIDGE EQWSYTMYNS QSKATSFIPV VGLLAGGADS QTKSLTVSFK GEKVSTYIFN 120
AGTSNVKTGI F 131
<212> Type : PRT
<211> Length : 131
SequenceName : SEQ ID 58
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MKKIACLSAL AAVLAFTAGT SVAATSTVTG GYAQSDAQGQ MNKMGGFNLK YRYEEDNSPL 60
GVIGSFTYTE KSRTASSGDY NKNQYYGITA GPAYRINDWA SIYGVVGVGY GKFQTTEYPT 120
YKHDTSDYGF SYGAGLQFNP MENVALDFSY EQSRIRSVDV GTWIAGVGYR F 171
<212> Type : PRT
<211> Length : 171
SequenceName : SEQ ID 59
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MKSIATLVVC AISGIACVNL SAHAAEGEHT ISLGYAHFQF PGLKDFVKDA TAHNRETFSH 60
FVNRNYFSSL GEYTDGRVSG YEGKDKNPQG INIRYRYEIT DDFGVITSFT WTRSLTNSQT 120
FIDVQSADHT RKIKNPAASA RTDIRANYWS LLAGPSWRVN QYMSLYAMAG MGVAKVSADL 180
KIKDNINSSG GFSESNSTKK TSLAWAAGAQ FNLNESVTLD VAYEGSGSGD WRTSGVTAGI 240
GLKF 244
<212> Type : PRT
<211> Length : 244
SequenceName : SEQ ID 60
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MRKLYAAILS AAICLTVSGA PAWASEQQAT LSAGYLHVST NAPGSDNLNG INVKYRYEFT 60
DTLGLVTSFS YAGDRNRQIT RYSDTRWHED SVRNRWFSVM AGPSVRVNEW FSAYAMAGVA 120
YSRVSTFSGD YLRVTDNKGK THDVLTGSDD GRHSNTSLAW GAGVQFNPTE SVAIDIAYEG 180
SGSGDWRTDG FIVGVGYKF 199
<212> Type : PRT
<211> Length : 199
SequenceName : SEQ ID 61
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MRKLYAAILS AAICLAVSGA PAWASEQQAT LSAGYLHART SAPGSDNLNG INVKYRYEFT 60
DTLGLVTSFS YAGDKNRQLT RYSDTRWHED SVRNRWFSVM AGPSVRVNEW FSAYAMAGVA 120
YSRVSTFSGD YLRVTDNKGK THDVLTGSDD GRHSNTSLAW GAGVQFNPTE SVAIDIAYEG 180
SGSGDWRTDG FIVGVGYKF 199
<212> Type : PRT
<211> Length : 199
SequenceName : SEQ ID 62
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MRKLYAAILS AAICLAVSGA PAWASEQQAT LSAGYLHART SAPGSDNLNG INVKYRYEFT 60
DTLGLVTSFS YAGDKNRQLT RYSDTRWHED SVRNRWFSVM AGPSVRVNEW FSAYAMAGVA 120
YSRVSTFSGD YLRVTDNKGK THDVLTGSDD GRHSNTSLAW GAGVQFNPTE SVAIDIAYEG 180
SGSGDWRTDG FIVGVGYKF 199
<212> Type : PRT
<211> Length : 199
SequenceName : SEQ ID 63
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MRKLYAAILS AAICLAVSGA PAWASEQQAT LSAGYLHART SAPGSDNLNG INVKYRYEFT 60
DTLGLVTSFS YAGDKNRQLT RYSDTRWHED SVRNRWFSVM AGPSVRVNEW FSAYAMAGVA 120
YSRVSTFSGD YLRVTDNKGK THDVLTGSDD GRHSNTSLAW GAGVQFNPTE SVAIDIAYEG 180
SGSGDWRTDG FIVGVGYKF 199
<212> Type : PRT
<211> Length : 199
SequenceName : SEQ ID 64
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7

<400> PreSequenceString :
MVMSQKTLFT KSALAVAVAL ISTQAWSAGF QLNEPSSSGL GRAYSGEGAI ADDAGNVSRN 60
PALITMFDRP TFSAGAVYID PDVNISGTSP SGRSLKADNI APTAWVPNMH FVAPINDQFG 120
WGASITSNYG LATEFNDTYA GGSVGGTTDL ETMNLNLSGA YRLNNAWSFG LGFNAVYARA 180
KIERFAGDLG QLVAGQIMQS PAGKTPQGQA LAATANGIDS NTKIAHLNGN QWGFGWNAGI 240
LYELDKNNRY ALTYRSEVKI DFKGNYSSDL NRVFNNYGLP IPTATGGATQ SGYLTLNLPE 300
MWEVSGYNRV DPQWAIHYSL AYTSWSQFQQ LKATSTSGDT LFQKHEGFKD AYRIALGTTY 360
YYDDNWTFRT GIAFDDSPVP AQNRSISIPD QDRFWLSAGT TYAFNKDASV DVGVSYMHGQ 420
SVKINEGPYQ FESEGKAWLF GTNFNYAF 448
<212> Type : PRT
<211> Length : 448
SequenceName : SEQ ID 65
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MAFSQAVSGL NAAATNLDVI GNNIANSATY GFKSGTASFA DMFAGSKVGL GVKVAGITQD 60
FTDGTTTNTG RGLDVAISQN GFFRLVDSNG SVFYSRNGQF KLDENRNLVN MQGLQLTGYP 120
ATGTPPTIQQ GANPTNISIP NTLMAAKTTT TASMQINLNS SDPLPSVNAF DASNADSYNK 180
KGSVTVFDSQ GNAHDMSVYF VKTGDNNWQV YTQDSSDPTG TAEPAMKLVF NANGVLTSNP 240
TENITTGAIN GAEPATFSLS FLNSMQQNTG ANNIVATTQN GYKPGDLVSY QINDDGTVVG 300
NYSNEQTQLL GQIVLANFAN NEGLASEGDN VWSATQSSGV ALLGTAGTGN FGTLTNGALE 360
ASNVDLSKEL VNMIVAQRNY QSNAQTIKTQ DQILNTLVNL R 401
<212> Type : PRT
<211> Length : 401
SequenceName : SEQ ID 66
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MSKSTFLHIL ISSIILVALI QSSAWANCTN TQIGQTEDGR TALIEFGKIN MTDTYFAPAG 60
SLLATTVVPP TNYTSGGATG SSVLWECDAT DLPNIYFLVA TNGDDRVGGF YDAGGPDGLS 120
DVYATWFAFV GLKQTMAGVT LGRYWKKVPI TSYATQGTKI QIRLQDIPPL HAELYRISTL 180
PDTSATTSWC GNNNTDSSGV GFAKPSGTIY NCVQPNAYIQ LSGTSGILFG HDEPGEDSSV 240
HWDFWGADNG FGYGMRSANR LYNNATCVAR SATPLVLLPT IAEAQLNAGM ESTGNFNVRV 300
ECSNSVQSGI SDTQTALGIQ VSEGAYTAAQ KLGIINSNGG VSALVSDNYD AAEMAKGVGI 360
YISNSAHPDT AMTLVGQPGI AKLTPGGNAA GWYPVFEGAT LEGATHPGYS SYSYSFIARL 420
KKLPNQTVSA GKVRATAYIL VKMQ 444
<212> Type : PRT
<211> Length : 444
SequenceName : SEQ ID 67
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MENNRNFPAR QFHSLTFFAG LCIGITPVAQ ALAAEGQTNA DDTLVVEAST PSLYAPQQSA 60
DPKFSRPVAD TTRTMTVISE QVIKDQGATN LTDALKNVPG VGAFFAGENG NSTTGDAIYM 120
RGADTSNSIY IDGIRDIGSV SRDTFNTEQV EVIKGPSGTD YGRSAPTGSI NMISKQPRND 180
SGIDASASIG SAWFRRGTLD VNQVIGDTTA VRLNVMGEKT HDAGRDKVKN ERYGVAPSIA 240
FGLGTANRLY LNYLHVTQHN TPDGGIPTIG LPGYSAPSAG TATLNHSGKV DTHNFYGTDS 300
DYDDSTTDTA TMRFEHDIND NTTIRNTTRW SRVKQDYLMT AIMGGASNIT QPTSDVNSWT 360
WSRTANTKDV SNKILTNQTN LTSTFYTASI GHDVSTGVEF TRETQTNYGV NPVTLPAVNI 420
YHPDSSIHPG GLTRNGANAN GQTDTFAIYA FDTLQITRDF ELNGGIRLDN YHTEYDSATA 480
CGGSGRGAIT CPAGVAKGSP VTTVDTAKSG NLVNWKAGAL YHLTENGNVY INYAVSQQPP 540
GGNNFALAQS GSGNSANRTD FKPQKANTSE IGTKWQVLDK RLLLTAALFR TDIENEVEQN 600
DDGTYSQYGK KRVEGYEISV AGNITPAWQV IGGYTQQKAT IKNGKDVAQD GSSSLPYTPE 660
HAFTLWSQYQ ATDDISVGAG ARYIGSMHKG SDGAVGTPAF TEGYWVADAK LGYRVNRNLD 720
FQLNVYNLFD TDYVASINKS GYRYHPGEPR TFLLTANMHF 760
<212> Type : PRT
<211> Length : 760
SequenceName : SEQ ID 68

SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MQMKKLLPIL IGLSLSGFSS LSQAENLMQV YQQARLSNPE LRKSAADRDA AFEKINEARS 60
PLLPQLGLGA DYTYSNGYRD ANGINSNATS ASLQLTQSIF DMSKWRALTL QEKAAGIQDV 120
TYQTDQQTLI LNTATAYFNV LNAIDVLSYT QAQKEAIYRQ LDQTTQRFNV GLVAITDVQN 180
ARAQYDTVLA NEVTARNNLD NAVEQLRQIT GNYYPELAAL NVENFKTDKP QPVNALLKSA 240
EKRNLSLLQA RLSQDIAREQ IRQAQDGHLP TLDLTASSGI SDTSYSGSKT RGAAGTQYDD 300
SNMGQNKVGL SFSLPIYQGG MVNSQVKQAQ YNFVGASEQL ESAHRSVVQT VRSSFNNINA 360
SISSINAYKQ AVVSAQSSLD AMEAGYSVGT RTIVDVLDAT TTLYNAKQEL ANARYNYLIN 420
QLNIKSALGT LNEQDLLALN NALSKPVSTN PENVAPQTPE QNAIADGYAP DSPAPVVQQT 480
SARTTTSNGH NPFRN 495
<212> Type : PRT
<211> Length : 495
SequenceName : SEQ ID 69
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MTKLKLLALG VLIATSAGVA HAEGKFSIGA GVGVVEHPYK DYDTDVYPVP VINYEGDNFW 60
FRGLGGGYYL WNDATDKLSI TAYWSPLYFK AKDSGDHQMR HLDDRKSTMM AGLSYAHFTQ 120
YGYLRTTLAG DTLDNSNGIV WDMAWLYRYT NGGLTVTPGI GVQWNSENQN EYYYGVSRKE 180
SARSGLRGYN SNDSWSPYLE LSASYNFLGD WSVYGTARYT RLSDEVTDSP IVDKSWTGLI 240
STGITYKF 248
<212> Type : PRT
<211> Length : 248
SequenceName : SEQ ID 70
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MKKTLLAAGA VLALSSSFTV NAAENDKPQY LSDWWHQSVN VVGSYHTRFG PQIRNDTYLE 60
YEAFAKKDWF DFYGYADAPV FFGGNSDAKG IWNHGSPLFM EIEPRFSIDK LTNTDLSFGP 120
FKEWYFANNY IYDMGRNKDG RQSTWYMGLG TDIDTGLPMS LSMNVYAKYQ WQNYGAANEN 180
EWDGYRFKIK YFVPITDLWG GQLSYIGFTN FDWGSDLGDD SGNAINGIKT RTNNSIASSH 240
ILALNYDHWH YSVVARYWHD GGQWNDDAEL NFGNGNFNVR STGWGGYLVV GYNF 294

<212> Type : PRT
<211> Length : 294
SequenceName : SEQ ID 71
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MLSTQFNRDN QYQAITKPSL LAGCIALALL PSAAFAAPAT EETVIVEGSA TAPDDGENDY 60
SVTSTSAGTK MQMTQRDIPQ SVTIVSQQRM EDQQLQTLGE VMENTLGISK SQADSDRALY 120
YSRGFQIDNY MVDGIPTYFE SRWNLGDALS DMALFERVEV VRGATGLMTG TGNPSAAINM 180
VRKHATSREF KGDVSAEYGS WNKERYVADL QSPLTEDGKI RARIVGGYQN NDSWLDRYNS 240
EKTFFSGIVD ADLGDLTTLS AGYEYQRIDV NSPTWGGLPR WNTDGSSNSY DRARSTAPDW 300
AYNDKEINKV PMTLKQRFAD TWQATLNATH SEVEFDSKMM YVDAYVNKAD GMLVGPYSNY 360
GPGFDYVGGT GWNSGKRKVD ALDLFADGSY ELFGRQHNLM FGGSYSKQNN RYFSSWANIF 420
PDEIGSFYNF NGNFPQTDWS PQSLAQDDTT HMKSLYAATR VTLADPLHLI LGARYTNWRV 480
DTLTYSMEKN HTTPYAGLVF DINDNWSTYA SYTSIFQPQN DRDSSGKYLA PITGNNYELG 540
LKSDWMNSRL TTTLAIFRIE QDNVAQSTGT PIPGSNGETA YKAVDGTVSK GVEFELNGAI 600
TDNWQLTFGA TRYIAEDNEG NAVNPNLPRT TVKMFTSYRL PVMPELTVGG GVNWQNRVYT 660
DTVTPYGTFR AEQGSYALVD LFTRYQVTKN FSLQGNVNNL FDKTYDTNVE GSIVYGAPRN 720
FSITGTYQF 729
<212> Type : PRT

<211> Length : 729
SequenceName : SEQ ID 72
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MARFQFKNRK NNGLIFFISF MVMGEAAIAA PLPQWANAPA VTPVAQLSLQ ESILRAFARN 60
PGVTQQAAQI GIGEAQIDEA KSAWYPHVGL TGNAGPSRQT DSSGRLDNNV SYGITLTQLV 120
YDFGKTNNDI NLQTAARDSY RFKLMATLTD VAEKTATAYM EVSRYQALCD AAQRNIHSLE 180
NVYNMAALRA NAGLNSSSDE LQAQTRIAGM RSTLEQYQAQ MASAKAQLAV LTGVQPEAIA 240
APPAELAEQP VSLKNIDYQS IPLVLAAENL RQSAQYGVEK TKAQYWPTLS IQGGKTRYQT 300
SDRSYWDDQL QLNVNAPLYQ GGAVSAQVQQ AEGQQKISAS QVEQAKLDVL QRASVAYANW 360
TGARGREEAG LAQSESAHKT RDVYQNEYKL GKRSLNDLLT VEQDVFQAQS AEINANYDGW 420
VAAVNYAAAV NNLIPLAGIK QGLYNDLPDL K 451
<212> Type : PRT
<211> Length : 451
SequenceName : SEQ ID 73
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MAKFTPSFSG IKGRALPSLL FAAPMIHATD TATTKDGETI TVTADANTAT EATDGYQPLS 60
TSTATLTDMP MLDIPQVVNT VSDQVLENQN ATTLDEALYN VSNVVQTNTL GGTQDAFVRR 120
GFGANRDGSI MTNGLRTVLP RSFNAATERV EVLKGPASTL YGILDPGGLI NVVTKRPEKT 180
FHGSVSATSS SFGGGTGQLD ITGPIEGTQL AYRLTGEVQD EDYWRNFGKE RSTFIAPSLT 240
WFGDNATVTM LYSHRDYKTP FDRGTIFDLT TKQPVNVDRK IRFDEPFNIT DGQSDLAQLN 300
ASYHLNSQWT ARFDYSYSQD KYSDNQARVT AYDATTGTLT RRVDATQGST QRMHSTRADL 360
QGNVDIAGFY NEILGGVSYE YYDLLRTDMI RCKNAKDFNI YNPVYGNTSK CTTVSASDSD 420
QTIKQESYSA YAQDALYLTD NWIAVAGIRY QYYTQYAGKG RPFNVNTDSR DEQWTPKLGL 480
VYKLTPSVSL FANYSQTFMP QSSIASYIGD LPPESSNAYE VGAKFELFDG ITADIALFDI 540
HKRNVLYTES IGDETIAKTA GRVRSRGVEV DLAGALTENI NIIASYGYTD AKVLEDPDYA 600
GKPLPNVPRH TGSLFLTYDI HNMPGNNTLT FGGGGHCVSR RSATNGADYY LPGYFVADAF 660
AAYKMKLQYP VTLQLNVKNL FDKTYYTSSI ATNNLGNQIG DPREVQFTVK MEF 713

<212> Type : PRT
<211> Length : 713
SequenceName : SEQ ID 74
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MRTLQGWLLP VFMLPMAVYA QEATVKEVHD APAVRGSIIA NMLQEHDNPF TLYPYDTNYL 60
IYTQTSDLNK EAIASYDWAE NARKDEVKFQ LSLAFPLWRG ILGPNSVLGA SYTQKSWWQL 120
SNSEESSPFR ETNYEPQLFL GFATDYRFAG WTLRDVEMGY NHDSNGRSDP TSRSWNRLYT 180
RLMAENGNWL VEVKPWYVVG NTDDNPDITK YMGYYQLKIG YHLGDAVLSA KGQYNWNTGY 240
GGAELGLSYP ITKHVRLYTQ VYSGYGESLI DYNFNQTRVG VGVMLNDLF 289
<212> Type : PRT
<211> Length : 289
SequenceName : SEQ ID 75
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MAVQKNVIKG ILAGTFALML SGCVTVPDAI KGSSPTPQQD LVRVMSAPQL YVGQEARFGG 60
KVVAVQNQQG KTRLEIATVP LDSGARPTLG EPSRGRIYAD VNGFLDPVDF RGQLVTVVGP 120
ITGAVDGKIG NTPYKFMVMQ ATGYKRWHLT QQVIMPPQPI DPWFYGGRGW PYGHGGWGWY 180
NPGPARVQTV VTE 193
<212> Type : PRT
<211> Length : 193

SequenceName : SEQ ID 76
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MRKQWLGICI AAGMLAACTS DDGQQQTVSV PQPAVCNGPI VEISGADPRF EPLNATANQD 60
YQRDGKSYKI VQDPSRFIQA GLAAIYDAEP GSNLTASGEA FDPTQLTAAH PTLPIPSYAR 120
ITNLANGRMI VVRINDRGPY GNDRVISLSR AAADRLNTSN NTKVRIDPII VAQDGSLSGP 180
GMACTTVAKQ TYALPAPPDL SGGAGTSSVS GPQGDILPVS NSTLKSEDPT GAPVTSSGFL 240
GAPTTLAPGV LEGSEPTPAP QPVVTAPSTT PATSPAMVTP QAASQSASGN FMVQVGAVSD 300
QARAQQVQQQ LGQKFGVPGR VTQNGAVWRI QLGPFANKAE ASTLQQRLQT EAQLQSFITT 360
AQ 362
<212> Type : PRT
<211> Length : 362
SequenceName : SEQ ID 77
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MIKRVLVVSM VGLSLVGCVN NDTLSGDVYT ASEAKQVQNV SYGTIVNVRP VQIQGGDDSN 60
VIGAIGGAVL GGFLGNTVGG GTGRSLATAA GAVAGGVAGQ GVQSAMNKTQ GVELEIRKDD 120
GNTIMVVQKQ GNTRFSPGQR VVLASNGSQV TVSPR 155
<212> Type : PRT
<211> Length : 155
SequenceName : SEQ ID 78
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MSKATEQNDK LKRAIIISAV LHVILFAALI WSSFDENIEA SAGGGGGSSI DAVMVDSGAV 60
VEQYKRMQSQ ESSAKRSDEQ RKMKEQQAAE ELREKQAAEQ ERLKQLEKER LAAQEQKKQA 120
EEAAKQAELK QKQAEEAAAK AAADAKAKAE ADDKAAEEAA KKAAADAKKK AEAEAAKAAA 180
EAQKKAEAAA AALKKKAEAA EAAAAEARKK AAAEKAAADK KAAEKAAAEK AAADKKAAAE 240
KAAADKKAAA AKAAAEKAAA AKAAAEADDI FGELSSGKNA PKTGGGAKGN NASPAGSGNT 300
KNNGASGADI NNYAGQIKSA IESKFYDASS YAGKTCTLRI KLAPDGMLLD IKPEGGDPAL 360
CQAALAAAKL AKIPKPPSQA VYEVFKNAPL DFKP 394
<212> Type : PRT
<211> Length : 394
SequenceName : SEQ ID 79
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MMKFKKCLLP VAMLASFTLA GCQSNADDHA ADVYQTDQLN TKQETKTVNI ISILPAKVAV 60
DNSQNKRNAQ AFGALIGAVA GGVIGHNVGS GSNSGTTAGA VGGGAVGAAA GSMVNDKTLV 120
EGVSLTYKEG TKVYTSTQVG KECQFTTGLA VVITTTYNET RIQPNTKCPE KS 172

<212> Type : PRT
<211> Length : 172
SequenceName : SEQ ID 80
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MLLSIITVAF RNLEGIVKTH ASLAHLAQAE DISFEWIVVD GGSNDGTREY LENLNGIYNL 60
RFVSEPDNGI YDAMNKGIAM AQGKFALFLN SGDIFHQDAA YFVRKLKMQK DNVMITGDAL 120
LDFGDGHKIK RSAKPGWYIY HSLPASHQAI FFPVSGLKKW RYDLEYKVSS DYALAAKMYK 180

AGYAFKKLNG LVSEFSMGGV STTNNMELCA DAKKVQRQIL HVPGFWAELS WHLRQRTTSK 240
TKALYNKS 248
<212> Type : PRT
<211> Length : 248
SequenceName : SEQ ID 81
SequenceDescription :

Sequence

<213> OrganismName : Haemophilus influenzae Rd
<400> PreSequenceString :
MKLTTLQTLK KGFTLIELMI VIAIIAILAT IAIPSYQNYT KKAAVSELLQ ASAPYKADVE 60
LCVYSTNETT SCTGGKNGIA ADIKTAKGYV ASVITQSGGI TVKGNGTLAN MEYILQAKGN 120
AAAGVTWTTT CKGTDASLFP ANFCGSVTK 149
<212> Type : PRT
<211> Length : 149
SequenceName : SEQ ID 82
SequenceDescription :

Sequence

<213> OrganismName : Haemophilus influenzae Rd
<400> PreSequenceString :
MLNKKFKLNF IALTVAYALT PYTEAALVRD DVDYQIFRDF AENKGRFSVG ATNVEVRDKN 60
NHSLGNVLPN GIPMIDFSVV DVDKRIATLI NPQYVVGVKH VSNGVSELHF GNLNGNMNNG 120
NAKSHRDVSS EENRYFSVEK NEYPTKLNGK AVTTEDQTQK RREDYYMPRL DKFVTEVAPI 180
EASTASSDAG TYNDQNKYPA FVRLGSGSQF IYKKGDNYSL ILNNHEVGGN NLKLVGDAYT 240
YGIAGTPYKV NHENNGLIGF GNSKEEHSDP KGILSQDPLT NYAVLGDSGS PLFVYDREKG 300
KWLFLGSYDF WAGYNKKSWQ EWNIYKPEFA KTVLDKDTAG SLTGSNTQYN WNPTGKTSVI 360
SNGSESLNVD LFDSSQDTDS KKNNHGKSVT LRGSGTLTLN NNIDQGAGGL FFEGDYEVKG 420
TSDSTTWKGA GVSVADGKTV TWKVHNPKSD RLAKIGKGTL IVEGKGENKG SLKVGDGTVI 480
LKQQADANNK VKAFSQVGIV SGRSTVVLND DKQVDPNSIY FGPRGGRLDA NGNNLTFEHI 540
RNIDDGARLV NHNTSKTSTV TITGESLITD PNTITPYNID APDEDNPYAF RRIKDGGQLY 600
LNLENYTYYA LRKGASTRSE LPKNSGESNE NWLYMGKTSD EAKRNVMNHI NNERMNGFNG 660
YFGEEEGKNN GNLNVTFKGK SEQNRFLLTG GTNLNGDLKV EKGTLFLSGR PTPHARDIAG 720
ISSTKKDQHF AENNEVVVED DWINRNFKAT NINVTNNATL YSGRNVANIT SNITASDNAK 780
VHIGYKAGDT VCVRSDYTGY VTCTTDKLSD KALNSFNATN VSGNVNLSGN ANFVLGKANL 840
FGTISGTGNS QVRLTENSHW HLTGDSNVNQ LNLDKGHIHL NAQNDANKVT TYNTLTVNSL 900
SGNGSFYYLT DLSNKQGDKV VVTKSATGNF TLQVADKTGE PTKNELTLFD ASNATRNNLN 960
VSLVGNTVDL GAWKYKLRNV NGRYDLYNPE VEKRNQTVDT TNITTPNNIQ ADVPSVPSNN 1020
EEIARVETPV PPPAPATPSE TTETVAENSK QESKTVEKNE QDATETTAQN GEVAEEAKPS 1080
VKANTQTNEV AQSGSETEET QTTEIKETAK VEKEEKAKVE KDEIQEAPQM ASETSPKQAK 1140
PAPKEVSTDT KVEETQVQAQ PQTQSTTVAA AEATSPNSKP AEETQPSEKT NAEPVTPVVS 1200
KNQTENTTDQ PTEREKTAKV ETEKTQEPPQ VASQASPKQE QSETVQPQAV LESENVPTVN 1260
NAEEVQAQLQ TQTSATVSTK QPAPENSINT GSATAITETA EKSDKPQTET AASTEDASQH 1320
KANTVADNSV ANNSESSDPK SRRRRSISQP QETSAEETTA ASTDETTIAD NSKRSKPNRR 1380
SRRSVRSEPT VTNGSDRSTV ALRDLTSTNT NAVISDAMAK AQFVALNVGK AVSQHISQLE 1440
MNNEGQYNVW VSNTSMNENY SSSQYRRPSS KSTQTQLGWD QTISNNVQLG GVFTYVRNSN 1500
NFDKASSKNT LAQVNFYSKY YADNHWYLGI DLGYGKFQSN LKTNHNAKFA RHTAQFGLTA 1560
GKAFNLGNFG ITPIVGVRYS YLSNANFALA KDRIKVNPIS VKTAFAQVDL SYTYHLGEFS 1620
VTPILSARYD TNQGSGKINV NQYDFAYNVE NQQQYNAGLK LKYHNVKLSL IGGLTKAKQA 1680
EKQKTAELKL SFSF 1694
<212> Type : PRT
<211> Length : 1694
SequenceName : SEQ ID 83
SequenceDescription :

Sequence

<213> OrganismName : Haemophilus influenzae Rd
<400> PreSequenceString :
MALVNKIKTL SSVGILAATL FLAGCQAQSN ILAFTPPAPS ASMNVNRTAV VSVTTKDSRA 60
IQEIASYTKH GELIKLNASP SVTQLFQQVM QQNLISKGFR VGQLNGSNAW VTVDVREFGT 120
QVEQGNLRYK LNTKIQATVY VQGAKGSYNK SFNVTHSQEG VFNAGNDEIH KVLSQTFNDI 180
VNNIYQDQEV AAAINQYSN 199
<212> Type : PRT
<211> Length : 199

SequenceName : SEQ ID 84
SequenceDescription :

Sequence

<213> OrganismName : Haemophilus influenzae Rd
<400> PreSequenceString :
MLCWIGYKNG ILPQQNSTLY PWLNPSKCGV IFDGFQLVGD DFNSDQTAEN TSPAWQVLYT 60
THLQSCSPIH SGENFAPIPL YKQLKNQPHL SQDLIKWQEN WQACDQLQMN GAVLEQQSLA 120
EISDHQSTLS KHGRYLAQEI EKETGIPTYY YLYRVGGQSL ESEKSRCCPS CGANWALKDA 180
IFDTFHFKCD TCRLVSNLSW NFL 203
<212> Type : PRT
<211> Length : 203
SequenceName : SEQ ID 85
SequenceDescription :

Sequence

<213> OrganismName : Haemophilus influenzae Rd
<400> PreSequenceString :
MGAFAFASVT NANIYAEGDI GLSQTKANGS NNTRVGPRVS VGYKVGNTRV AGDYTHHGKV 60
DGTKIQGLGA SVLYDFDTNS KVQPYVGARV ATNQFKYTNR AEQKFKSSSD IKLGYGVVAG 120
AKYKLDGNWY ANGGVEYNRL GNFDSTKVNN YGAKVGVGYG F 161
<212> Type : PRT
<211> Length : 161
SequenceName : SEQ ID 86
SequenceDescription :

Sequence

<213> OrganismName : Haemophilus influenzae Rd
<400> PreSequenceString :
MKKLLIASLL FGTTTTVFAA PFVAKDIRVD GVQGDLEQQI RASLPVRAGQ RVTDNDVANI 60
VRSLFVSGRF DDVKAHQEGD VLVVSVVAKS IISDVKIKGN SIIPTEALKQ NLDANGFKVG 120
DVLIREKLNE FAKSVKEHYA SVGRYNATVE PIVNTLPNNR AEILIQINED DKAKLASLTF 180
KGNESVSSST LQEQMELQPD SWWKLWGNKF EGAQFEKDLQ SIRDYYLNNG YAKAQITKTD 240
VQLNDEKTKV NVTIDVNEGL QYDLRSARII GNLGGMSAEL EPLLSALHLN DTFRRSDIAD 300
VENAIKAKLG ERGYGSATVN SVPDFDDANK TLAITLVVDA GRRLTVRQLR FEGNTVSADS 360
TLRQEMRQQE GTWYNSQLVE LGKIRLDRTG FFETVENRID PINGSNDEVD VVYKVKERNT 420
GSINFGIGYG TESGISYQAS VKQDNFLGTG AAVSIAGTKN DYGTSVNLGY TEPYFTKDGV 480
SLGGNVFFEN YDNSKSDTSS NYKRTTYGSN VTLGFPVNEN NSYYVGLGHT YNKISNFALE 540
YNRNLYIQSM KFKGNGIKTN DFDFSFGWNY NSLNRGYFPT KGVKASLGGR VTIPGSDNKY 600
YKLSADVQGF YPLDRDHLWV VSAKASAGYA NGFGNKRLPF YQTYTAGGIG SLRGFAYGSI 660
GPNAIYAEHG NGNGTFKKIS SDVIGGNAIT TASAELIVPT PFVSDKSQNT VRTSLFVDAA 720
SVWNTKWKSD KSGLDNNVLK SLPDYGKSSR IRASTGVGFQ WQSPIGPLVF SYAKPIKKYE 780
NDDVEQFQFS IGGSF 795
<212> Type : PRT
<211> Length : 795
SequenceName : SEQ ID 87
SequenceDescription :

Sequence

<213> OrganismName : Haemophilus influenzae Rd
<400> PreSequenceString :
MLKKTSLIFT ALLMTGCVQN ANVTTPQAQK MQVEKVDKAL QKGEADRYLC QDDRVVRVVH 60
ATHKKYKKNL HYVTVTFQGV SEKLTLMISE RGKNYANIRW MWQERDDFST LKTNLGEILA 120
TQCVSQTSER LSGQ 134
<212> Type : PRT
<211> Length : 134
SequenceName : SEQ ID 88
SequenceDescription :

Sequence

<213> OrganismName : Haemophilus influenzae Rd
<400> PreSequenceString :

MRIIIIFFMG LNMTNFRLER ACLFRYAWAN GRCCLCSSTN QPTNQPTNQP TNQPTNQPTN 60
QPTNQNSNVS EQLEQINVSG STENSDTKTP PKIAETVKTA KTLEREQANN IKDIVKYETG 120
VTVVEAGRFG QSGFAIRGVD ENRVAINIDG LRQAETLSSQ GFKELFEGYG NFNNTRNGAE 180
IETLKEVNIT KGADSIKNGS GSLGGSVIYK TKDARDYLIN KDYYVSYKKG YATENNQSFD 240
TLTLAGRYKK FDVLVVTTSR NGHELENYGY KNYNDKIQGK KREKADPYKI EQDSTLLKLS 300
FNPTENHRFT FAADLYEHRS RGQDLSYTLK YQRSGNETPE VDSRHTNDKT KRRNISFSYE 360
NFSQTPFWDT LKLTYSDQRI KTRARTDEYC DAGVRHCEGT DNPTGLKVTN GKITRRDGSD 420
LQFEEKNNTA KSSDKTYDFK KFIDTDKRVI DDKLVLNNPS DTWYDCSIFN CENNAKIKVF 480
KGNNYYGYDG KWKEVDLEIK ELNGKKFAKI KDNDRKIKSI LPSSPGYLER LWQERDLDTN 540
TQQLNLDLTK DFKIWHIEHN LQYGGSYNTA MKRMVNRAGN DASDVQWWAT PTLGEDSWTG 600
KPHTCATTYE WNANLCPRVD PEFSYLLPIK TTGKSVYLFD NFVITDYLSF DLGYRYDNIH 660
YQPKYKHGIT PKLPDDIVKG LFIPLPNNSN SDPNKVKENV QQNIDYIAKQ NKKYKAHSYS 720
FVSTIDPTSF LRLQLKYSKG FRTPTSDEMY FTFKHPDFTI LPNTDLKPEI AKTKEIAFTL 780
HNDDWGFIST SLFKTNYKNF IDLIFKKQET FKVGGSGRGE TLPFSLYQNI NRDNASLKGI 840
EINSKVFLGK MAKFMDGFNL SYKYTYQKGR MNGNIPMNAI QPRTMVYGLG YDHPNHKFGF 900
DFYTTHVASK NPEDTYNMFY KEENKKDSTI KWRSKSYTIL DLIGYVQPIK NLTIRAGVYN 960
LTNRKYITWD SARSIRSFGT SNVIDQSTGL GINRFYAPGR NYKMSVQFEF 1010

<212> Type : PRT
<211> Length : 1010
SequenceName : SEQ ID 89
SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :
MTYRNGKIDL KERFSKNRSF KGIKKKIAKK YTIKNSLSII YSLKTHSNSS LSINKKIFLG 60
LGFVSALSAQ SEDYNSSVYW LNSVNENNNN KSYYISPLRT WAGGNRSFTQ NYNNSQLYIG 120
TKNASATPNH SSVWFGEKGY IGFITGVFKA RDIFITGAVG SGNELKTGGG AILVFESSNE 180
LTTNGAYFQN NRAGTQTSWI NLISNNSVNL TNTDFGNQTP NGGFNVMGRK ITYNGGSVNG 240
GNFGFDNVDS NGATTISGVT FNNNGALTYK GGNGIGGSIT FTNSNINHYK LNLNANSVTF 300
NNSTLGSMPN GNANTIGNAY ILNANNITFN NLTFNGGWFV FNRSDAHVNF QGTTTINNPT 360
SPFVNMTGKV TINPNAIFNI QNYTPTIGNA YTLFSMKNGN IAYDDVNNLW NIIRLKNTQA 420
TKDNSKNATS NNNTHTYYVT YNLGGTLYHF RQIFSPDSIV LQSVYYGANN LYYTNSVNIH 480
DNVFNLKNIN DDRADTIFYL NGLNTWNYTQ ARFAQTYGGK NSALVFNATT PWANGAIPKS 540
NSTVRFGGYE GVNWGKTGYI TGTFTADRVY ITGNMMSGNG AQTGGGATLN FVGATEINIA 600
GATFKNLKTT SQNSYMTFMA LGNGSGSGKI NVSQSDFYDW TDGGYDFTGN GVFDSVNFNK 660
AYYKFQGAEN SYNFKNTNFL AGNFKFQGKT TIEKSVLNDA SYAFDGVNNA FNEDKFNGGS 720
FNFNHAEQTN AFNNNSFSGG SFSFNAKQVD FNGNSFNGGV FNFNNTPKAS FTNDTFNVNN 780
QFKINGAQTD FTFSKGVVFN MQGLLSSLSV GTTYQLLNAK SVGYKDNNNA LYQMLRWTSG 840
ENPSGKLVDE NKTAPNSAKI YNVQFTDNGL TYYIKENFNN GITLTRLCTL GYTHCVNIDN 900
DAFNLKNVNN NASNTVFYLN GMTTWKTAGT GVFTQDYSGT NSVLVFNQTT PFLAGANPTS 960
NSVVGFGKTS GAEWGLVGYI QGVFKANQID ITGTIRSGNG AKTGGGATLV FNAQERLNIA 1020
NANLNNDKAG LQNSWMNFIV NNGNLNVTNA NFSNQTPHGG FNLKANNITW DKGSVSGGGN 1080
FGVDNANANG NAVIKNVNFS DNGTLIYKGG ENSAGNSLTL ENNTFNSYNI NAKAQNLIFN 1140
NNSFNSGSYS FNDTKNVTFK GTNTLINSDP FSRLKGSVSI DNNSIFNIER DLTDKTTYTL 1200
LSGDNIKYNN QALADNVFSK NLWDLIHYDG EQGTLLRTDN NTYFVQFTQS NGQKFVFEET 1260
FNPGSITYKY FTIHSSPFHT EADSKDIWNQ VRKQFDFIPG KTPVCVGVCY IAPYKNQDLI 1320
GSSAFAWSLN FGATVVGTLL LGSAQEKANN NGGSIWFGKN NLLYLHGNFN ATNIFLTNNF 1380
NVGNPNAGGG ATINFNADET LSADGLNYTN FQTVAMGLQT SASQHSWANF NSKLSMEIKN 1440
SNFRDFTWGG FRFNSGRITF ENTTFSGWTN INGATESGSS YVNMVANTDL IFTDSILGGG 1500
IRYDLKANNI IFNNTQMVVD VSKNVNQSSL NGNVTFNHSR LSVKPNAAIN IGGDQTQTTL 1560
ENASSLSFYN DSVANFNGTT AFNGVSYLNL NPNAQVSFNQ ANFNNANVTF YGIPLFGKTP 1620
NFGNSVRLIN FKGDAKFNQA TLNLRAKNIH LNFQGASTFE NNSTMNLAES SQASFNALSV 1680
EGETNFNLNG SSLLSFNGNS VFNAPVNFYA NNSQISFTHS ATFNADASFD LGNNSTLNFQ 1740
SVLLNSALNL LGNGGNNLAI NAKGNFSFGS QGILNLSYMN LFGGDKKASV YDVLQAQNID 1800
GLRGNNGYEK IRFYGIQIEK ADYSFNNGVH SWSFTNPLNT TETITETLHN NRLKVQISQN 1860
GASNNAMFNL APSLYDYQQN PYDESENSYN HTSDKAGTYY LSSSIKGFGK NNEIPGTYNA 1920
QNQPLQALHI YNQAISKQDL NMIASLGKEF LPKVAKLIAS GALDNLNLNS PDSFETIFSI 1980
LKEYGITLNQ ANWKSLLKII NNFSNTANYH FSQGSLVVGA IKEGQTNTNS VVWFGGDGYK 2040
NPCAVGDNTC QMFRQTNLGQ LLNSSVPYLG YINANFKAKN IYITGTIGSG NAWGSGGSAN 2100
VSFESATNLV LNQANIDAQG TDKIFSYLGK EGIDKLFGEK GLGNVLSNIV YEESLNDNAI 2160
PKDLANMIPK DLGSKTLSSL LSPTEVNNLL GVSAFKNAIM EILNSKTVGD VFGENGLLNA 2220
LDPVKRKEID QMLLEQIQAH SSGFEKFIVK TLGIENVENF INNWYGKQSL SSFANNFVPG 2280
GLNQALDKIG SSSDAKDLQS FLDKTTFGDI LNQMINQAPL INKLISWLGP QDLSVLVNIA 2340
LNSITNPSKE LLGAISGMGQ KVLNDLLGEG VVNKIMSNQV LGQMINKIIA DKGFGGVYHQ 2400
GLGSILPKSL QDELKKLGMG SLLKPKGLHN LWQKGNFNFV AKNHVFVNNS LFSNATGGEL 2460

NFVAGKSIIF NGKNTINFTQ YQGRLSFVSK DFSNISLDTL NATNGLTLNA SKNDISVQKG 2520
QICVNVLDCM TAKGKTTQTN SSSSATAPTN ETLEVSANNF APLGTIKANG LVDFSKVLQN 2580
TTIGTLDLGP NATFKANNLI VNNAFNNNSN YRANISGNFN VAKGATFSTN ENGLNVGGNF 2640
NSEGPLIFNL NNPTHQTIIN VTGTSTIMSY NNQALINFNT QLKQGAYTLI NANRMVYGYD 2700
NQTILGGSLS DYLKLYTLID FNGKRMQLNG DSLSYDNQPV SIKDGGLVVS FKDNQGQMVY 2760
SSILYDKIQV TVSDKPMSIQ APSLEYYVKR IQGSAGLNAI KSAGNNSIMW LSELFAAKGG 2820
NPLFAPYYLQ DNPTEHIVTL MKDITSALGM LSNSNLKNNS TDVLQLNTYT QQMSRLAKLS 2880
NFASFDSTDF SERLSSLKNQ RFADAVPNAM DVILKYSQRD KLKNNLWATG VGGVSFVENG 2940
TGTLYGVNVG YDRFVRGVIV GGYAAYGYSG FYERITSSKS DNVDVGLYAR AFIKKSELTF 3000
SVNETWGANK TQISSNDALL SMINQSYKYS TWTTNAKVNY GYDFMFKNKS IILKPQIGLR 3060
YYYIGMSGLE GVMNNVLYNQ FKANADPSKK SVLTIDFALE NRHYFNTNSY FYAIGGVGRD 3120
LLVNSMGDKL VRFIGNNTLS YRKGDLYNTF ANITTGGEVR LFKSFYANAG VGARFGLDYK 3180
MIDIIGNIGM RLAF 3194

<212> Type : PRT

<211> Length : 3194

SequenceName : SEQ ID 90

SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori J99

<400> PreSequenceString :

MKQFKKKPKK IKRSHQNQKT ILKRPLWLMP LLIGGFASGV YADGTDILGL SWGEKSQKVC 60
VHRPWYAIWS CDKWEEKTQQ FTGNQLITKT WAGGNAANYY HSQNNQDITA NLKNDNGTYF 120
LSGLYNYTGG EYNGGNLDIE LGSNATFNLG ASSGNSFTSW YPNGHTDVTF SAGTINVNNS 180
VEVGNRVGSG AGTHTGTATL NLNANKVTIN SNISAYKTSQ VNVGNANSVI TINSVSLNGD 240
TCSSLARVGV GANCSTSGPS YSFKGTTNAT NTTFSNSSGS FTFEENATFS GAKLNGGAFT 300
FNKKFNATNN TAFNSGSFTF KGTSSFNGAN FSNASYTFNN QATFQNSSFN GGTFTFNDQT 360
NQSTQHPQIQ NSSFSGSATT LKGFATFEQA FNNSNHQLTI QNASFNNATF NNTGKITIEK 420
DASFNNTSFN TPVDTNNMTI SGGVTLSGKN DLKNGATLDF GSSKITLTQG TTFNLTSLGS 480
EKSVTILNSR GGITYNHLLN HAINSLTNAL KTNESSSKPQ SFAQGLWDMI TYNGVTGQLL 540
NENAATSKPT DSSPSKSSTN STQVYQVGYK IGDTIYKLQE TFSHNSIIIQ ALESGTYTPP 600
PVINGSKFDL SASNYINADM PWYNHKYYIP KSQNFTESGT YYLPSVQIWG SYTNSFKQTF 660
SASNSNLVIG YNATWTDHNV SSSDTVAFGD TSGSALNGHC GPWPYYQCTG TTNGTYSAYH 720
VYITANLRSG NRIGTGGAAN LIFNGVDSIN IANATITQHN AGAYSSSMTF STQNMDNSQN 780
LNGLNSNGKL LVYGTTFTNQ AKDGKFIFNA GQATFENTNF NGGSYQFSGD SLNFSNNNQF 840
NSGSFEIGAK NTIFNNANFN NSTSFNFNNS SATTSFVGDF TNANSNLQIA GNAVFGNSTN 900
GSQNTANFNN TGSVNIAGNA TFDNVVFNSP TNTSVKGKVT LNNITLKNLN APLSFGDGTI 960
VFSAHSVINI GEAITNGNPI TLVSSSKAIE YNDAFSKNLW QLINYQGHGA SSEKLVSSAG 1020
NGVYDVVYSF NNQTYNFQEV FSPNSISIRR LGVGMVFDYV DMEKSDRLYY QNALGFMTYM 1080
PNSYNNNLGN LNNTIYYYDN SIDFYASGKT LFTKAEFSQT FTGQNSAIVF GAKNIWTSVS 1140
DAPQSNVIIR FGDNKGAGSN DASGHCWNLQ CIGFITGHYE AQKIYITGSI ESGNRISSGG 1200
GASLNFNGLQ GILLTNATLY NRAAGTQSSS MNFVSNSANI QAQNSYFIDD TAQNKGNPNF 1260
SFNALNLDFS NSSFRGYVGQ TQSVFKFNAV NAISFTNSSN LSSGLYQMQA KSVLFDNSNL 1320
SVSVGTSSIK ANAINLSQNA SINASNHSTL ELQGDLNLND TSSLNLNQSA INVSNNATIN 1380
DYASLIASNG SHLNFNGAVN FNSANITTSL SSSSIVFKGA VSLRGQFNLS NNSSLDFQGS 1440
SAITSNTAFN FYDNAFSQSP ITTFHQALDIK VPLSLGGNLL NPNNSSVLNL KNSQLVFSDQ 1500
GSLNIANIDL LSDLNGNKNR VYNIIQADMN GNWYERINFF GMRINDGIYD AKNQTYSFTN 1560
PLNNALKITE SFKNNQLSVT LSQIPGIKNT LYNIGSEIFN YQKVYNNANG VYSYSDDAQG 1620
VFYLTSSVKG YYNPNQSYQA SGSNNTTKNN NLTSESSVIS QTYNAQGNPI SALHVYNKGY 1680
NFSNIKALGQ MALKLYPEIK KILGNDFSLS SLSNLKGDAL NQLTKLITPS DWKNINELID 1740
NANNSVVQNF NNGTLIIGAT KIGQTDTNSA VVFGGLGYQK PCDYTDIVCQ KFRGTYLGQL 1800
LESISADLGY IDTTFNAKEI YLTGTLGSGN AWGTGGSASV TFNSQTSLIL NQANIVSSQT 1860
DGIFSMLGQE GINKVFNQAG LANILGEVAM QSINKAGGLG NLIVNTLGSD SVIGGYLTPE 1920
QKNQTLSQLL GQNNFDNLMN DSGLNTAIKD LIRQKLGFWT GLVGGLAGLG GIDLQNPEKL 1980
IGSMSINDLL SKKGLFNQIT GFISANDIGQ VISVMLQDIV KPSDALKNDV AALGKQMIGE 2040
FLGQDTLNSL ESLLQNQQIK SVLDKVLAAK GLGSIYEQGL GDLIPNLGKK GIFAPYGLSQ 2100
VWQKGDFSFN AQGNVFVQNS TFSNANGGTL SFNAGNSLIF AGNNHIAFTN HSGTLNLLSN 2160
QVSNINVTML NASNGLKINA TNNNVSVSQG NLFINASCVQ QSDPTTASAT NPCTTAQNNA 2220
SSSNASNNAP IALNNNDESL VVTANGFNFS GNIYANGVVD FSKIKGSANV KNLYLYNNAQ 2280
FQANNLTISN QAVLEKNASF VTNNLNIQGA FNNNATQKIE VLQNLVIASN ASLSTGIYGL 2340
EVGGALNNLG AIHFNLENSQ TPVNPLIQVG GIINLNTTQT PFMNVSVANG GTYTLLKSSR 2400
YIDYNINPNS LQSYLKLYTL ININGNHIEE KNGVLTYLGQ RVLLQDKGLL LSVALPNSNN 2460
ASQNNILSLS VLHNQIKMSY GNKVMDFTPP TLQDYIVGIQ GQSALNQIEA VGGNNAIKWL 2520
STLMMETKEN PLFAPIYLEN HSLNEILGVT KDLQNTASLI SNPNFRNNAT SLLEMASYTQ 2580
QTSRLTKLSD FRAREGESNF SERLLELKNK RFSDPNPSEV FVKYSQLSKH PNNLWIQGVG 2640
GASFISGGNG TLYGLNVGYD RLVKSVILGG YVAYGYSGFN GNIMHSLANN VDVGMYARAF 2700

LKRNEFTLSA NETYGGNASH INSSNSLLSV LNQRYNYNTW TTSVNGNYGY DFMFKQKSVV 2760
LKPQVGLSYH FIGLSGMKGK MQNPAYQQFV MHSNPSNESV LTLNMGLESR KYFGKNSYYF 2820
VTARLGRDLL IKAKGDNVVR FVGENTLLYR KGEIFNTFAS VITGGEMHLW RLMYVNAGVG 2880
LKMGLQYQDL NITGNVGMRV AF 2902

<212> Type : PRT
<211> Length : 2902
SequenceName : SEQ ID 91
SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :
MAFKKARLIS RFISKGSFKL NKISKKFFTL NQILKREKPL KRHKKTKSIE KPFNKNKSFL 60
KASVLLIGAL GGLSHLRANE CRYWSWSSWS YQDNIESGPN SPTHNSYCLF SSAQGSGTYY 120
LNTLTTYSAG GASFTQKFNG GTLDIGGNIR FGGTGINGGD VGYITGTYNA QTMNFNSSHI 180
TTGNSYADGG GTTLNFNATN NITINQASFD NSDAGTQKSY MNFKGSNIKI SGSSFTDDTN 240
GGFNFSGNNN NSTISFNQTS FNQGTYNFSN SATLSFNNSN FNQGTYHFNS AQSTFENSNF 300
NQGTYNFNDN TSFNNDTFNQ GTYNFNSSKV SFSGANTLNS SSPFASLKGS VSFNSGAIFN 360
LNQTLNNNQT YDILTTNGAI QYGVYQSYLW DLINYKGDKA ISHVEVSNNT YDVTFDINGQ 420
DETLQETFSN QSIITQFLGD DLQQQAQQTY QEDVANSQNA LNKVASDNTI ANNDTSYTQS 480
SNPTILKDAQ GLENTNQQIQ QDEKALEKDL AQIKQLANST TGFNEQAFTQ AQKQEQQDEQ 540
ALQNDENAFN TEQEGLEQAI ANAKHANPTP NPTPSPTPTP IKHTAPNTPP SQVPPTPPSQ 600
NLPKTNVWNG VYWLQNKTYS NKGIYYIDPN LSGQSGQSGN TLSTYTANLL GRSFGVNANN 660
GTLIIGNNTE SVNDNGLIWI GHGGFGYITG TFSAANIYLT NNFKTGEGVS NSDGGGANIT 720
FKASDNITMD GLNYNNAETV TKMIQTGASQ HSYTTFDATN NISVTDSDFS DMTWGKFSFS 780
AKNISFSNAS FSGFTNPGGS STISTNASNS LSFTDSRLNG GAIYNLQANS LIFNNTQAVF 840
NVLYSRGTSN FNATTQLLGN TSFTLSSQSL LNFNGDTTLQ NNANITLGNK SQAAFKNSLT 900
LDNNSNLSLD NQSVLNANGT SAFNNQASLN IYNGSQAAFS SLFFNGGTLS LNANSKLNAS 960
SASFSNNTTI NLDDSVLNAN NTSSLNNANN FQGASQADFG GNTTIDTASF NFDSASSLNF 1020
NNLTANGALN FNGYAPSLTK ALMNVSGQFV LGNNGDINLS DINIFDNITK SVTYNILNAQ 1080
KGITGISGAN GYEKILFYGM KIQNATYSDN NNIQTWSFIN PLNSSQIIQE SIKNGDLTIE 1140
VLNNPNSASN TIFNIAPELY NYQDSKQNPT GYSYDYSDNQ AGTYYLTSNI KGLFTPKGSQ 1200
TPQTPGTYSP FNQPLNSLNI YNKGFSSENL KTLLGILSQN SATLKEMIES NQLDNITNIN 1260
EVLQLLDKIK ITQAQKQALL ETINHLTDNI NQTFNNGNLV IGATQDNVTN STSSIWFGGN 1320
GYSSPCALDS ATCSSFRNTY LGQLLGSTSP YLGYINADFK AKSIYITGTI GSSNAFESGG 1380
SADVTFQSAN NLVLNKANIE AQATDNIFNL LGQEGIDKIF NQGNLANVLS QMAMEKIKQA 1440
GGLGNFIENA LSPLSKELPA SLQDETLGQL IGQNNLDDLL NNSGVMNEIQ NIISQKLSIF 1500
GNFVTPSIIE NYLAKQSLKS MLDDKGLLNF IGGYIDASEL SSILGVILKD ITNPPTSLQK 1560
DIGVVANDLL NEFLGQDVVK KLESQGLVSN IINNVISQGG LSGVYNQGLG SVLPPSLQNA 1620
LKENDLGTLL SPRGLHDFWQ KGYFNFLSNG YVFVNNSSFS NATGGSLNFV ANKSIIFNGD 1680
NTIDFSKYQG ALIFASNGVS NINITTLNAT NGLSLNAGLN NVSVQKGEIC INLANCPTTK 1740
NSSPANSSVT PTNESLSVHA NNFTFLGTII SNGAIDLSQV TNNSVIGTLN LNENATLQAN 1800
NLTITNAFNN ASNSTANIDG NFTLNQQATL STNASGLNVM GNFNSYGDLV FNLSHSVSHA 1860
IINTQGTATI MANNNPLIQF NASSKEVGTY TLIDSAKAIY YGYNNQITGG SSLDNYLKLY 1920
ALIDINGKHM VMTDNGLTYN GQAVSVKDGG LVVGFKDSQN QYIYTSILYN KVKIAVSNDP 1980
INNPQAPTLK QYIAQIQGVQ SVDSIDQAGG NQAINWLNKI PETKGSPLFA PYYLESHSTK 2040
DLTTIAGDIA NTLEVIANPN FKNDATNILQ INTYTQQMSR LAKLSDTSTF ARSDFLERLE 2100
ALKNKRFADA IPNAMDVILK YSQRNRVKNN VWATGVGGAS FISGGTGTLY GINVGYDRFI 2160
KGVIVGGYAA YGYSGFHANI TQSGSSNVNV GVYSRAFIKR SELTMSLNET WGYNKTFINS 2220
YDPLLSIINQ SYRYDTWTTD AKINYGYDFM FKDKSVIFKP QVGLSYYYIG LSGLRGIMDD 2280
PIYNQFRANA DPNKKSVLTI NFALESRHYF NKNSYYFVIA DVGRDLFINS MGDKMVRFIG 2340
NNTLSYRDGG RYNTFASIIT GGEIRLFKTF YVNAGIGARF GLDYKDINIT GNIGMRYAF 2399

<212> Type : PRT
<211> Length : 2399
SequenceName : SEQ ID 92
SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :
MEIQQTHRKI NRPLVSLVLA GALISAIPQE SHAAFFTTVI IPAIVGGIAT GTAVGTVSGL 60
LSWGLKQAEE ANKTPDKPDK VWRIQAGKGF NEFPNKEYDL YKSLLSSKID GGWDWGNAAR 120
HYWVKGGQWN KLEVDMKDAV GTYKLSGLRN FTGGDLDVNM QKATLRLGQF NGNSFTSYKD 180
SADRTTRVNF NAKNISIDNF VEINNRVGSG AGRKASSTVL TLQASEGITS SKNAEISLYD 240

GATLNLASNS VKLNGNVWMG RLQYVGAYLA PSYSTINTSK VQGEVDFNHL TVGDQNAAQA 300
GIIASNKTHI GTLDLWQSAG LNIIAPPEGG YKDKPNSTTS QSGTKNDKKE ISQNNNSNTE 360
VINPPNNTQK TETEPTQVID GPFAGGKDTV VNIFHLNTKA DGTIKVGGFK ASLTTNAAHL 420
NIGKGGVNLS NQASGRTLLV ENLTGNITVD GPLRVNNQVG GYALAGSSAN FEFKAGVDTK 480
NGTATPNNDI SLGRFVNLKV DAHTANFKGI DTGNGGFNTL DFSGVTDKVN INKLITASTN 540
VAVKNFNINE LIVKTNGISV GEYTHFSEDI GSQSRINTVR LETGTRSIFS GGVKFKSGEK 600
LVINDFYYSP WNYFDARNVK NVEITRKFAS STPENPWGTS KLMFNNLTLG QNAVMDYSQF 660
SNLTIQGDFI NNQGTINYLV RGGKVATLNV GNAAAMMFNN DIDSATGFYK PLIKINSAQD 720
LIKNTEHVLL KAKIIGYGNV STGTNGISNV NLEEQFKERL ALYNNNNRMD TCVVRNTDDI 780
KACGMAIGNQ SMVNNPDNYK YLIGKAWRNI GISKTANGSK ISVYYLGNST PTENGGNTTN 840
LPTNTINNAH SANYALVKNA PFAHSATPNL VAINQHDFGT IESVFELANR SKDIDTLYTH 900
SGAQGRDLLQ TLLIDSHDAG YARQMIDNTS TGEITKQLNA ATDALNNVAS LEHKQSGLQT 960
LSLSNAMILN SRLVNLSRKH TNHINSFAQR LQALKGQEFA SLESAAEVLY QFAPKYEKPT 1020
NVWANAIGGA SLNSGSNASL YGTSAGVDAF LNGNVEAIVG GFGSYGYSSF SNQANSLNSG 1080
ANNANFGVYS RFFANQHEFD FEAQGALGSD QSSLNFKSTL LQDLNQSYNY LAYSATARAS 1140
YGYDFAFFRN ALVLKPSVGV SYNHLGSTNF KSNSQSQVAL KNGASSQHLF NANANVEARY 1200
YYGDTSYFYL HAGVLQEFAH FGSNDVASLN TFKINAARSP LSTYARAMMG GELQLAKEVF 1260
LNLGVVYLHN LISNASHFAS NLGMRYSF 1288

<212> Type : PRT
<211> Length : 1288
SequenceName : SEQ ID 93
SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :
MKKHILSLTL GSLLVSTLSA EDDGFYTSVG YQIGEAAQMV TNTKGIQDLS DRYESLNNLL 60
NRYSTLNTLI KLSADPSAIN AVRENLGASA KNLIGDKANS PAYQAVLLAI NAAVGFWNVV 120
GYVTQCGGNA NGQKSISSKT IFNNEPGYRS TSITCSLNGH SPGYYGPMSI ENFKKLNEAY 180
QILQTALKRG LPALKENNGK VNVTYTYTCS GDGNNNCSSQ VTGVNNQKDG TKTKIQTIDG 240
KSVTTTISSK VVDSRADGNT TGVSYTEITN KLEGVPDSAQ ALLAQASTLI NTINNACPYF 300
HASNSSEANA PKFSTTTGKI CGAFSEEISA IQKMITDAQE LVNQTSVINE HEQTTPVGNN 360
NGKPFNPFTD ASFAQGMLAN ASAQAKMLNL AEQVGQAINP ERLSGTFQNF VKGFLATCNN 420
PSTAGTGGTQ GSAPGTVTTQ TFASGCAYVG QTITNLKNSI AHFGTQEQQI QQAENIADTL 480
VNFKSRYSEL GNTYNSITTA LSNIPNAQSL QNAVSKKNNP YSPQGIDTNY YLNQNSYNQI 540
QTINQKLGRN PFRKVGIVSS QTNNGAMNGI GIQVGYKQFF GQKRKWGARY YGFFDYNHAF 600
IKSSFFNSAS DVWTYGFGAD ALYNFINDKA TNFLGKNNKL SVGLFGGIAL AGTSWLNSEY 660
VNLATMNNVY NAKMNVANFQ FLFNMGVRMN LARPKKKDSD HAAQHGIELG LKIPTINTNY 720
YSFMGAELKY RRLYSVYLNY VFAY 744

<212> Type : PRT
<211> Length : 744
SequenceName : SEQ ID 94
SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :
MIKKAKKFIP FFLIGSLLAE DNGWYMSVGY QIGGTQQFIN NKQLLENQNI INSITQSAIN 60
IAGPTTGLIT LSSQTVIDAL GYGVSNTVGN QLEGISNILN QIGKRKDFYS SRQISSISQQ 120
IIGLKGSSDP LKAHSSQITA KLLSNTQSAF DQGIALSSNI ISAVNSLNPS NNSQEVKAQL 180
QNTAQSMAEL LQQIEHSITK TTSTTYAQSL LSNLTDAVNA SSNNTTYVSA LVNALNTLGV 240
GVFPTTTSTH VVLNPPGQVV FYPTNSLLGS TSSNSNNQQQ YNNTLLMNTL QGELSTNNQN 300
NPNGCANQIQ CLEQFIQNLT PLAATPTSTN QANQQVQAIA QKLQSVAINA LDNNAINNTT 360
YNLNNLHNAL NFQAYQSTIE QYNNALKQIS WISFSEPKNL LKNTSNNYQI GTVTNDQGQN 420
ISAYDCTSAT GSLSSDASSG ISCSATSSTN NTNSFDNSLV ATSKVQTING KEQIGVNSFN 480
LVSQVWSVYN SLKTSEENLQ KNAKILCNNG SQSGTSPCNS SSGGLSISGN AQLQNILSPT 540
NGTTTNTQAK SNASKLKAMV MVNNEEEAKT TNFNQSSGPT TQSSNSTVMG ALNTVLQNVS 600
NFQQSIQSAF QNQENNIQAW ANALYNTSNP NGNQSQNLTT NNNQDLRIQL RANFYQLINT 660
INQQVPTDMN ALINQSQQTQ QTSGSASTTN NACASGMGSS GNWCYQQWSD SKAYYSGLQS 720
ALGYQTQATT QNGSSGGSNI TYNVQQITLT SGGLLNQIIT NLKSVNGGSN GGSSGNGTSQ 780
INTAYQMLTD ASDGKLGTYN SSNSSNSSNS GNNNGYTPCN STNGSNGTSG SNCYEPNKQQ 840
NATTATTTTD SNLQKVYNDA QKIANIIASS GNNKGVENGL KQFFEALKSN SSSLSNLCGN 900
GSSGSSSTCS GGLINLLGAI PTNGVSDTNN LINLLTEFIK TAGFIQNKDS NVSTSLTSAF 960
QAITSAISQG FQALQNDISP NAILTLLQEI TSNTTTIQSF SQTLRQLLGD KTFFMVQQKL 1020
IDAMINARNQ VQNAQNQANN YGSQPVLSQY AAAKSTQHGM SNGLGVGIGY KYFFGKARKL 1080

GLRHYFFFDY GFSEIGLANQ SVKANIFAYG VGTDFLWNLF RRTYNTKALN FGLFAGVQLG 1140
GATWLSSLRQ QIIDNWGNAN DIHSTNFQVA LNFGVRTNFA EFKRFAKKFH NQGVISQKSV 1200
EFGIKVPLIN QAYLNSAGAD VSYRRLYTFY INYIMGF 1237

<212> Type : PRT
<211> Length : 1237
SequenceName : SEQ ID 95
SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :
MKQNLKPFKM IKENLMTQSQ KVRFLAPLSL ALSLSFNPVG AEEDGGFMTF GYELGQVVQQ 60
VKNPGKIKAE ELAGLLNSTT TNNTNINIAG TGGNVAGTLG NLFMNQLGNL IDLYPTLKTN 120
NLHQCGSTNS GNGATAAAAT NNSPCFQGNL ALYNEMVDSI KTLSQNISKN IFQGDNNTTS 180
ANLSNQLSEL NTASVYLTYM NSFLNANNQA GGIFQNNTNQ AYENGVTAQQ IAYVLKQASI 240
TMGPSGDSGA AGAFLDAALA QHVFNSANAG NDLSAKEFTS LVQNIVNNSQ NALTLANNAN 300
ISNSTGYQVS YGGNIDQARS TQLLNNTTNT LAKVTALNNE LKANPWLGNF AAGNSSQVNA 360
FNGFITKIGY KQFFGENKNV GLRYYGFFSY NGAGVGNGPT YNQVNLLTYG VGTDVLYNVF 420
SRSFGSRSLN AGFFGGIQLA GDTYISTLRN SPQLASRPTA TKFQFLFDVG LRMNFGILKK 480
DLKSHNQHSI EIGVQIPTIY NTYYKAGGAE VKYFRPYSVY WVYGYAF 527

<212> Type : PRT
<211> Length : 527
SequenceName : SEQ ID 96
SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :
MKKTLLLSLS LSFGLHAEDD GFYASAGIRI GEAAQMVKNT KGIQQLSENY EKLNNLLNNY 60
NTLNTLVKLS SDPSAVNDAR DNLGSSTRNL LDVKANSPAY QAVLLALNAA VGLWQVTSYA 120
FTACGPGSNE NANGGIQTFN NVPGQNTTTI TCNSYYEPGH GGPISTKNYA IINKAYQIIQ 180
KALTANGEGI PVLSNTTTKL DFTINGDKRT GGEPNKKLVY PWSHGKAIST SWNATITAPT 240
TENINITTNSA QELLKQASII ITTLNSACPN FQNGGSGYWA GISGNGTMCG MFKNEISAIQ 300
GMIANAQEAV AQAKIVSENT QNQNSLDAGK PFNPYTDASF AESMLKNAQA QAEILNQAEQ 360
VVKNFEKIPT AFVNDSLGVC YEVQGGERRG TNPGQTTSNT WGAGCAYVGQ TITNLKNSIA 420
HFGTQEQQIQ QAENIADTLV NFKSRYSELG NTYNSITTAL SNIPNAQSLQ NAVSKKNNPY 480
SPQGIDTNYY LNQNSYNQIQ TINQELGRNP FRKVGIVSSQ TNNGAMNGIG IQVGYKQFFG 540
QKRKWGARYY GFFDYNHAFI KSSFFNSASD VWTYGFGADA LYNFINDKAT NFLGKNNKLS 600
VGLFGGIALA GTSWLNSEYV NLATMNNVYN AKMNVANFQF LFNMGVRMNL ARPKKKDSDH 660
AAQHGIELGL KIPTINTNYY SFMGAELKYR RLYSVYLNYV FAY 703

<212> Type : PRT
<211> Length : 703
SequenceName : SEQ ID 97
SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :
MIKKNRTLFL SLALCASISY AEDDGGFFTV GYQLGQVMQD VQNPGGAKSD ELARELNADV 60
TNNILNNNTG GNVAGALSNA FSQYLYSLLG AYPTKLNGND VSANALLSGA VGSGTCAAAG 120
TAGGTTLNTQ SACTAAGYYW LPSLTDRILS TIGSQTNYGT NTNFPNMQQQ LTYLNAGNVF 180
FNAMNKALEK NGTATANSTS STSGATGSDG QTYSQQAIQY LQGQQNILNN AANLLKQDEL 240
LLEAFNSAVA ANIGNKEFNS AAFTGLVQGI IDQSQLVYNE LTKNTISGSA VNNAGINSNQ 300
ANAVQGRASQ LPNALYNVQV TLDKINALNN QVRSMPYLPQ FRAGNSRATN ILNGFYTKVG 360
YKQFFGKKRN IGLRYYGFFS YNGASVGFRS TQNNVGLYTY GVGTDVLYNI FSRSYQNRSV 420
DMGFFSGIQL AGETFQSTLR DDPNVKLHGK INNTHFQFLF DFGMRMNFGK LDGKSNRHNQ 480
HTVEFGVVVP TIYNTYYKSA GTTVKYFRPY SVYWSYGYSF 520

<212> Type : PRT
<211> Length : 520
SequenceName : SEQ ID 98
SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :
MKKKFLSLTL GSLLVSALSA EDNGFFVSAG YQIGESAQMV KNTKGIQDLS DSYERLNNLL 60
TNYSVLNALI RQSADPNAIN NARGNLNASA KNLINDKKNS PAYQAVLLAL NAAAGLWQVM 120
SYAISPCGPG KDTSKNGGVQ TFHNTPSNQW GGTTITCGTT GYEPGPYSIL STENYAKINK 180
AYQIIQKAFG SSGKDIPALS DTNTELKFTI NKNNGNTNTN NNGEEIVTKN NAQVLLEQAS 240
TIITTLNSAC PWINNGGAGG ASSGSLWEGI YLKGDGSACG IFKNEISAIQ DMIKNAAIAV 300
EQSKIVAANA QNQRNLDTGK TFNPYKDANF AQSMFANAKA QAEILNRAQA VVKDFERIPA 360
EFVKDSLGVC HEVQNGHLRG TPSGTVTDNT WGAGCAYVGE TVTNLKDSIA HFGDQAERIH 420
NARNLAYTLA NFSSQYQKLG EHYDSITAAI SSLPDAQSLQ NVVSKKTNPN SPQGIQDNYY 480
IDSNIHSQVQ SRSQELGSNP FRRAGLIAAS TTNNGAMNGI GFQVGYKQFF GKNKRWGARY 540
YGFVDYNHTY NKSQFFNASS DVWTYGVGSD LLVNFINDKA TKHNKISFGA FGGIALAGTS 600
WLNSQYVNLA NVNNYYKAKI NTANFQFLFN LGLRMNLARK KHRATDNAAQ HGIELGTKIP 660
TINTNYYSLL-GTTLQYRRLY SVYLNYVFAY 690
<212> Type : PRT
<211> Length : 690
SequenceName : SEQ ID 99
SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :
MKIKKSLFAL SFSLMASLSR AEDDGFYMSV GYQIGEAVQK VKNTGALQNL ADRYDNLSNL 60
LNQYNYLNSL VNLASTPSAI TGAIDNLSSS AINLTSATTT SPAYQAVALA LNAAVGMWQV 120
IAFGISCGPG PNLGPEHLEN GGVRSFDNTP NYSYNTGSGT TTTTCNGASN VGPNGILSSS 180
EYQVLNTAYQ TIQTALNQNQ GGGMPALNSS KNMVVNINQT FTKNPTTEYT YPDGNGNYYS 240
GGSSIPIQLK ISSVNDAENL LQQAATIINV LTTQNPHVNG GGGAWGFGGK TGNVMDIFGD 300
SFNAINEMIK NAQAVLEKTQ QLNANENTQI TQPDNFNPYT SKDTQFAQEM LNRANAQAEI 360
LSLAQQVADN FHSIQGPIQQ DLEECTAGSA GVINDNTYGS GCAFVKETLN SLEQHTAYYG 420
NQVNQDRALS QTILNFKEAL STLGNDSKAI NSGISNLPNA KSLQNMTHAT QNPNSPEGLL 480
TYSLDTSKYN QLQTVAQELG KNPFRRIGVI NYQNNNGAMN GIGVQAGYKQ FFGKKRNWGL 540
RYYGFFDYNH AYIKSNFFNS ASDVWTYGVG MDALYNFIND KNTNFLGKNN KLSVGLFGGF 600
ALAGTSWLNS QQVNLTMMNG IYNANVSASN FQFLFDLGLR MNLARPKKKD SDHAAQHGME 660
LGVKIPTINT DYYSFMGAEL KYRRLYSVYL NYVFAY 696
<212> Type : PRT
<211> Length : 696
SequenceName : SEQ ID 100
SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :
MKIKKSLFAL SFSLMASLSR AEDDGFYMSV GYQIGEAVQK VKNTGALQNL ADRYDNLSNL 60
LNQYNYLNSL VNLASTPSAI TGAIDNLSSS AINLTSATTT SPAYQAVALA LNAAVGMWQV 120
IAFGISCGPG PNLGPEHLEN GGVRSFDNTP NYSYNTGSGT TTTTCNGASN VGPNGILSSS 180
EYQVLNTAYQ TIQTALNQNQ GGGMPALNSS KNMVVNINQT FTKNPTTEYT YPDGNGNYYS 240
GGSSIPIQLK ISSVNDAENL LQQAATIINV LTTQNPHVNG GGGAWGFGGK TGNVMDIFGD 300
SFNAINEMIK NAQAVLEKTQ QLNANENTQI TQPDNFNPYT SKDTQFAQEM LNRANAQAEI 360
LSLAQQVADN FHSIQGPIQQ DLEECTAGSA GVINDNTYGS GCAFVKETLN SLEQHTAYYG 420
NQVNQDRALS QTILNFKEAL STLGNDSKAI NSGISNLPNA KSLQNMTHAT QNPNSPEGLL 480
TYSLDTSKYN QLQTVAQELG KNPFRRIGVI NYQNNNGAMN GIGVQAGYKQ FFGKKRNWGL 540
RYYGFFDYNH AYIKSNFFNS ASDVWTYGVG MDALYNFIND KNTNFLGKNN KLSVGLFGGF 600
ALAGTSWLNS QQVNLTMMNG IYNANVSASN FQFLFDLGLR MNLARPKKKD SDHAAQHGME 660
LGVKIPTINT DYYSFMGAEL KYRRLYSVYL NYVFAY 696
<212> Type : PRT
<211> Length : 696
SequenceName : SEQ ID 101
SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :
MHKKVLLALT ASLICQESLF AKDKDYTLGK VSTAGKKDRS DYSGQVNLGY SGITAPKSWQ 60
DEEVKKYTGS RTVISNKALT QQANQSIEEA LQNVPGLQIR NATGVGAMPT IQIRGFGAGG 120

SGHSDATLML VNGIPVYMAP YAHIELDIFP VTFQAIDRID VIKGGGSVQY GPNTYGGIVN 180
IITKPIPNQW ENQAAERITY WAKARNAGFA APPDKTGDPS FIKSLGNNLL YNTYVRSGGM 240
INKHVGIQAQ ANWVRGQGFR DNSPSSISNY WLDGVYDINE SNGIKAYYQY YDFAIAQPGS 300
LSEQDYKINR FANLRPLNQK GGRSQRFGAV YENRFGDLDR VGGTFSFTYY GQLMTRDFQV 360
SSSYNSANMV TCFSEAACRA AGLPAGYNLA VPYYATNYNG WAEVENPVRS INNAFEPKVN 420
LIVNTGKVRQ TFIMGLRFMT TTFLQRQYLN TNECATKTSG EGAGFLCEGP NVMSGWKPHI 480
KHGVYRNWNN WRNNYTAVYL SDRIEAWDGR FFIVPGLRYA FVQYNNENAS NWMQIPEKDL 540
RKIKHMNNWM PSTNIGFIPV QGDHNVLTYF NYQRSFVPPQ LDVLSYGGAE YFTQHFDTVE 600
AGARYTYKDK FSFNADYFRI WARDFATGQY SVYTSGPMKG NVRPINGYSQ GVELELYYRP 660
IRGLQFHAAF NYIDTRVTSH GPLTDLNGDV LKGTSYNKHF PFVSPFQFIF DARYNWRKTT 720
IGISSYFYSR AYSGISNSAA GGYYGMQYYS GGNNYESVLN SGYQCEAWCM TQHEGLLPWY 780
WVWNIQVSQI FWENGRHRVT GSLQINNIFN MKYYFTGIGS SPAGLQPAPG RSVTAYLNYT 840
F 841

<212> Type : PRT
<211> Length : 841
SequenceName : SEQ ID 102
SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :
MKKTLLLLSLS ASSLLNAEDN GFFISAGYQI GEAAQMVKNT GELKKLSDTY ENLSNLLTNF 60
NNLNQAVTNA SSPSEINAAI DNLKANTQGL IGEKTNSPAY QAVYLALNAA VGLWNVIAYN 120
VQCGPGNSGQ QSVTFEGQPG HNSSSINCNL TGYNNGVSGP LSIENFKKLN QAYQTIQQAL 180
KQDSGFPVLD SAGKQVTITI TTQTNGANKS ETTTTTTTTN DAQTLLQEAS KMISVLTTNC 240
PWVNHNQGQN GGAPWGLDTA GNVCQVFATE FSAVTSMIKN AQEIVTQAQS LNQQNNQNAP 300
QDFNPYTSAD RAFAQNMLNH AQAQAKILEL ADQMKKDLNT IPSQFITNYL AACHNGGGTL 360
PDAGVTNNTW GAGCAYVEET ITALNNSLAH FGTQAEQIKQ SELLARTILD FRGSLSNLNN 420
TYNSITTTAS NTPNSPFLKN LISQSTNPNN PGGLQAVYQV NQSAYSQLLS ATQELGHNPF 480
RRVGLISSQT NNGAMNGIGV QVGYKQFFGE KRRWGLRYYG FFDYNHAYIK SSFFNSASDV 540
FTYGVGTDVL YNFINDKTTK NSKISFGVFG GIALAGTSWL NSQYVNLATF NNFYSAKMNV 600
ANFQFLFNLG LRMNLAKNKK KASDHAAQHG VELGVKIPTI NTNYYSLLGT QLQYRRLYSV 660
YLNYVFAY 668

<212> Type : PRT
<211> Length : 668
SequenceName : SEQ ID 103
SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :
MRKLFIPLLL FSALEANEKN GFFIEAGFET GLLEGTQTQE KRHTTTKNTY ATYNYLPTDT 60
ILKRAANLFT NAEAISKLKF SSLSPVRVLY MYNGQLTIEN FLPYNLNNVK LSFTDAQGNT 120
IDLGVIETIP KHSKIVLPGE AFDSLKEAFD KIDPYTLFLP KFEATSTSIS DTNTQRVFET 180
LNNIKTNLIM KYSNENPNNF NTCPYNNNGN TKNDCWQNFT PQTAEEFTNL MLNMIAVLDS 240
QSWGDAILNA PFEFTNSSTD CDSDPSKCVN PGVNGRVDTK VDQQYILNKQ GIINNFRKKI 300
EIDAVVLKNS GVVGLANGYG NDGEYGTLGV EAYALDPKKL FGNDLKTINL EDLRTILHEF 360
SHTKGYGHNG NMTYQRVPVT KDGQVEKDSN GKPKDSDGLP YNVCSLYGGS NQPAFPSNYP 420
NSIYHNCADV PAGFLGVTAA VWQQLINQNA LPINYANLGS QTNYNLNASL NTQDLANSML 480
STIQKTFVTS SVTNHHFSNA SQSFRSPILG VNAKIGYQNY FNDFIGLAYY GIIKYNYAKA 540
VNQKVQQLSY GGGIDLLLDF ITTYSNKNSP TGIQTKRNFS SSFGIFGGLR GLYNSYYVLN 600
KVKGSGNLDV ATGLNYRYKH SKYSVGISIP LIQRKASVVS SGGDYTNSFV FNEGASHFKV 660
FFNYGWVF 668

<212> Type : PRT
<211> Length : 668
SequenceName : SEQ ID 104
SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :
MNKTTIKILM GMALLSSLQA AEAELDEKSK KPKFADRNTF YLGVGYQLSA INTSFSTSSI 60
DKSYFMTGNG FGVVLGGKFV AKTQAVEHVG FRYGLFYDQT FSSHKSYIST YGLEFSGLWD 120
AFNSPKMFLG LEFGLGIAGA TYMPGGAMHG IIAQYLGKEN SLFQLLVKVG FRFGFFHNEI 180

TFGLKFPVIP NKKTEIVDGL SATTLWQRLP VAYFNYIYNF 220

<212> Type : PRT
<211> Length : 220
SequenceName : SEQ ID 105
SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :
MKKTKKTILL SLTLAASLLH AEDNGVFLSV GYQIGEAVQK VKNADKVQKL SDVYEQLSKL 60
LANDNGTSSK TSAQAINQAV NNLNESAKTL AGGTTNSPAY QATLLALRSA LGLWNSMGYA 120
VVCGGYIKKP GENNQKNFHY TDENGNGTTI NCGGSTNSNG THSPNGTNTL KADKNVSLSI 180
EQYEKIHEAY QILSKALKQA GLAPLNSKGE KLEAHVTTSK DQQGTSSDQT TTTTSVIDTT 240
NDAQNLLTQA QTIVNTLKDY CPMLIAKSSS NGGTNGANTP SWQTAGGGKN SCATFGAEFS 300
AISDMISNAQ KIVQETQQLN ANQPKNITQP NNPNLNSPGS LTALAQSMLK NAQSQTEILK 360
LANQVASDFD KLSSGYLKDY IGKCDVSGVS SSNMTPQNMN TTWGKGCAGV EETLTSLKAS 420
TTDFNNQTTP QLDQAQTLAN TLTQELGNNP FKRVGIIGSQ TNNGAMNGLG VQAGYKQFFG 480
QKRRWGLRYY GFFDYNHTYI KSSFFNSSSD VLTYGVGSDL LFNFINDKNT NFLGKNNKIS 540
VGLFGGIALA GTSWLNSQFV NLKTISNVYS AKVNTANFQF LFNLGLRTNL ARPKKKDSDH 600
SAQHGMELGV KIPTINTNYY SYLGTKLEYR RLYSVYLNYV FAY 643

<212> Type : PRT
<211> Length : 643
SequenceName : SEQ ID 106
SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :
MKKTILLSLM VSSLFAENDG VYMSVGYQIG EAAQMVKNTG EIQKVSNAYE NLNNLLTRYN 60
ELKQTASNTD SSTAQAIDNL EKSASRLKTT PNTANQAVSS ALSSAVGMWQ VIASNLANNS 120
LSSSEYEKLK ATSQLLQNTL ENKNNNLKIE NDYDQLLTQA STIINTLQSQ CPGVDGGNGK 180
PWGINTSGNA CAIFGSTFNA INSMIDSAKK AAADARRTAP ESPNQQNAFT NADFNKNLNQ 240
VSSVINDTIS YLKGDNLETI YNTIQKTPNS KGFQSLVSRS SYSYSLNETQ YSQFQTTTKE 300
FGHNPFRSVG LINSQSNNGA MNGVGVQLGY KQFFGKNKFF GIRYYGFFDY NYAYIKSNFF 360
NSASNVFTYG AGSDLLLNFI NGGSDRNRKV SFGIFGGIAL AGTTWLNNQS ANLKITNSAY 420
SAKINNTNFQ FLFNTGLRLQ GIHHGIELGV KIPTINTNYY SFMGAKLAYR RLYSLYLNYV 480
LAY 483

<212> Type : PRT
<211> Length : 483
SequenceName : SEQ ID 107
SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :
MPKASQVLFF GAFLSTSLQG FEAKLNGFVD QSSTIGFNQH KINKERGIYP MQQFATIAGY 60
LGLGFSLLPK KVSDHVLKGK IGGMVGSIFY DGTKKFEDGS VAYNLFGYYD GFMGVYTNIL 120
QTDSLETQNM KHNKNVRNYV FSDAYLEYAY KNYFEIKAGR YLSTMPYKSG QTQGFQVSGQ 180
YKHARLTWFS SWGRAFAYGS FLMDWFAART TYSGGFTKNN NGGYDSHGRK VLYGTHAVQL 240
TYKPHRFLIE GFYYLSPQIF NAPGVKIGWD SNPNFSGTGF RSDTAIIGFF PIYYPWMIVK 300
SNGSPVYRYD TPATQNGQNL IIRQRFDINN YNVSIAFYKV FQNANGWIGN MGNPSGVIMG 360
SNSVYAGFTG TALKRDAATI FLSCGGTHFA KKFTWKFATQ YSNSVVSWEA RAMISLGYKF 420
TEYLSGSVDL AYYGVHTNKG FKPGENGPVP KNFPALYSDR SALYTALVAS F 471

<212> Type : PRT
<211> Length : 471
SequenceName : SEQ ID 108
SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :
MLRLVSKTIC LSLISLFNPL EAFQKHQKDV FFVEAGFETG LLEGAQTKEQ AIAQNTQNTQ 60

KIYENPLTHP QTKEQPKEQN KSDTATPQSV YGRYYILQNT ILEKATELFT AANINGNGLT 120
FYSQNPVYVM AYNKDNAEFE GYGNNSVVVI QNFLPYNLNN IELSYTDAQG KAVNLGVIET 180
IPKDSQIILP ASLFNNFSND SPFNSDGLQQ LQTTTTPFSD ANTQSLFEKL SQITTNLQMT 240
YENTDPFSSG NNDPNGPLAS PKPHYECPGY KKSCQVASVS FTPQTAEELT NLMLDMIAVF 300
DSKSWEEAVL NAPFQFSNSP SECGIDYPKC VNPFNNGLVD PKDEKYALTP EEVINSYRVA 360
NELTVNLLNA AKGFLGLGSQ LGSANAPDDD GFNQGVLGIA PFALDPEKLF GKNLNKVAIL 420
ALRDIIHEYG HTLGYTHNGN MTYQRVRLCQ EGNGPEARCE GGHEVEKNGK EELEFSNGHE 480
VRDHDGYTYD VCSRFGGKNQ PAFPSNYPNS IYTNCAQVPA GLIGVTTAVW QQLINQNALP 540
INFANLNSQT SHLNAGLNAQ NFATSMVSAI AQNFSTTSTT TYRSSSKNFR SPILGVNVKI 600
GYQHYFNDYI GLAYYGIIQY NYAQANDEKI QQLSYGGGMD VLFDFITTYT NKKQDHPTKK 660
VFASSFGVFG GLRGLYNSYY VFNQVKGSGN LDIVTGFNYR YKHSKYSIGV SVPLIQSGIK 720
IASNNGIYAD SVVLNEGGSH PKVFFNYGWV F 751

<212> Type : PRT
<211> Length : 751
SequenceName : SEQ ID 109
SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :
MQNFVFNKKW LIYSSLLPLF FLNPLMAEDD GFFMGVSYQT SLAVQRVDNS GLNASQDAST 60
YIRQNAIALE SAAVPLAYYL EAMGQQTRVL MQMLCPDPSK RCLLYAGGYQ NGQNNNGDTG 120
NNPPRGNVNA TFDMQSLVNN LNKLTQLIGE TLIRNPENLP NSKVFNVKFG NQSTVIALPR 180
GLANTMDALN NDITNALTTL WYNQTLTNKS FSTPSNTSVN FSPQVLQHLL QDGLATANNN 240
QTICSTQNQC TATNEAKSIA QNAQNIFQAL MQAGILGGLA NEKQFGFTYN KAPNGSDSQQ 300
GYQSFSGPGY VTKNDNTTQA PLKALPAGAT IGSGNGQYTY HPSSAVYYLA DSIIANGITA 360
SMIFSGMQNF ANKAAKLIGT SSYNQMQDAI NYGESLLSNT VAYGDFITNW VAPYLDLNNK 420
GLNFLPNYGG QLNGANNQTP QLTPQQAQQE QKVIMNQLEQ ATNAPTPAQI NRILANPYSP 480
TAKTLMAYGL YRSKAVIGGV IDEMQTKVNQ VYQMGFARNF LEHNSNSNNM NGFGVKMGYK 540
QFFGKKRMFG LRYYGFYDFG YAQFGTESSL VKATLSSYGA GTDFLYNVFT RKRGTEAIDI 600
GFFAGIQLAG QTWKTNFLDQ VDGNHLKPKD TSFQFLFDLG IRTNFSKIAH QKRSRFSQGI 660
EFGLKIPVLY HTYYQSEGVT AKYRRDFSFY VGYNIGF 697

<212> Type : PRT
<211> Length : 697
SequenceName : SEQ ID 110
SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :
MKKTILLSLS LSLASSLLHA EDNGFFVSAG YQIGEAVQMV KNTGELKNLN EKYEQLSQYL 60
NQVASLKQSI QNANNIELVN SSLNYLKSFT NNNYNSTTQS PIFNAVQAVI TSVLGFWSLY 120
AGNYLTFFVV NKDTQKPASV QGNPPFSTIV QNCSGIENCA MNQTTYDKMK KLAEDLQAAQ 180
QNATTKANNL CALSGCATTQ GQNPSSTVSN ALNLAQQLMD LIANTKTAMM WKNIVIAGVS 240
NVSGAIDSTG YPTQYAVFNN IKAMIPILQQ AVTLSQSNHT LSASLQAQAT GSQTNPKFAK 300
DIYAFAQNQK QVISYAQDIF NLFSSIPKDQ YRYLEKAYLK IPNAGKTPTN PYRQEVNLNQ 360
EIQTIQNNVS YYGNRVDAAL SVAKDVYNLK SNQTEIVTTY NNAKNLSQEI SKLPYNQVNT 420
KDIITLPYDQ NAPAAGQYNY QINPEQQSNL SQALAAMSNN PFKKVGMISS QNNNGALNGL 480
GVQVGYKQFF GESKRWGLRY YGFFDYNHGY IKSSFFNSSS DIWTYGGGSD LLVNFINDSI 540
TRKNNKLSVG LFGGIQLAGT TWLNSQYMNL TAFNNPYSAK VNASNFQFLF NLGLRTNLAT 600
AKKKDSERSA QHGVELGIKI PTINTNYYSF LGTKLEYRRL YSVYLNYVFA Y 651

<212> Type : PRT
<211> Length : 651
SequenceName : SEQ ID 111
SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :
MLKLASKTIC LSLISSFTAV EAFQKHQKDG FFIEAGFETG LLQGTQTQEQ TIATTQEKPK 60
PKPKPKPITP QSTYGKYYIS QSTILKNATE LFAEDNITNL TFYSQNPVYV TAYNQESAEE 120
AGYGNNSLIM IQNFLPYNLN NIELSYTDDQ GNVVSLGVIE TIPKQSQIIL PASLFNDPQL 180
NADGFQQLQT NTTRFSDAST QNLFNKLSKV TTNLQMTYIN YNQFSSGNGS GSKPPCPPYE 240

NQANCVAKVP PFTSQDAKNL TNLMLNMMAV FDSKSWEDAV LNAPFQFSDN NLSAPCYSDY 300
LTCVNPYNDG LVDPKLIAKN KGDEYNIENG QTGSVILTPQ DVIYSYRVAN NIYVNLLPTR 360
GGDLGLGSQY GGPNGPGDDG TNFGALGILS PFLDPEILFG KELNKVAIMQ LRDIIHEYGH 420
TLGYTHNGNM TYQRVRMCEE NNGPEERCQG GRIEQVDGKE VQVFDNGHEV RDTDGSTYDV 480
CSRFKDKPYT AGSYPNSIYT DCSQVPAGLI GVTSAVWQQL IDQNALPVDF TNLSSQTNYL 540
NASLNTQDFA TTMLSAISQS LSSSKSSATT YRTSKTSRPF GAPLLGVNLK MGYQKYFNDY 600
LGLSSYGIIK YNYAQANNEK IQQLSYGVGM DVLFDFITNY TNEKNPKSNL TKKVFTSSLG 660
VFGGLRGLYN SYYLLNQYKG SGNLNVTGGL NYRYKHSKYS IGISVPLVQL KSRIVSSDGA 720
YTNSITLNEG GSHFKVFFNY GWIF 744

<212> Type : PRT
<211> Length : 744
SequenceName : SEQ ID 112
SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :
MRKLFIPLLL FSALEANEKN GFFIEAGFET GLLEGTQTQE KRHTTTKNTY ATYNYLPTDT 60
ILKRAANLFT NAEAISKLKF SSLSPVRVLY MYNGQLTIEN FLPYNLNNVK LSFTDAQGNV 120
IDLGVIETIP KHSKIVLPGE AFDSLKIDPY TLFLPKIEAT STSISDANTQ RVFETLNKIK 180
TNLVVNYRNE NKFKDHENHW EAFTPQTAEE FTNLMLNMIA VLDSQSWGDA ILNAPFEFTN 240
SPTDCDNDPS KCVNPGTNGL VNSKVDQKYV LNKQDIVNKF KNKADLDVIV LKDSGVVGLG 300
SDITPSNNDD GKHYGQLGVV ASALDPKKLF GDNLKTINLE DLRTILHEFS HTKGYGHNGN 360
MTYQRVPVTK DGQVEKDSNG KPKDSDGLPY NVCSLYGGSN QPAFPSNYPN SIYHNCADVP 420
AGFLGVTAAV WQQLINQNAL PINYANLGSQ TNYNLNASLN TQDLANSMLS TIQKTFVTSS 480
VTNHHFSNAS QSFRSPILGV NAKIGYQNYF NDFIGLAYYG IIKYNYAKAV NQKVQQLSYG 540
GGIDLLLDFI TTYSNKNSPT GIQTKRNFSS SFGIFGGLRG LYNSYYVLNK VKGSGNLDVA 600
TGLNYRYKHS KYSVGISIPL IQRKASVVSS GGDYTNSFVF NEGASHFKVF FNYGWVF 657

<212> Type : PRT
<211> Length : 657
SequenceName : SEQ ID 113
SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :
MSLATSYNVS NNFSKFNIKR VRGYLICLVC NTPKMIQRGL NGVSFYGCSD YVNKGDCKGV 60
LREINGSMKM VCLHCENTPI MEKVESGRGG AYACKNCNRK FYFIDLAKQN ERKKDLEKEK 120
KELLNKIEKQ KIKHLERFIL AGVKANIKEN SFFLGCKNYP KCEWTASMDS QDLKCPKCNR 180
LMKRKKNFKN NEFFTATSLT LNAIEFCLYI NLKKKETNV 219

<212> Type : PRT
<211> Length : 219
SequenceName : SEQ ID 114
SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :
MEIKKYFLYA LFFLLFSGLF LSKLQAYKFN MSIVGKVSSY TKFGFNNQRY QPSKDIYPTG 60
SYTSLLGELN LSMGLYKGLR AEVGAMMAAL PYDSTAYQGN NIPNGQPGSR TDPFGAGIFW 120
QYIGWYAGHS GLNVQKPRLA MVHNAFLSYN YKKDKFSFGV KGGRYDAEEY DWFTSYTQGV 180
EGFVKYKDTR LRVMYSDARA SASSDWFWYF GRYYTSGKAL MIADLKYEKD NLKINPYFYA 240
IFQRMYAPGI NITYDTNPNF NNKGFRFVGT FVGFFPIFAT PANQNDIILF QQVPLGKSGQ 300
TYFFRTRFYY NKWQFGGSVY KNIGNANGDI GIYGDPLGYN IWTNSIYDAE INNIVGADVI 360
NGFLYVGSQY RGFSWKILGR WTDSPRADER SLALFLSYFS NKYNIRMDLK LEYYGNITKK 420
GYCIGYCGMY VPVDPNGPGT QPLTHNVYSD RSHIMFNITY GFRIY 465

<212> Type : PRT
<211> Length : 465
SequenceName : SEQ ID 115
SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :
MKKTILLSLS LSLASSLLHA EDNGFFVSAG YQIGEAVQMV KNTGELKNLN DKYEQLSQSL 60
AQLASLKKSI QTANNIQAVN NALSDLKSFA SNNHTNKETS PIYNTAQAVI TSVLAFWSLY 120
AGNALSFHVT GLNDGSNSPL GRIHRDGNCT GLQQCFMSKE TYDKMKTLAE NLQKAQGNLC 180
ALSECSSNQS NGGKTSMTTA LQTAQQLMDL IEQTKVSMVW KNIVIAGVTN KPNGAGAITS 240
TGHVTDYAVF NNIKAMLPIL QQALTLSQSN HTLSTQLQAR AMGSQTNREF AKDIYALAQN 300
QKQILSNASS IFNLFNSIPK DQLKYLENAY LKVPHLGKTP TNPYRQNVNL NKEINAVQDN 360
VANYGNRLDS ALSVAKDVYN LKSNQTEIVT TYNDAKNLSE EISKLPYNQV NVTNIVMSPK 420
DSTAGQYQIN PEQQSNLNQA LAAMSNNPFK KVGMISSQNN NGALNGLGVQ VGYKQFFGES 480
KRWGLRYYGF FDYNHGYIKS SFFNSSSDIW TYGGGSDLLV NFINDSITRK NNKLSVGLFG 540
GIQLAGTTWL NSQYMNLTAF NNPYSAKVNA SNFQFLFNLG LRTNLATAKK KDSERSAQHG 600
VELGIKIPTI NTNYYSFLGT KLEYRRLYSV YLNYVFAY 638
<212> Type : PRT
<211> Length : 638
SequenceName : SEQ ID 116
SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :
MKLKKRKVAA TLLKRLTLPL LFTTGSLGAV TYEVHGDFIN FSKVGFNRSP INPVKGIYPT 60
ETFVNLTGKL EGSVHLGRGW TVNVGGVLGG QVYDNTRYDR WAKDFTPPSY WDKTSCGTDS 120
LSLCMNATKM WQQQGPGGII DPRGIGYMYM GEWNGLFPNY YPANAYLPGH SRRYEVYKAN 180
LTYDSDRVHM VMGRFDVTEQ EQMDWIYQLF QGFYGTFKLT KNMKFLLFSS WGRGIADGQW 240
LFPIYREKPW GIHKAGIIYR PTKNLMIHPY VYLIPMVGTL PGAKIEYDTN PEFSGRGIRN 300
KTTFYVLYDY RWNNAEYGRY APARYNTWDP FLDNGKWRGL QGPGGATLYL HHHIDINNYF 360
VVGGAYLNIG NPNMNLGTWG NPVALDGIEQ WVGGIYSLGF AGIDNITDAD AFTEYVKGGG 420
KHGKFSWSVY QRFTTAPRAL EYGIGMYLDY QFSKHVKAGL KLVWLEFQIR AGYNPGTGFL 480
GPNGQPLNLN NGLFESSAFA QGPQNMGGIA KSITQDRSHL MTHISYSF 528
<212> Type : PRT
<211> Length : 528
SequenceName : SEQ ID 117
SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :
MKNFSPLYCL KKLKKRHLIA LSLPLLSYAN GFKIQEQSLN GTALGSAYVA GARGADASFY 60
NPANMGFTND WGENRSEFEM TTTVINIPAF SFKVPTTNQG LYSVTSLEID KSQQNILGII 120
NTIGLGNILK ALGNTAATNG LSQAINRVQG LMNLTNQKVV TLASKPDTQI VNGWTGTTNF 180
VLPKFFYKTR THNGFTFGGS FTAPSGLGMK WNGKGGEFLH DVFIMMVELA PSMSYTINKR 240
FSVGVGLRGL YATGSFNNTV YVPLEGASVL SAEQILNLPN NVFADQVPSN MMTLLGNIGY 300
QPALNCQKAG GDMSDQSCQE FYNGLKKIMG YSGLIKASAN LYGTTQVVQK SNGQGVSGGY 360
RVGSSLRVFD HGMFSVVYNS SVTFNNMKGGL VAITELGPSL GSVLTKGSLN INVSLPQTLS 420
LAYAHQFFKD RLRVEGVFER TFWSQGNKFL VTPDFANATY KGLSGTVASL DSETLKKMVG 480
LANFKSVMNM GAGWRDTNTF RLGVTYMGKS LRLMGAIDYD QAPSPQDAIG IPDSNGYTVA 540
FGTKYNFRGF DLGVAGSFTF KSNRSSLYQS PTIGQLRIFS ASLGYRW 587
<212> Type : PRT
<211> Length : 587
SequenceName : SEQ ID 118
SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :
MAFQVNTNIN AMNAHVQSAL TQNALKTSLE RLSSGLRINK AADDASGMTV ADSLRSQASS 60
LGQAIANTND GMGIIQVADK AMDEQLKILD TVKVKATQAA QDGQTTESRK AIQSDIVRLI 120
QGLDNIGNTT TYNGQALLSG QFTNKEFQVG AYSNQSIKAS IGSTTSDKIG QVRIATGALI 180
TASGDISLTF KQVDGVNDVT LESVKVSSSA GTGIGVLAEV INKNSNRTGV KAYASVITTS 240
DVAVQSGSLS NLTLNGIHLG NIADIKKNDS DGRLVAAINA VTSETGVEAY TDQKGRLNLR 300
SIDGRGIEIK TDSVSNGPSA LTMVNGGQDL TKGSTNYGRL SLTRLDAKSI NVVSASDSQH 360
LGFTAIGFGE SQVAETTVNL RDVTGNFNAN VKSASGANYN AVIASGNQSL GSGVTTLRGA 420
MVVIDIAESA MKMLDKVRSD LGSVQNQMIS TVNNISITQV NVKAAESQIR DVDFAEESAN 480

FNKNNILAQS GSYAMSQANT VQQNILRLLT 510
<212> Type : PRT
<211> Length : 510
SequenceName : SEQ ID 119
SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :
MAGTQAIYES SSAGFLSQVS SIISSTSGVA GPFAGIVAGA MTAAIIPIVV GFTNPQMTAI 60
MTQYNQSIAE AVSVPMKAAN QQYNQLYQGF NDQSMAVGNN ILNISKLTGE FNAQGNTQSA 120
QISAVNSQIA SILASNTTPK NPSAIEAYAT NQIAVPSVPT TVEMMSGILG NITSAAPKYA 180
LALQEQLRSQ ASNSSMNDTA DSLDSCTALG ALVGSSKVFF SCMQISMTPM SVSMPTVYAK 240
YQAVATKALT SGVNPMTTPA CPIGDKVLAV YCYAEKVAEI LREYYIEFVK NNTNLLQNAS 300
QMILNQSGLA TSTYDTQAIS NISSLYNYNI VANKSFLKSH LTYLDYIKDK LKGQKDSYLT 360
ERVQTKIIVK 370
<212> Type : PRT
<211> Length : 370
SequenceName : SEQ ID 120
SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :
MTNEAINQQP QTEAAFNPQQ FINNLQVAFI KVDNVVASFD PNQKPIVDKN DRDNRQAFEK 60
ISQLREEFAN KAIKNPTKKN QYFSSFISKS NDLIDKDNLI DTGSSIKSFQ KFGTQRYQIF 120
MNWVSHQNDP SKINTQKIRG FMENIIQPPI SDDKEKAEFL RSAKQAFAGI IIGNQIRSDQ 180
KFMGVFDESL KERQEAEKNG EPNGDPTGGD WLDIFLSFVF NKKQSSDLKE TLNQEPVPHV 240
QPDVATTTTD IQSLPPEARD LLDERGNFSK FTLGDMNMLD VEGVADIDPN YKFNQLLIHN 300
NALSSVLMGS HNGIEPEKVS LLYGNNGGPE ARHDWNATVG YKNQRGDNVA TLINVHMKNG 360
SGLVIAGGEK GINNPSFYLY KEDQLTGSQR ALSQEEIQNK VDFMEFLAQN NAKLDNLSKK 420
EKEKFQNEIE DFQKDSKAYL DALGNDHIAF VSKKDKKHLA LVAEFGNGEL SYTLKDYGKK 480
ADKALDREAK TTLQGSLKHD GVMFVDYSNF KYTNASKSPD KGVGATNGVS HLEAGFSKVA 540
VFNLPNLNNL AITSVVRQDL EDKLIAKGLS PQEANKLVKD FLSSNKELVG KALNFNKAVA 600
EAKNTGNYDE VKQAQKDLEK SLKKRERLEK DVAKNLESKS GNKNKMEAKS QANSQKDEIF 660
ALINKEANRD ARAIAYAQNL KGIKRELSDK LENINKDLKD FSKSFDEFKN GKNKDFSKAE 720
ETLKALKGSV KDLGINPEWI SKVENLNAAL NEFKNGKNKD FSKVTQAKSD LENSIKDVII 780
NQKITDKVDN LNQAVSVAKA TGDFSGVEQA LADLKNFSKE QLAQQAQKNE DFNTGKNSAL 840
YQSVKNGVNG TLVGNGLSKA EATTLSKNFS DIKKELNAKL GNFNNNNNNG LENSTEPIYT 900
QVAKKVKAKI DRLDQIASGL GDVGQAASFL LKRHDKVDDL SKVGLSANHE PIYATIDDLG 960
GPFPLKRHDK VDDLSKVGLS REQKLTQKID NLNQAVSEAK ASHFDNLDQM IDKLKDSTKK 1020
NVVNLYVESA KKVPTSLSAK LDNYATNSHT RINSNVKNGT INEKATGMLT QKNSEWLKLV 1080
NDKIVAHNVG SAPLSAYDKI GFNQKNMKDY SDSFKFSTRL SNAVKDIKSG FVQFLTNIFS 1140
MGSYSLMKAS VEHGVKNTNT KGGFQKS 1167
<212> Type : PRT
<211> Length : 1167
SequenceName : SEQ ID 121
SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :
MKTNGHFKDF AWKKCFLGAS VVALLVGCSP HIIETNEVAL KLNYHPASEK VQALDEKILL 60
LRPAFQYSDN IAKEYENKFK NQTTLKVEEI LQNQGYKVIN VDSSDKDDFS FAQKKEGYLA 120
VAMNGEIVLR PDPKRTIQKK SEPGLLFSTG LDKMEGVLIP AGFVKVTILE PMSGESLDSF 180
TMDLSELDIQ EKFLKTTHSS HSGGLVSTMV KGTDNSNDAI KSALNKIFAS IMQEMDKKLT 240
QRNLESYQKD AKELKNKRNR 260
<212> Type : PRT
<211> Length : 260
SequenceName : SEQ ID 122
SequenceDescription :

Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
MKSKLKLKRY LLFLPLLPLG TLSLANTYLL QDHNTLTPYT PFTTPLNGGL DVVRAAHLHP 60
SYELVDWKRV GDTKLVALVR SALVRVKFQD TTSSDQSNTN QNALSFDTQE SQKALNGSQS 120
GSSDTSGSNS QDFASYVLIF KAAPRATWVF ERKIKLALPY VKQESQGSGD QGSNGKGSLY 180
KTLQDLLVEQ PVTPYTPNAG LARVNGVAQD TVHFGSGQES SWNSQRSQKG LKNNPGPKAV 240
TGFKLDKGRA YRKLNESWPV YEPLDSTKEG KGKDESSWKN SEKTTAENDA PLVGMVGSGA 300
AGSASSLQGN GSNSSGLKSL LRSAPVSVPP SSTSNQTLSL SNPAPVGPQA VVSQPAGGAT 360
AAVSVNRTAS DTATFSKYLN TAQALHQMGV IVPGLEKWGG NNGTGVVASR QDATSTNLPH 420
AAGASQTGLG TGSPREPALT ATSQRAVTVV AGPLRAGNSS ETDALPNVIT QLYHTSTAQL 480
AYLNGQIVVM GSDRVPSLWY WVVGEDQESG KATWWAKTEL NWGTDKQKQF VENQLGFKDD 540
SNSDSKNSNL KAQGLTQPAY LIAGLDVVAD HLVFAAFKAG AVGYDMTTDS SASTYNQALA 600
WSTTAGLDSD GGYKALVENT AGLNGPINGL FTLLDTFAYV TPVSGMKGGS QNNEEVQTTY 660
PVKSDQKATA KIASLINASP LNSYGDDGVT VFDALGLNFN FKLNEERLPS RTDQLLVYGL 720
VNESELKSAR ENAQSTSDDN SNTKVKWTNT ASHYLPVPYY YSANFPEAGN RRRAEQRNGV 780
KISTLESQAT DGFANSLLNF GTGLKAGVDP APVARGHKPN YSAVLLVRGG VVRLNFNPDT 840
DKLLDSTDKN SEPISFSYTP FGSAESAVDL TTLKDVTYIA ESGLWFYTFD NGEKPTYDGK 900
QQQVKNRKGY AVITVSRTGI EFNEDANTTT LSQAPAALAV QNGIASSQDD LTGILPLSDE 960
FSAVITKDQT WTGKVDIYKN TNGLFEKDDQ LSENVKRRDN GLVPIYNEGI VDIWGRVDFA 1020
ANSVLQARNL TDKTVDEVIN NPDILQSFFK FTPAFDNQRA MLVGEKTSDT TLTVKPKIEY 1080
LDGNFYGEDS KIAGIPLNID FPSRIFAGFA ALPSWVIPVS VGSSVGILLI LLILGLGIGI 1140
PMYKVRKLQD SSFVDVFKKV DTLTTAVGSV YKKIITQTSV IKKAPSALKA ANNAAPKAPV 1200
KPAAPTAPRP PVQPPKKA 1218
<212> Type : PRT
<211> Length : 1218
SequenceName : SEQ ID 123
SequenceDescription :

Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
MHQTKKTALS KSTWILLLTA TASLATGLTV VGHFTSTTTT LKRQQFSYTR PDEVALRHTN 60
AINPRLTPWT YRNTSFSSLP LTGENPGAWA LVRDNSAKGI TAGSGSQQTT YDPTRTEAAL 120
TASTTFALRR YDLAGRALYD LDFSKLNPQT PTRDQTGQIT FNPFGGFGLS GAAPQQWNEV 180
KNKVPVEVAQ DPSNPYRFAV LLVPRSVVYY EQLQRGLGLP QQRTESGQNT STTGAMFGLK 240
VKNAEADTAK SNEKLQGAEA TGSSTTSGSG QSTQRGGSSG DTKVKALKIE VKKKSDSEDN 300
GQLQLEKNDL ANAPIKRSEE SGQSVQLKAD DFGTALSSSG SGGNSNPGSP TPWRPWLATE 360
QIHKDLPKWS ASILILYDAP YARNRTAIDR VDHLDPKAMT ANYPPSWRTP KWNHHGLWDW 420
KARDVLLQTT GFFNPRRHPE WFDGGQTVAD NEKTGFDVDN SENTKQGFQK EADSDKSAPI 480
ALPFEAYFAN IGNLTWFGQA LLVFGGNGHV TKSAHTAPLS IGVFRVRYNA TGTSATVTGW 540
PYALLFSGMV NKQTDGLKDL PFNNNRWFEY VPRMAVAGAK FVGRELVLAG TITMGDTATV 600
PRLLYDELES NLNLVAQGQG LLREDLQLFT PYGWANRPDL PIGAWSSSSS SSHNAPYYFH 660
NNPDWQDRPI QNVVDAFIKP WEDKNGKDDA KYIYPYRYSG MWAWQVYNWS NKLTDQPLSA 720
DFVNENAYQP NSLFAAILNP ELLAALPDKV KYGKENEFAA NEYERFNQKL TVAPTQGTNW 780
SHFSPTLSRF STGFNLVGSV LDQVLDYVPW IGNGYRYGNN HRGVDDITAP QTSAGSSSGI 840
STNTSGSRSF LPTFSNIGVG LKANVQATLG GSQTMITGGS PRRTLDQANL QLWTGAGWRN 900
DKASSGQSDE NHTKFTSATG MDQQGQSGTS AGNPDSLKQD NISKSGDSLT TQDGNAIDQQ 960
EATNYTNLPP NLTPTADWPN ALSFTNKNNA QRAQLFLRGL LGSIPVLVNR SGSDSNKFQA 1020
TDQKWSYTDL HSDQTKLNLP AYGEVNGLLN PALVETYFGN TRAGGSGSNT TSSPGIGFKI 1080
PEQNNDSKAT LITPGLAWTP QDVGNLVVSG TTVSFQLGGW LVTFTDFVKP RAGYLGLQLT 1140
GLDASDATQR ALIWAPRPWA AFRGSWVNRL GRVESVWDLK GVWADQAQSD SQGSTTTATR 1200
NALPEHPNAL AFQVSVVEAS AYKPNTSSGQ TQSTNSSPYL HLVKPKKVTQ SDKLDDDLKN 1260
LLDPNQVRTK LRQSFGTDHS TQPQPQSLKT TTPVFGTSSG NLSSVLSGGG AGGGSSGSGQ 1320
SGVDLSPVEK VSGWLVGQLP STSDGNTSST NNLAPNTNTG NDVVGVGRLS ESNAAKMNDD 1380
VDGIVRTPLA ELLDGEGQTA DTGPQSVKFK SPDQIDFNRL FTHPVTDLFD PVTMLVYDQY 1440
IPLFIDIPAS VNPKMVRLKV LSFDTNEQSL GLRLEFFKPD QDTQPNNNVQ VNPNNGDFLP 1500
LLTASSQGPQ TLFSPFNQWP DYVLPLAITV PIVVIVLSVT LGLAIGIPMH KNKQALKAGF 1560
ALSNQKVDVL TKAVGSVFKE IINRTGISQA PKRLKQTSAA KPGAPRPPVP PKPGAPKPPV 1620
QPPKKPA 1627
<212> Type : PRT
<211> Length : 1627
SequenceName : SEQ ID 124
SequenceDescription :

Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
MGYKLKRWPL VAFTFTGIGL GVVLAACSAL NTSNLFPRQN RSKQLIGFTE NNIIKPEAVL 60
KAALAEDNGT ETILRVNFGE ALKSWYQNNK DRNIATRLTI FSENVEDEHD NLLDQKQQAE 120
PINWPIELQK EYDQWGGSES SWKALKLYDR LIADFQSLIF SNIVANVQLT DGSDQFKPTT 180
KDNLDSTSNK IKFVNSKPND PNGEFFANLQ AYLFAQWVVE ENPLPLTQAF FAYQAPKDGL 240
DSLYDQAAIG SALQLGYAFP AFREPNNGQS QGKTTFDPTP NSAQNFGDFI KAVFPEQKNG 300
QTQQSNTSSR TGLFDWQTKW NTNGAANKLL VTKSNLRGAF KGVGLATAII DQYEYLVGGS 360
KTSSLPEVKV DSNKSNQNPL DSFFMEGKDA VAIRSIVSRA KIAMTDQTPG FKVNPAFVKV 420
KQSQQNDTFY QNQRKLSGGQ SGDNNSQGKH HYLQDAVRLT SSQAMAAAST GADSSSGTNV 480
GGSSGGNSVL IPLPRSAALT HTQQQVQQTT STLQTPVYAR GDDGTYALAI DGGDYFLANN 540
KRDFTKQADI LLYRYLQAKS NNFKENGVEF SLNLLESGSL FQTWAQTGLT AKLYGALVAM 600
MGSGQGTQVK GSVQGSSRAA SVSVQTTQQN RQQSTDTQES EVVKLAKSLL KSSADLAKPF 660
TDNPTFKKAL TDIQSEYKDY LAAAGKLSEF KKDLGEVSGL QQAIIDRADK YIQLEKQAQK 720
SAIGLGQPLP YQRASDGSYP ALEKFFIPED SAADGKVKAS ESGSAALVTL KTTDSQKSTN 780
TVKQPDIKPT RENNDKKLKQ LTSDVETKAS SLITKWGATP QIGSQFSEIV SLKSKDNKPQ 840
TNMILALLSD VGIKWTKILN SFKEWFFTNT NDFKNNYDSE KKELKGNEYK DFNDLVKQTL 900
YLRSWQRLTS KEKFGYYKEL GSVKAQAAQS GMVSLSSSAA VANAVASSGM QKSGDQTLLE 960
LGKKAFESEL EASSSDGQYK YLRFLSTLMW LVKDGAKNYK RLLQQAITVG TRAFVSWTVS 1020
YDDTATASAA AAKAQVAVLK TAQATNTQSD NPFNKFVQNP DYVQGSETNW FNDKSTPIKP 1080
DSLLESESTY NFTAEPFDDK TKSQKRSTGG TTNEKHFFGF NGLTTNSPQS VSTASAGLTE 1140
QIFNNFGQLV TSSDKSGALS QYKDKATLKR LIQNTNSDAE LNAFGEVLHR AVNVDTSNLG 1200
RFNSSGEPLI SFDNKKKFLV DVVDKLDDVY FNKFEGYVGQ TKVKMSDSSS SSQGTKTIRK 1260
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<212> Type : PRT
<211> Length : 1300
SequenceName : SEQ ID 125
SequenceDescription :

Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
MKKLLIKPQF WFLTLGGFIS SSVILVACAT PSNSALQTVF KARSNQFFNG EQGSLQNALA 60
TALKDPEANK QFVAAPLLKA LTAWYENNQD KQVTQFFKDT KKSVDEQYNQ AVDKVVSASR 120
NKNLFVQQDL LDSAGGVRNL KSPEVVWTAH 150
<212> Type : PRT
<211> Length : 150
SequenceName : SEQ ID 126
SequenceDescription :

Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
MQQQGETKDQ YNTFGLRLVR NSVGVSVLGL DGFVKFIKGG SGGSNGGSSS AKKIDKEEQK 60
KFLKFRAFQA KIGTFYNTNF AFSFPLNETL KGWFDKHRGL ILANALVKVT LDTKEKASKA 120
LVDAFSSYKN WLSEYTPVGL ATTMISFYFD QMKALNNKLL ERVRSLNQNV NQANPTPWLN 180
GLSAKLPYVN TNGNYEKLNN YFTFLITKVL WPKVGTEDTN VSEEKSKLKT KTEDVNKIRE 240
KILNNIDSKL KTFVQKLKPT LAPRPAYSNV ILLNINNDKV WSAGANWSLA VLLDPKKVNP 300
LSFMLLKQMF DQNSLFKKAK TLFENIQNKA KTSGSGKSGT TTNDDADALS KVIGNYYYNT 360
WAKLTDKSIY GNLKDDKFDD LFKLAPDSSI NEKSFNVDYK AVIEHYRFIY TLEWLVDKNL 420
KNFKDLLKAN LKFGEIAFIA YKNTETQNFS NPQGIFGSYF NYENETNAAK SATQIIDPNS 480
FFYKTTTKPE AKTTQSANTA VMVQNTQMNN QQTNSYGFTG LSTSSGSMLG AATQQAILDQ 540
ITKTSLQQYG SQADLKKIIG ETKNQLLLDR IANQLIALKP NTSGNSGTQK TIAAYFQTDA 600
VGNPTLDFKA KQKLLLDVLD QYKDFFGNNA QAVQRDSGKS GTGNYLTYTD GSDKITYLQF 660
SYKDIDGLSL SSSNGTSSKF ASDVVAALLL FQAAYKGTQQ LALSSINKPQ LPIGDKRIKT 720
GIDLLK 726
<212> Type : PRT
<211> Length : 726
SequenceName : SEQ ID 127
SequenceDescription :

Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :

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TALRDPETNK KFVAAPLLKA LEAWYENNQD KNITQFLKDT KTNVDNQYKT VVDKVVSAPR     120
NKSLFVQQDL LDSSGGSEAT WKARKLFEQL ISDFASRVFQ KNYLSYKENG KVSAGPFLYD     180
TISKNSNWQN IVFDAVNFPE TNDDFFAKIQ SEVFDQWAEY TDPTIISSVT LKYSAPN        237

<212> Type : PRT
<211> Length : 237
      SequenceName : SEQ ID 128
      SequenceDescription :

Sequence
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<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
MINFLFNQMN ALNNKFLERA KALNQNVNQA NPTPWLNGLS AKLPYVRTNG NYEKLNNYFT      60
FLIVKYMWKK VGNEDASLSK DSSINKLKTK TEDVNKIRDK ILEDIQKKVQ EPVKNKLKPT     120
LAPRQTYSNV ILLNVNNDKV WSMGANWALA NLLDTSKINP LSFMLLKQTF DQNDLFKKAK     180
KLFEDIQSKT NGGSSGGMQG SNTSSSEGAD ALSKVIGNYY YNSWAKLTDK SIYGNPKDNK     240
FDDLFKLAFE DSINEKSFNV DYKAVIEHYR FIYTLEWLVN GNLKNFKDLL KANLKFGEIA     300
FIAYKNTETK EFSNPQGVFG SAFNYENETN EVKIAAQNLD PNNFFYKTTT KPEEVKTAQN     360
GASMMVMQQK MQSTMQDSNH YGFTGLNTST SSMLGAATQQ AILDQITKNS LQQYGSQQEL     420
KTLIEKTNNQ LLLDRIASQL SGLNPSTTGN SNNGKGKNIA TYFQLDAIGN PTLSFQQKRK     480
LLLDVLDQYK DFFGTNTQAA QRDSGKGGHG SYSTYQDGSD KITYLQFSYK DIDNLSLSDK     540
GNSKLASDVV AALLLFQAAD KGTQQLALSA IN                                   572

<212> Type : PRT
<211> Length : 572
      SequenceName : SEQ ID 129
      SequenceDescription :

Sequence
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<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
MKKFLRKPQF WLLTLGGFLS TSVILAACAT PSNSALQTVF KARSSQFFNG EQGSLQSALT      60
TALKNPVANK QFIAAPLLKA LEAWYENNED KKITQFLKDT KSNVDSQYTT AVDKVVSASR     120
NKSLFVQQDL LDNAGGSEAT WKAQKLLEQL ISDFASRVFQ KNYLNYKKDG QVSTGPFTYD     180
ELHKEESWKN FEFSAPRFSE TNDDFFAKIQ SQVFDQWVEY TDPTLISQVN YKYSAPSQGL     240
GQIYNREKLK DKLTPSYAFP FFAEEKDIAP NQNVGNKRWK QLVKGEGAIT DNNIGQSGTN     300
SQKTGLLKYR NESNKGDFLD FPLNLSDTNE TKQLVDASNI VDQLEAANLG AALNLKLQVF     360
EQDNDELPQI KELKEDLNNT IVVDKSKDVE KASKTNALFY NDQEGKQQQS DSDPIAGALD     420
DIFAQNTSEG TNLSKLAEQV KKAAATKMEA KTAVLRTNNS KGQQNNYVVL DAAIPTFNST     480
TSKSKNNSAS NEVLVALKSG SINLRQVQQT DQNSYSPIKF RIVRNSTGVT VFGLDGGSYY     540
LKQDSTNKKS VSKQSLTLLT KSSSGNSNKV LRDLDKQKQF LKFRAFQAKT NTFYSTNFAF     600
SFPLNETLKS WFDKHRELIL ANALVNASLD QKDKASKALT EAFNPYKELI KEFAPVALAT     660
IMISFYFDQM KALNNKLLER ARNLNQNVNQ ANPTPWLNGL SAKLPYVNTN GNYEKLNNYF     720
TFLITKTLWP KVGQEETSIS EESNKLKTKT ADVDKIRDKI LENIQTKVND FVKNKLKPAL     780
APRPAYSNVI LLNVNNDKVL SSGANWSLAS LLQSDKVNPL SFMLLKQAFD NNDLFKKAQK     840
LFKDIQEKSS NNGGMQSSST TNSDADALSK VIGNYYYTTW AKLTDKSIYG NPKDNKFDEL     900
FKLAFEASID EKSFNVDYKA VIDHYRFIYT LQWLVDQKLK NFKSLLKTNL KFGEVAFIAY     960
KNTETTNFSN PQGVFGSYFN YENSASEVKE STQTLDPNNF FYKTTTKPTV QAIQQVASLA    1020
LVQKQQMQQN STDHYGFTGL STSTSSMFDA SSRDAILQQI TKTSLQQYGS KDQLKKIIQG    1080
TNNQLLLDRI AVQLSGLNPS TTNGGSGKTI ATYFQVDAVG NPTLDFQAKR KLLLDLLDQY    1140
QNYFGNGAQK SQRDSTPSGT GNYLTYQNGS DKYTYTQFTY QDIDSLSLTT TSGTNNKIAS    1200
DVVAALLLFQ AADKGTQQLA LSAINKPQLN IGDKRIESGL KLLK                      1244

<212> Type : PRT
<211> Length : 1244
      SequenceName : SEQ ID 130
      SequenceDescription :

Sequence
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<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
MVGSGAAGSA SSLQGNGSNS SGLKSLLRSA PVSVPPSSTS NQTLSLSNPA PVGPQAVVSQ      60
PAGGATAAVS VNRTASDTAT PSKYLNTAQA LHQMGVIVPG LEKWGGNNGT GVVASRRDAT     120
STNLPHAAGA SQTGLGTGSP REPALTATSQ RAVTVVAGPL RAGNSSETDA LPNVITQLYH     180
TSTAQLAYLN GQIVVMSSAR VPSLWYWVVG EDQESGKATW WAKTELNWGT DKQKQFVENQ     240
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LGFKDDSNSD SKNSNLKTQG LTQPAYLIAG LDVVADHLVF AAFKAGAVGY DMTTDSNAST 300
YNQALVWSTT AGLDSDGGTR LW 322
<212> Type : PRT
<211> Length : 322
SequenceName : SEQ ID 131
SequenceDescription :

Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
MPVFLKLTHT IRKVLRVARL SRLALLSLTA VIFSGCANIN LISAVGSSSV QPLLSKLSSH 60
YVLNHNDKDN LVEISVQAGG SSAGVKAITK GLADIGNVSK NTKSYAEENK QLWMDKKLKT 120
ITLGKDAIAV IYKAPSEFKG KLVLTKDNLN DLYDLFAGSK SVDINKFVEN GQTTKNSNHN 180
LIGFPRTGGA FASGTAEAFL KFSGLTQTKT LDKDSKEILE GQRNYGPNAR PTSETNIEAF 240
NTFVTTLRQP NLYGMVYLSL GFVNNNMNLI KSEGFEVLKV KYDNNAVTPS SQAVSSNTYK 300
WVRPLNSVVS LLPKQKTLPS IQRFFNWLLF SNNSEIKKIY DDFGVLELTA DEKKKMFKTG 360
NAEMSNIANF WVDDYSLNNQ TFGAL 385
<212> Type : PRT
<211> Length : 385
SequenceName : SEQ ID 132
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MSFAVLPPEI NSARLYVGAG LAPMLDAAAA WDGLADELGS AAASFSAVTA GLAGSSWLGA 60
ASTAMTGAAA PYLGWLSAAA AQAQQAATQT RLAAAAFEAA LAATVHPAII SANRALFVSL 120
VVSNLLGQNA PAIAATEAAY EQMWAQDVAA MFGYHAGASA AVSALTPFGQ ALPTVAGGGA 180
LVSAAAAQVT TRVFRNLGLA NVGEGNVGNG NVGNFNLGSA NIGNGNIGSG NIGSSNIGFG 240
NVGPGLTAAL NNIGFGNTGS NNIGFGNTGS NNIGFGNTGD GNRGIGLTGS GLLGFGGLNS 300
GTGNIGLFNS GTGNVGIGNS GTGNWGIGNS GNSYNTGFGN SGDANTGFFN SGIANTGVGN 360
AGNYNTGSYN PGNSNTGGFN MGQYNTGYLN SGNYNTGLAN SGNVNTGAFI TGNFNNGFLW 420
RGDHQGLIFG SPGFFNSTSA PSSGFFNSGA GSASGFLNSG ANNSGFFNSS SGAIGNSGLA 480
NAGVLVSGVI NSGNTVSGLF NMSLVAITTP ALISGFFNTG SNMSGFFGGP PVFNLGLANR 540
GVVNILGNAN IGNYNILGSG NVGDFNILGS GNLGSQNILG SGNVGSFNIG SGNIGVFNVG 600
SGSLGNYNIG SGNLGIYNIG FGNVGDYNVG FGNAGDFNQG FANTGNNNIG FANTGNNNIG 660
IGLSGDNQQG FNIASGWNSG TGNSGLFNSG TNNVGIFNAG TGNVGIANSG TGNWGIGNPG 720
TDNTGILNAG SYNTGILNAG DFNTGFYNTG SYNTGGFNVG NTNTGNFNVG DTNTGSYNPG 780
DTNTGFFNPG NVNTGAFDTG DFNNGFLVAG DNQGQIAIDL SVTTPFIPIN EQMVIDVHNV 840
MTFGGNMITV TEASTVFPQT FYLSGLFFFG PVNLSASTLT VPTITLTIGG PTVTVPISIV 900
GALESRTITF LKIDPAPGIG NSTTNPSSGF FNSGTGGTSG FQNVGGGSSG VWNSGLSSAI 960
GNSGFQNLGS LQSGWANLGN SVSGFFNTST VNLSTPANVS GLNNIGTNLS GVFRGPTGTI 1020
FNAGLANLGQ LNIGSANLGD FNLGSGNVGS FNVFSGNQGS YNIGPANLGN YNIGFANLGN 1080
YNIGFGNAGD FNQGFANTGN NNIGFANTGN NNIGIGLSGD NQQGFNFAGG WNSGTANIGL 1140
FNSGTNNVGI GNSGTGNWGI GNSGSGNTGI GNTGSTNTGF FNTGIVNTGV ANAGSYNTGW 1200
YNTGDTNTGI ANLGDFNTGF YNTGNFSTGF ANQGDIATGA FITGDMGNGA FWRGDQQGLF 1260
SAGYRVHVPE IPAHVTVEVP VNIPITASFT NTVYSGITLE QINFGFTIDI AGIPLLAGAI 1320
SKAVLPPITG TGPAITVNIG DPGGSTAIRI PATASVGPFD VTFVNIAATT GFFNATTDPS 1380
SGFFNGGPGT VSGIANIGAN ISGFQNVANS ATSGFNNYGS LQSGLANLGD TVSGVFNTGI 1440
GAPANVSGMF NIGSNLAGFF HDQATGMSMF NLGLGNIGQF NVGFSNVGDS NAGLANIGSF 1500
NLGSGNLGSF NVFGGNQGSY NIGPANLGNY NIGLGNLGSY NFGFGNAGDF NLGFANTGNN 1560
NIGFANTGNN NIGIGLSGDN QQGFNFAGGW NSGSGNSGLF NSGTNNIGLF NSGTGNIGIG 1620
NSGTGNWGIA NTGDTNTGIF NTGDVNTGLL NAGNVNTGIF NTGHYNTGSF NAGSFNTAGF 1680
NPGSYNTGYL NTGSYNTGLA NSGDVNTGGF ITGNYSNGFW WRGDYQGLAG ISQTITVPDT 1740
AVPVKLHVPI FLDIPVTGTL GTFTVHGFRF PEITGDIFLI GIPFNAATLD AFSFPNISIV 1800
LPNIGINLGS GPDPLIDIAG TGGLLPIKIP LIDIPAAPGF GNSTTTPSSG FFNAGTGTVS 1860
GVGNVGSNSS GFFNLTSGSS GISGVQNFGE LISGGFNFGN TVSGLVNAST LGLSMPANLS 1920
GGGNVGATVA GFVNNTQILN LGFGNVGSGN VGHGNIGDSN VGLGNLGNAN VGHGNIGSFN 1980
VFSGNRGSYN IGPANLGNYN IGLGNLGSYN FGFGNAGDFN LGFANSGSNN IGFANTGNNN 2040
IGIGLSGHNQ QGFGSWNSGT ANTGLFNSGT NNIGLFNSGT GNIGIGNSGI GNTGIGNPGV 2100
GNTGLGNSGT GNWGLWNPGT GNMGVANVGT YNTGGYNVGS TNTGIANVGI ANTGSYNTGS 2160
TNTGSFNDGD FNTGFYNTGD YNTGFYNTGD VNTGAFIGGN FSNGAFWQSD HQGQWGAHYA 2220
ITVPQIPLLN FSLNIPVNIP IHLDFGTLAV NGFQIPAITL RALGVTHFSV GPIIVPRIAG 2280
TLPVIDINIG DPGGSSSIPI TITSGAGPVV IPLLDIPPAP GFGNSTTGPS SGFFNSGTGS 2340
SSGFGNVGAN NSGFWNTAFA GIGNSGLQNF GSLQSGWANL GNTVSGFYNT SAADFATPAN 2400

LSGLSNVGAD LTGVLRGPNG STFNAGLANL GQFNVGSANL GSANLGSANL GSANLGNSNV 2460
GFGNIGNANI GGANIGDFNV GIANTGPGLT AAVNNIGIGN TGNYNIGVGN TGNYNIGFGN 2520
TGNNNIGIGL SGDNQIGFGP LNAGIANMGL FNLGDNNFGM ANAGNFNQGI ANTGNNNIGL 2580
FNTGNNNVGI WLTGDGLSGF SSLNSGAGNT GFFNSGTANT GLFNSGTGNT GLFNSGTGNV 2640
GIGNMGTGGF GVGLSGDSQV GIGGTNSGSF NIGLFNSGTG NVGIGNSGTG NVGIGNTGTG 2700
NTGIGNSGNY NTGLLNAGLV NTGIANPGNH NTGLFNIGTF NTGIANPGHY NTGSYNTGSY 2760
NTGMANAGDY GTGAFITGSM NNGLLWRADR QGLLAANYTI TIERPAAFLN VDIPVNIPIT 2820
GDITNVSIPA ITFPRIDASG SVDIGILSGT VLAPVGPITL HGGDASAPLD TPIEIDFGPS 2880
PAINLNIGKP DGSTVINIVG GAGAGPISIP IIDLRPAPGF FNATTGPSSG FLNWGAGSAS 2940
GLLNFGNNSG LYNFATSSMG NSGFQNYGSL QSGWANLGNS ISGIYNTGLG APANVSGLLN 3000
IGTNLAGWLQ NGPTETTFSV GLANLGFWNL GSANIGNYNL GSANIGVYNL GSANIGDFNL 3060
GSANIGDFNL GSANIGSSNI GFGNVGPGLT AAIGNIGFGN TGNGNIGIGN TGTGNIGFGN 3120
TGNGNIGIGL TGDTMTGFGG WNSGTGNIGL FNSGTGNIGF GNSGTGNWGI GNSGDYNTGI 3180
GNTGSTNSGF FNTGLVNTGI GNSGDYNTGL FNAGNTNTGS FNPGDYNTGG FNPGNYNTGY 3240
FNPGNSNTGI ANSGDVNTGA FNSGNYSNGF FWRGDYQGLG GFAYQSAVSE IPWSYDRFQH 3300

<212> Type : PRT
<211> Length : 3300
SequenceName : SEQ ID 133
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
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LRDGAGTAAI NLGLANHGNL NVGFASLGGF NFGGATIGHN NVGIGNTGIF DVGLANLGSY 120
NIGFGNLGDD NLGFGNFGSY NIGFGNVGND NLGFANAGGG NIGFANTGSN NVGFGNTGSN 180
NVGIGLTGNG QIGFGSFNSG SGNIGLFNSG SNNIGFFNSG SGNFGIANSG SFNTGIGNTG 240
NTNTGLFNSG DVNTGAFNPG SFNTGSFNTG SFNTGGFNPG NTNTGYLNIG NYNTGIANTG 300
DVDTGAFITG NYSNGLFLSG DYQGLVGLNL VIDMPLPISL GVNIPIDIPI TASAGNITLM 360
GVTIPPTGDI VLSSIAGQRA HFGPITIPNI TVVGPTTTVA IGGPNTAITI TGGGAIRIPL 420
ISIPAAPGFG NSTTNPSSGF FNTGAGGASG FGNFGGANSG FWNLASATSG ASGLLNVGAL 480
GSGLANVGTT VSGFYNTSTS DLATPAFNSG LANISTSIAG LLRDSTGTMV LNLGLANHGT 540
LNVGIANLGD YNIGFANLGS ANFGSANIGG NNIGGANTGI FDIGLANLGS YNIGFGNFGD 600
DNLGFGNLGS YNVGFGNLGN DNLGFANTGS NNIGFANTGS NNIGIGLTGD GQIGFGSLNS 660
GSGNIGLFNS GSGNIGFFNS GNGNVGIGNT GTANFGLGNT GSTNTGFFNS GDVNTGIGNT 720
GSFNTGSFNP GDSNTGDFNP GSYNTGLGNT GDVDTGAFIS GSYSNGFLWS GNYQGLIGLH 780
AALAIPEIAL TFGVDIPIHI PINIDAGVVT LQGFSIVAAE NNIDFTPIII PTINITLPTA 840
AITVGGPTTS IGITASAGIG SITIPIIDIP ATSGFGNSTT SPSSGFFNSG AGSASGFLNV 900
VAGASGISGY LNVGALGSGV TNVGHTVSGF YNASALDLVT PAFASGLMRD GMGTMTLNLG 960
LANLGSNNAG FGNTGIFDVG VANLGNYNIG FGNFGDDNLG FANLGSYNIG VANTGSNNIG 1020
FANTGSNNIG IGLTGTGQIG IGALNSGSGN IGLFNSGDGN IGFFNSGTGN FGIGNTGTGN 1080
FGIGNSGSTS TGLFNSGDGN TGGFNPGNFN TGNFNTGSFN TGGFNAGNTN TGHFNTGNYN 1140
TGIANTGDVS TGAFISGNYS NGILWRGDYQ GLIGYSYALT IPEIPAHLDV NIPIDIPITG 1200
SFTDLVVDNF TIPIIGFESF AFSFHIHTEP DIGPIIVPSF VLSVPTFAIA VGGPTTAINI 1260
SATAGLGPIT IPIIDIPAAP GIGNSTTSPS SGFFNTGAGT ASGFGNVGGN TSGLWNLASA 1320
ASGVSGLLNV GALGSGVANV GNTISGIYNT SPLDLGTPAF GSGLANIAGL LQGGAGTTIL 1380
DLAGLGNLNV GLANLGGSNF GIGNTGIFNV GFANVGNHNI GLANLGNYSV GFANSGNYHI 1440
GIANTGSANI GFANTGSGNI GIGLTGTGQI GFGSFNSGSH NIGLFNSGDG NVGFFNSGTG 1500
NVGIGNTGTA NFGIANSGSF NTGLGNTGST NTGLFNPGNV NTGVGNTGSI NTGSINTGSF 1560
NTGSTNTGSF NLGDHNTGSF NSGDYNTGYF NAGDYNTGVA NTGNVNTGAF ISGNYSNGFF 1620
WRGDYQGLIG LSTTITIPEI PYRYDLSVPI DIPITGTVVA TTPNSFTIPG FQIRVLLGPA 1680
AVLVNEMIGP ITIDVNQVIA IDSPIQQTIS MVGTGGFGPI PIGISIGGTP GFGNSTTGPS 1740
SGFFHTGAGH VSGFGNFGAG NMSGSGNFGA GNSGFFNAGG LGNSGLLNFG ALQSGLANLG 1800
NTISGVYNTS TLDLATPAFG SGIANIGANL AGLFLDNTGN LTLNFGVANQ GGLNAGIGNL 1860
GSVNIGFVNT GDSNLGIGNL GDLNFGGVNI GGNNIGIANT GIFDIGLANL GSYNIGLANL 1920
GDDNLGFGNA GSYNIGFANF GSDNLGFANT GSYNIGFANT GNNNIGVGLT GNGQIGIGSL 1980
NSGSNNIGLF NSGSGNIGFF NSGTGNVGIF NTGTGNFGLA NSGGFNTGIG NAGSTNTGVF 2040
NPGDLNTGSF NPGSFNTGGF NPGSGNTGYL NTGDYNTGVA NTGDVDTGAF ITGSYSNGFL 2100
VSGDYQGLIG LPLLGIPVTP GYFNLTGGPS SGFFNSGAGS VSGFVNSGAG LSGYLNTGAL 2160
GSGVANVGNT ISGWLNASAL DLATPGFLSG IGNFGTNLAG FFRG 2204

<212> Type : PRT
<211> Length : 2204
SequenceName : SEQ ID 134
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
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EYQAISAQVA AYHQRFVQAL STGAGAYASA EAAAAEQIVL GVINAPTQAL LGRPLIGDGA 120
NATTPGGAGG AGGLLFGNGG AGAAGAPGQA GGPGGPAGLW GNGGPGGAGG SGGGTGGAGG 180
AGGWLFGVGG AGGVGGAGGG TGGAGGPGGL IWGGGGAGGV GGAGGGTGGA GGRAELLFGA 240
GGAGGAGTDG GPGATGGTGG HGGVGGDGGW LAPGGAGGAG GQGGAGGAGS DGGALGGTGG 300
TGGTGGAGGA GGRGALLLGA GGQGGLGGAG GQGGTGGAGG DGVLGGVGGT GGKGGVGGVA 360
GLGGAGGAAG QLFSAGGAAG AVGVGGTGGQ GGAGGAGAAG ADAPASTGLT GGTGFAGGAG 420
GVGGQGGNAI AGGINGSGGA GGTGGQGGAG GMGGSGADNA SGIGADGGAG GTGGNAGAGG 480
AGGAAGTGGT GGVVGAAGKA GIGGTGGQGG AGGAGSAGTD ATATGATGGT GFSGGAGGAG 540
GAGGNTGVGG TNGSGGQGGT GGAGGAGGAG GVGADNPTGI GGTGGTGGKG GAGGAGGQGG 600
SSGAGGTNGS GGAGGTGGQG GAGGAGGAGA DNPTGIGGAG GTGGTGGAAG AGGAGGAIGT 660
GGTGGAVGSV GNAGIGGTGG TGGVGGAGGA GAAAAAGSSA TGGAGFAGGA GGEGGAGGNS 720
GVGGTNGSGG AGGAGGKGGT GGAGGSGADN PTGAGFAGGA GGTGGAAGAG GAGGATGTGG 780
TGGVVGATGS AGIGGAGGRG GDGGDGASGL GLGLSGFDGG QGGQGGAGGS AGAGGINGAG 840
GAGGNGGDGG DGATGAAGLG DNGGVGGDGG AGGAAGNGGN AGVGLTAKAG DGGAAGNGGN 900
GGAGGAGGAG DNNFNGGQGG AGGQGGQGGL GGASTTSINA NGGAGGNGGT GGKGGAGGAG 960
TLGVGGSGGT GGDGGDAGSG GGGGFGGAAG KAGGGGNGGR GGDGGDGASG LGLGLSGFDG 1020
GQGGQGGAGG SAGAGGINGA GGAGGNGGDG GDGATGAAGL GDNGGVGGDG GAGGAAGNGG 1080
NAGVGLTAKA GDGGAAGNGG NGGAGGAGGA GDNNFNGGQG GAGGQGGQGG LGGASTTSIN 1140
ANGGAGGNGG TGGKGGAGGA GTLGVGGSGG TGGDGGDAGS GGGGGFGGAA GKAGGGGNGG 1200
VGGDGGEGAS GLGLGLSGFD GGQGGQGGAG GSAGAGGING AGGAGGTGGA GGDGAPATLI 1260
GGPDGGDGGQ GGIGGDGGNA GFGAGVPGDG GDGGNAGFGA GVPGDGGIGG TGGAGGAGGA 1320
GADGDPSIDG GQGGAGGHGG QGGKGGLNST GLASAASGDG GNGGAGGAGG NGGDGDGFIG 1380
GSGGTGGTGG DAGVGGLANT GGTAGNAGIG GAGGRGGDGG AGDSGALSQD GNGFAGGQGG 1440
QGGVGGNAGA GGINGAGGTG GTGGAGGDGQ NGTTGVASEG GAGGQGGDGG QGGIGGAGGN 1500
AGFGAGVPGD GGIGGTGGAG GAGGAGADGD PSIDGGQGGA GGHGGQGGKG GLNSTGLASA 1560
ASGDGGNGGA GGAGGNGGDG DGFIGGSGGT GGTGGDAGVG GLANTGGTAG NAGIGGAGGR 1620
GGDGGAGDSG ALSQDGNGFA GGQGGQGGVG GNAGAGGING AGGTGGTGGA GGDGQNGTTG 1680
VASEGGAGGQ GGDGGQGGIG GAGGNAGFGA GVPGDGGIGG TGGAGGAGGA GADGDPSIDG 1740
GQGGAGGHGG QGGKGGLNST GLASAASGDG GNGGAGGAGG NGGAGGLGGG GGTGGTNGNG 1800
GLGGGGGNGG AGGAGGTPTG SGTEGTGGDG GDAGAGGNGG SATGVGNGGN GGDGGNGGDG 1860
GNGAPGGFGG GAGAGGLGGS GAGGGTDGDD GNGGSPGTDG S 1901
<212> Type : PRT
<211> Length : 1901
SequenceName : SEQ ID 135
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
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EYQAISTQVA AFHDRFAQTL SAAVGSYVSA EATNAAPLAT LEHNVLNALN APTQALLGRP 120
LIGDGAAGAP GTGQAGGAGG ILWGNGGAGG SGAPGQVGGA GGAAGLFGTG GAGGAGGAGA 180
AGGAGGSGGW LLGNGGVGGA GGQSLLGGAT GGAGGNAGLF GVGGTGGPGG PGGPGGVGGT 240
GGAGGLGGTL YGAGGHGGAG GPGPIGGVGG HGGVGGAAGL LGVGGHGGAG GHGAEGVAGA 300
AGEDLSPHGT SGGVGGDAGD GGTGGRGGWL AGAGGAGGAG GVGGTGGAGG AGFSRALIVA 360
GDNGGDPGAG GAGGTGGAGS TIGAHGAAGA SPTSGGNGGA GGNGAHFSSG GKAGGNGGAG 420
GAGGLVGNGG AGGAGGNGAP GAPPSGGDPN GGGGGAGGAG GKGGDGGAQA GDGGAGGAGG 480
KGGNGGNGAT GATGLNGLGA GADGTDGGKG GNGGAGGGGG AGGQGGKALA ATHQDGSMGA 540
GGAGGNGGAG GMGGDGGNGA KGTFDNGGDG VGGNGGNGGS RGIGGAGGIG GAGSTAGADG 600
ARGATPTSGG NGGTGGNGAN ATVAGGAGGA GGKGGNGGLV GNGGAGGKGG DGMAGVAGSS 660
PTTAGESGTS GQNGGAGGAG GAGGRGGDFG GDGGTGGAGG NGANGANATT PGAKGGDGGH 720
GGPGAQGGNG GQGGPGGLAG NLFGQNGIQG VGGSGGKGGA GGLAGDGGNG ANGNFAFGDG 780
NGGHGGNGGN PGAGGQGGSG GAGSTPGAKG AHGFTPTSGG DGGDGGNGGN SQVVGGNGGD 840
GGNGGNGGSA GTGGNGGRGG DGAFGGMSAN ATNPGENGPN GNPGGNGGAG GAGGAGLNGG 900
NGGAGGNGGL GGFGGNGAAG ANGVAVGAPG QPGGAGGHGG AGGNGGAGGN GGQGVVSDGA 960
GGAGGAGGDG GAPGDGANGG NGQGAGAFAG GGGGRGGDGG NAGNAGAGGP GGTGSTAGKA 1020
GPAGSILHDG GNGGHGGHGA ASGGNGGPGG HGGNGGNGGT GANGGNGGIG GTGGAGSTGA 1080
KGVLGTNEGD GGDGGRGGNG GRGGNGGQGL TGAGGNGGTG GTPGNGGNGG NGASGDLVTS 1140
PGDGGGGGRG GDAGRGGDAG LGGSSGPGGT PGDWGTGGTG GTGGTGGQGA NGGLTGGRGG 1200
TGGNGGNGNT GGTGGAGGTG GTGHNGSQPG MGGNGGAGGF GGNGFAGVGG RGGMGGSGGT 1260
GGTGDAGPFG TGTGGTGGHG GQGGGGGFSI LLGLGGLGGL GSPGSIATGT AGGAGGGGGF 1320

GGLGGGEFV 1329
<212> Type : PRT
<211> Length : 1329
SequenceName : SEQ ID 136
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
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EYQALSAQAA AFHDQFVHTL TAAARWYTAT EIANAAAMRV VLGAVNAPTQ TLLGRPLIGD 120
GAHGTAPGQP GGAGGLLFGN GGNGAAGAVG QVGGAGGAAG LFGIGGAGGA GGAGAPGGTG 180
GTGGWLAGGG GVGGMGGAGG GAGGAGGNAG LFGNGGAGGA GGAGGGAGGA GGNAGWFGHG 240
GAGGVGGVGA AGANGATPGQ DGAAGVAGSD DGAGGDGLAG SDGGDGGAGG VGGNGGRGGW 300
LLGNGGAGGV GGVGGAGGAG AAGGAGGAGA TGINGPAGIS AAGGDGGAGG NGGAGGNGGV 360
GGAGGAGGSA GLLGYVGRAG DGGAGGGGGL GGAPGDGGAG GNGGSWLAAG DGGAGGHGGD 420
PGLGGAGGAG GASGGAGARA GANGLAAGND GPVSGGNGGK GGNGAHAPVA GGHGGNGGAG 480
GNGGLVGDGG AGGHGGDGAA GAGYADMTAI FLGSSGTPGE DGGNGGAGGA GGAGGAHAGD 540
GGAGGAGGNG GAGGAGGNGA HGFNAVLVSD GGNGGDGGAG GRGGDGGAGG AGGDAPAGRA 600
GSQGVGGDGG AGGAGGAPGN GGSGGRGDMA FKDGDGGAGG DGGDPGAGGK GGAGGAGATE 660
GVTGATGATV HSGGNGGKGG NGADATVAGA NGGKGGAGGN GGLVGDGGAG GDGGSGAAGA 720
NGANVGEDGA DGTLSGQPGE GSEANGGQGG VGGGGAGGAG GDGGAGSSAL GSGGNGGRGD 780
AGQAGGAGGA GGAGGAGGSV SGDGGPGGKG GAGGAGGAGA SGGGGGKGAS GADSAEAVGG 840
AGGKGGDGGV GGVGGDGGPG GDGGAGGAAP AGQVGSHGVG GVGGDGGLGG AGGNGGDGGH 900
GSDGGDGGDG GDPGAGGLGG LGGDSGNGTR AASGVDASDH GPGSGGNGGN GGNGAQASVA 960
GGAGGNGGDG GNAGRVGDGG AGGNGGDGAA GANGANSGAP GSDALALGQP GGNGGQGDAG 1020
QAGGAGGAGG AGGAGGSVSG DGGAGGNGGA GGNGGVGASG GAGARGANGI DSIGGTGGAG 1080
GGGGDGGAGG VGGHGGDGGV GGAAPSGTVG SHGTGGVGGD GGLGGAGGVG GAGGNGGIGI 1140
TVGGAGGAGG NGGDPGAGGR GGLGGDSGNG TSAANGVDAS KHGPLTGGDG GVGGNGAKAA 1200
AAGGDGGQGG DGGNAGLFGD GGAGGDGADG TAAEALGGDG GAGGAGGKGG DAGDIGDGGD 1260
GGKGGDGAHG ALGGLTVAGG NGGAGGAGGA GGAGGAFLGD GGNGGAGGQG GAGRGGSPGG 1320
GGGVGGHGGA GGDAGMNGGG GTGGQGGNGA AGGAGWSPDS DLKGFDGFDG GSGGAGGDGG 1380
AGGAGGTQTG DGGDGGAGGL GGAGGVGGNG VDGFDINETT GRDGGDGGDG GYGGWGGAGG 1440
NGGAGGSAPA GEVGNRGVGG DGGDGGSGGD AGNGGLGGDG FTYLADFDGE PGGDGGDGGD 1500
GGWGRPGGQG GFGSTSGAHG KAGFGAPGGD GGDGGNGGHG GDGNGSFADA GDGGPGGNGG 1560
NGGLGGAGRD GGAPGGDGGD GGTGGSGGFG APPPRSIGGG DGGDGGRGGD GGRGAGGLTS 1620
GGVGSSGESG GSGNGRGDPG SGGSGGEGGE GGPSISVNVT 1660
<212> Type : PRT
<211> Length : 1660
SequenceName : SEQ ID 137
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MSFVLVSPET VAAVATDLKR IGASLAHENA SAAASTTAVV SAAADEVSTA VAALFSQHAQ 60
GYQAAAAQVA AFHSRFVQAL TAGAGAYAFA EAANASPLQS AMGAVSASAQ TLLSRPLIGN 120
GANATTPGGN GGDGGWLFGS GGNGAPGAAG QSGGNGGSAG LWGNGGAGGA GGSGGAAGGN 180
GGNGGWLFGA GGTGGIGGTG APGAMGGTGG NGGNGALLIG GGGLGGAGGM GGTGGGTGGT 240
GGNGGNGALL IGAGGVGGAG GIGGQGTGAG GAAGAGGTGG NGGAGGLFMN GGDGGAGGQG 300
GDGAAGDAAA SAGGTGGKGG QGGDGGTGGA GGAGPVLFGH GGAGGMGGQG GTGGMGGAGG 360
DGTTVIAAGT GGEGGTGGAA GAGGAAGARG ALTSGGLAGG VGAGGTGGTG GTGGNGADAA 420
AVVGFGANGD PGFAGGKGGN GGIGGAAVTG GVAGDGGTGG KGGTGGAGGA GNDAGSTGNP 480
GGKGGDGGIG GAGGAGGAAG TGNGGHAGNT GDGGDGGTGG NGGNGTGGVN GADNTLNPDT 540
PGGAGEPGGA GGAGGAGGAA GGPGGTGGTG GNGGNGGNGG NGGNGGNGGN GGNAGNNSTN 600
APVGGEGGAG GDGGAGGAGG AANGGTAGSQ GTGGVGGDGG AGGNGGGGKA GTGNSGNFGV 660
DGEAGFSGGA GGNGGVGGAA GANGGTGGSG GNGGDGGAGG IGGAGGNGIP GTGTEPAGGT 720
GAKGGDGGDG GAGGAGGNAG GAGGQGGNAG QGGAGGAGGN AVIPGDGVGK APHGDAGGSG 780
GDGGKGGQGG SGGTGGSGAP IGGGAGGTGG SGGHAGKGGA GGIGAQGTTI TVPGNGGNAG 840
DGGNGGNAGA GGNGGSGDFG GNTTSGASGS GGNGGNAGTA GSGGAGGTGG TGLSGGNGGN 900
GGNGGNGGDG GNGAHGTVGA QFVPATSLPT PNGGAGGNGG TGSNGGAPGP AGAPGPTTGG 960
NAGSQGIGGD GGNGGDGGKG GDGADAVNVV FMPTEPQAAT GTAGSAGDPT GGNGGPGTPG 1020
SPMVAPPPPT PITQVQQGGD GGAGGTGSTN ANDGTATGGK GGEGGVGSIL GGPGGNGGTG 1080
GNASATGTNG VANAGNGGKG GDGGQFGAGG NGGAGGSVTD GSAGSTAGNG GNGGNATNGT 1140
IAGQPAGGNG SAGGKGGDGG NIAAGATGTA GNGGNGGNGN DGAVNAGTGG SGGNGGNAGG 1200

GGANGGDGGA GGAGGAGGRG GKGIDGGPGG DGGNGGSNNG TGAGGNGGNG GTGGVGSVGA 1260
AGGDGGNGGT GGPAGPGGTA GNGGSGGTGG AGGDGGTGGD GGNGVIAGGG GTGGNGGASG 1320
AGGAGGTGGP AGNGNAGGNG GTGGASEDGD NGNAGSGATG GTGGNGGTGG DGGAAGLGGV 1380
A 1381

<212> Type : PRT
<211> Length : 1381
SequenceName : SEQ ID 138
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MSFVIATPEM LTTAATDLAK IGSTITAANT AAAAVAKVLP ASADEVSVAV AALPGTHAQE 60
YQTVSAQVAT FHDRFVQTLS AAASSYVAAE AVNVEQSLLA AVNAPTQALP GRPLIGNGAD 120
GSPGTGQAGG PGGILYGNGG NGGSGAPGQR GGAGGAAGLI GNGGNGGAGG VGTTGGAGGH 180
GGAGGWLYGN GGAGGFGGAG AVGGNGGAGG TAGLFGVGGA GGAGGNGIAG VTGTSASTPG 240
GSGTAGGAGG IGGNGGAGGA GGVLMGNGGN GGAGGEGGPG GAGGAGASGA HATNLGADGQ 300
AGGNGGNGGA GGTGGVGGPG GGHGLLGLGG SHGAGGAGGS GGDGGAPGDG GNGATGTWGH 360
NLGAGGTGGN GGNPGAGGAG GAGGASVGGS AHGANGAPGT TSTSGGNGGD GGKGADAISS 420
GQTGANGGRG GDGGQVGNGG AGGAGGRGGA GGLGFGSEAP GRPGGAGGTG GAGGNGGTQA 480
GDGGTGGAGG AGGDGGSGGA GSIGFNASAP GAAGSPGGNG GNGGPGGAGG EGGAGGLALA 540
ASGQNGSQGA GGDGGAGGNG GTPGNGGHGA AGALGVNGGV GGAGGHGGDP GVGGAGGQGG 600
SGSTPGANGA PGNTPTSGGN GGNGGRGADA TGFGQTGASG GRGGDGGLVG NGGAGGAGGN 660
GSKGLPGLGR LGNPGLDGGT GGNGGAGGSG GAWAGNGGTG GAGGTGGVGG TGGSGSDGVN 720
GSSAGADGHP GGTGGVGGTG GKGGDGGDGG AAPNGVAGSQ GPGGAGGDGG TGGVGGNGGR 780
GIDGADGATA GARGQDGGAG GAGGKGGRGG TGGPGGAGPA GTTGSQGAGG NGGSGGTGGD 840
PGDGGNGANG SVPTNNGIGG NGGNGGNAGP SGAGGSGGAG STFGATGSSS SIHVNGGNGG 900
NGGNGDHALS GNGAAGGNGG NGGNGSLRGS GGAGGHGGNG GNASRGMGGD GGTGGAGGNA 960
GQIGNGGAGG NGGDGGTGSD GNPGAITGSG GRGGDGGVGG QGGSVAGDGA DGGRGGAGGT 1020
GGTGLRGTTG ATGATGTFDA GADGHGGNGG TGGVGGTGGA GGGGGNGGAG GKALSPTGNN 1080
GSQGAGGDGG AGGAGGTGGT GGDGGRGAHG TLFSSLAGTG GTGGNGGTGG TGGTGGAGGA 1140
GGTGSTLGAT GATGAAGRAG NGGVGGSGGL GSAFGPGGTG GMGGAGGTST VSAGGDGGRG 1200
GPGGDGLDAS SGGNGGDGGH GGDGFRTAGA GGRGGDGGKG ADPGGLFPIP GAGGKGGTGG 1260
TGGTAHLGPL AIIGQSGQPG QFGSPGADGR GGAGGAGGGG GAGGSF 1306

<212> Type : PRT
<211> Length : 1306
SequenceName : SEQ ID 139
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
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QRSATQAAAL VAEFEAVRAA MVQPALVAAN RSDLVSLVFS NFFGQNAPAI AAIEAAYEQM 120
WAIDVSVMSA YHAGASAVAS ALTPFTAPPQ NLTDLPAQLA AAPAAVVTAA ITSSKGVLAN 180
LSLGLANSGF GQMGAANLGI LNLGSLNPGG NNFGLGNVGS NNVGLGNTGN GNIGFGNTGN 240
GNIGFGLTGD NQQGFGGWNS GTGNIGLFNS GTGNIGIGNT GTGNFGIGNS GTSYNTGIGN 300
TGQANTGFFN AGIANTGIGN TGNYNTGSFN LGSFNTGDFN TGSSNTGFFN PGNLNTGVGN 360
TGNVNTGGFN SGNYSNGFFW RGDYQGLIGF SGTLTIPAAG LDLNGLGSVG PITIPSITIP 420
EIGLGINSSG ALVGPINVPP ITVPAIGLGI NSTGALVGPI NIPPITLNSI GLELSAFQVI 480
NVGSISIPAS PLAIGLFGVN PTVGSIGPGS ISIQLGTPEI PAIPPFFPGF PPDYVTVSGQ 540
IGPITFLSGG YSLPAIPLGI DVGGGLGPFT VFPDGYSLPA IPLGIDVGGG LGPFTVFPDG 600
YSLPAIPLGI DVGGGLGPFT VFPDGYSLPA IPLGIDVGGA IGPLTTPPIT IPSIPLGIDV 660
SGSLGPINIP IEIAGTPGFG NSTTTPSSGF FNSGTGGTSG FGNVGSGGSG FWNIAGNLGN 720
SGFLNVGPLT SGILNFGNTV SGLYNTSTLG LATSAFHSGV GNTDSQLAGF MRNAAGGTLF 780
NFGFANDGTL NLGNANLGDY NVGSGNVGSY NFGSGNIGNG SFGFGNIGSN NFGFGNVGSN 840
NLGFANTGPG LTEALHNIGF GNIGGNNYGF ANIGNGNIGF GNTGTGNIGI GLTGDNQVGF 900
GALNSGSGNI GFFNSGNGNI GFFNSGNGNV GIGNSGNYNT GLGNVGNANT GLFNTGNVNT 960
GIGNAGSYNT GSYNAGDTNT GDLNPGNANT GYLNLGDLNT GWGNIGDLNT GALISGSYSN 1020
GILWRGDYQG LIGYSDTLSI PAIPLSVEVN GGIGPIVVPD ITIPGIPLSL NALGGVGPIV 1080
VPDITIPGIP LSLNALGGVG PIVVPDITIP GIPLSLNALG GVGPIVVPDI TIPGIPLSLN 1140
ALGGVGPIVV PDITIPGIPL SLNALGGVGP ITVPGVPISR IPLTINIRIP VNITLNELPF 1200
NVAGIFTGYI GPIPLSTFVL GVTLAGGTLE SGIQGFSVNP FGLNIPLSGA TNAVTIPGFA 1260
INPFGLNVPL SGGTSPVTIP GFAINPFGLN VPLSGGTSPV TIPGFTIPGS PLNLTANGGL 1320
GPINIPINIT SAPGFGNSTT TPSSGFFNSG DGSASGFGNV GPGISGLWNQ VPNALQGGVS 1380

GIYNVGQLAS GVANLGNTVS GFNNTSTVGH LTAAFNSGVN NIGQMLLGFF SPGAGP 1436

<212> Type : PRT
<211> Length : 1436
SequenceName : SEQ ID 140
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :

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AAAAMAAAAA PYAGWLGSVA AAAEAVAGQA RVVVGVFEAA LAATVDPALV AANRARLVAL 120
AVSNLLGQNT PAIAAAEAEY ELMWAADVAA MAGYHSGASA AAAALPAFSP PAQALGGGVG 180
AFLTALFASP AKALSLNAGL GNVGNYNVGL GNVGVFNLGA GNVGGQNLGF GNAGGTNVGF 240
GNLGNGNVGF GNSGLGAGLA GLGNIGLGNA GSSNYGFANL GVGNIGFGNT GTNNVGVGLT 300
GNHLTGIGGL NSGTGNIGLF NSGTGNVGFF NSGTGNFGVF NSGNYNTGVG NAGTASTGLF 360
NAGNFNTGVV NVGSYNTGSF NAGDTNTGGF NPGGVNTGWL NTGNTNTGIA NSGNVNTGAF 420
ISGNFNNGVL WVGDYQGLFG VSAGSSIPAI PIGLVLNGDI GPITIQPIPI LPTIPLSIHQ 480
TVNLGPLVVP DIVIPAFGGG IGIPINIGPL TITPITLFAQ QTFVNQLPFP TFSLGKITIP 540
QIQTFDSNGQ LVSFIGPIVI DTTIPGPTNP QIDLTIRWDT PPITLFPNGI SAPDNPLGLL 600
VSVSISNPGF TIPGFSVPAQ PLPLSIDIEG QIDGFSTPPI TIDRIPLTVG GGVTIGPITI 660
QGLHIPAAPG VGNTTTAPSS GFFNSGAGGV SGFGNVGAGS SGWWNQAPSA LLGAGSGVGN 720
VGTLGSGVLN LGSGISGFYN TSVLPFGTPA AVSGIGNLGQ QLSGVSAAGT TLRSMLAGNL 780
GLANVGNFNT GFGNVGDVNL GAANIGGHNL GLGNVGDGNL GLGNIGHGNL GFANLGLTAG 840
AAGVGNVGFG NAGINNYGLA NMGVGNIGFA NTGTGNIGIG LVGDHRTGIG GLNSGIGNIG 900
LFNSGTGNVG FFNSGTGNFG IGNSGRFNTG IGNSGTASTG LFNAGSFSTG IANTGDYNTG 960
SFNAGDTNTG GFNPGGINTG WFNTGHANTG LANAGTFGTG AFMTGDYSNG LLWRGGYEGL 1020
VGVRVGPTIS QFPVTVHAIG GVGPLHVAPV PVPAVHVEIT DATVGLGPFT VPPISIPSLP 1080
IASITGSVDL AANTISPIRA LDPLAGSIGL FLEPFRLSDP FITIDAFQVV AGVLFLENII 1140
VPGLTVSGQI LVTPTPIPLT LNILDTTPWTL FPNGFTIPAQ TPVTVGMEVA NDGFTFFPGG 1200
LTFPRASAGV TGLSVGLDAF TLLPDGFTLD TVPATFDGTI LIGDIPIPII DVPAVPGFGN 1260
TTTAPSSGFF NTGGGGSGF ANVGAGTSGW WNQGHDVLAG AGSGVANAGT LSSGVLNVGS 1320
GISGWYNTST LGAGTPAVVS GIGNLGQQLS GFLANGTVLN RSPIVNIGWA DVGAFNTGLG 1380
NVGDLNWGAA NIGAQNLGLG NLGSGNVGFG NIGAGNVGFA NSGPAVGLAG LGNVGLSNAG 1440
SNNWGLANLG VGNIGLANTG TGNIGIGLVG DYQTGIGGLN SGSGNIGLFN SGTGNVGFFN 1500
TGTGNFGLFN SGSFNTGIGN SGTGSTGLFN AGNFNTGIAN PGSYNTGSFN VGDTNTGGFN 1560
PGDINTGWFN TGIMNTGTRN TGALMSGTDS NGMLWRGDHE GLFGLSYGIT IPQFPIRITT 1620
TGGIGPIVIP DTTILPPLHL QITGDADYSF TVPDIPIPAI HIGINGVVTV GFTAPEATLL 1680
SALKNNGSFI SFGPITLSNI DIPPMDFTLG LPVLGPITGQ LGPIHLEPIV VAGIGVPLEI 1740
EPIPLDAISL SESIPIRIPV DIPASVIDGI SMSEVVPIDA SVDIPAVTIT GTTISAIPLG 1800
FDIRTSAGPL NIPIIDIPAA PGFGNSTQMP SSGFFNTGAG GGSGIGNLGA GVSGLLNQAG 1860
AGSLVGTLSG LGNAGTLASG VLNSGTAISG LFNVSTLDAT TPAVISGFSN LGDHMSGVSI 1920
DGLIAILTFP PAESVFDQII DAAIAELQHL DIGNALALGN VGGVNLGLAN VGEFNLGAGN 1980
VGNINVGAGN LGGSNLGLGN VGTGNLGFGN IGAGNFGFGN AGLTAGAGGL GNVGLGNAGS 2040
GSWGLANVGV GNIGLANTGT GNIGIGLTGD YRTGIGGLNS GTGNLGLFNS GTGNIGFFNT 2100
GTGNFGLFNS GSYSTGVGNA GTASTGLFNA GNFNTGLANA GSYNTGSLNV GSFNTGGVNP 2160
GTVNTGWFNT GHTNTGLFNT GNVNTGAFNS GSFNNGALWT GDYHGLVGFS FSIDIAGSTL 2220
LDLNETLNLG PIHIEQIDIP GMSLFDVHEI VEIGPFTIPQ VDVPAIPLEI HESIHMDPIV 2280
LVPATTIPAQ TRTIPLDIPA SPGSTMTLPL ISMRFEGEDW ILGSTAAIPN FGDPFPAPTQ 2340
GITIHTGPGP GTTGELKISI PGFEIPQIAT TRFLLDVNIS GGLPAFTLFA GGLTIPTNAI 2400
PLTIDASGAL DPITIFPGGY TIDPLPLHLA LNLTVPDSSI PIIDVPPTPG FGNTTATPSS 2460
GFFNSGAGGV SGFGNVGSNL SGWWNQAASA LAGSGSGVLN VGTLGSGVLN VGSGVSGIYN 2520
TSVLPLGTPA VLSGLGNVGH QLSGVSAAGT ALNQIPILNI GLADVGNFNV GFGNVGDVNL 2580
GAANLGAQNL GLGNVGTGNL GFANVGHGNI GFGNSGLTAG AAGLGNTGFG NAGSANYGFA 2640
NQGVRNIGLA NTGTGNIGIG LVGDNLTGIG GLNSGAGNIG LFNSGTGNIG FFNSGTGNFG 2700
IGNSGSFNTG IGNSGTGSTG LFNAGSFNTG VANAGSYNTG SFNAGDTNTG GFNPGTINTG 2760
WFNTGHTNTG IANSGNVGTG AFMSGNFSNG LLWRGDHEGL FSLFYSLDVP RITIVDAHLD 2820
GGFGPVVLPP IPVPAVNAHL TGNVAMGAFT IPQIDIPALT PNITGSAAFR IVVGSVRIPP 2880
VSVIVEQIIN ASVGAEMRID PFEMWTQGTN GLGITFYSFG SADGSPYATG PLVFGAGTSD 2940
GSHLTISASS GAFTTPQLET GPITLGFQVP GSVNAITLFP GGLTFPATSL LNLDVTAGAG 3000
GVDIPAITWP EIAASADGSV YVLASSIPLI NIPPTPGIGN STITPSSGFF NAGAGGGSGF 3060
GNFGAGTSGW WNQAHTALAG AGSGFANVGT LHSGVLNLGS GVSGIYNTST LGVGTPALVS 3120
GLGNVGHQLS GLLSGGSAVN PVTVLNIGLA NVGSHNAGFG NVGEVNLGAA NLGAHNLGFG 3180
NIGAGNLGFG NIGHGNVGVG NSGLTAGVPG LGNVGLGNAG GNNWGLANVG VGNIGLANTG 3240
TGNIGIGLTG DYQTGIGGLN SGAGNLGLFN SGAGNVGFFN TGTGNFGLFN SGSFNTGVGN 3300
SGTGSTGLFN AGSFNTGVAN AGSYNTGSFN VGDTNTGGFN PGSINTGWLN AGNANTGVAN 3360

AGNVNTGAFV TGNFSNGILW RGDYQGLAGF AVGYTLPLFP AVGADVSGGI GPITVLPPIH 3420
IPPIPVGFAA VGGIGPIAIP DISVPSIHLG LDPAVHVGSI TVNPITVRTP PVLVSYSQGA 3480
VTSTSGPTSE IWVKPSFFPG IRIAPSSGGG ATSTQGAYFV GPISIPSGTV TFPGFTIPLD 3540
PIDIGLPVSL TIPGFTIPGG TLIPTLPLGL ALSNGIPPVD IPAIVLDRIL LDLHADTTIG 3600
PINVPIAGFG GAPGFGNSTT LPSSGFFNTG AGGGSGFSNT GAGMSGLLNA MSDPLLGSAS 3660
GFANFGTQLS GILNRGAGIS GVYNTGALGV VTAAVVSGFG NVGQQLSGLL FTGVGP 3716

<212> Type : PRT
<211> Length : 3716
SequenceName : SEQ ID 141
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MNFPVLPPEI NSVLMYSGAG SSPLLAAAAA WDGLAEELGS AAVSFGQVTS GLTAGVWQGA 60
AAAAMAAAAA PYAGWLGSVA AQAVAVAGQA RAAVAAFEAA LAATVDPAAV AVNRMAMRAL 120
AMSNLLGQNA AAIAAVEAEY ELMWAADVAA MAGYHSGASA AAAALPAFSP PAQALGGGVG 180
AFLNALPAGP AKMLRLNAGL GNVGNYNVGL GNVGIFNLGA ANVGAQNLGA ANAGSGNFGF 240
GNIGNANFGF GNSGLGLPPG MGNIGLGNAG SSNYGLANLG VGNIGFANTG SNNIGIGLTG 300
DNLTGIGGLN SGTGNLGLFN SGTGNIGFFN SGTGNFGVFN SGSYNTGVGN AGTASTGLFN 360
VGGFNTGVAN VGSYNTGSFN AGNTNTGGFN PGNVNTGWLN TGNTNTGIAN SGNVNTGAFI 420
SGNFSNGVLW RGDYEGLWGL SGGSTIPAIP IGLELNGGVG PITVLPIQIL PTIPLNIHQT 480
FSLGPLVVPD IVIPAFGGGT AIPISVGPIT ISPITLFPAQ NFNTTFPVGP FFGLGVVNIS 540
GIEIKDLAGN VTLQLGNLNI DTRINQSFPV TVNWSTPAVT IFPNGISIPN NPLALLASAS 600
IGTLGFTIPG FTIPAAPLPL TIDIDGQIDG FSTPPITIDR IPLNLGASVT VGPILINGVN 660
IPATPGFGNT TTAPSSGFFN SGDGGVSGFG NFGAGSSGWW NQAQTEVAGA GSGFANFGSL 720
GSGVLNFGSG VSGLYNTGGL PPGTPAVVSG IGNVGEQLSG LSSAGTALNQ SLIINLGLAD 780
VGSVNVGFGN VGDFNLGAAN IGDLNVGLGN VGGGNVGFGN IGDANFGLGN AGLAAGLAGV 840
GNIGLGNAGS GNVGFGNMGV GNIGFGNTGT NNLGIGLTGD NQTGIGGLNS GAGNIGLFNS 900
GTGNVGLFNS GTGNFGLFNS GSFNTGIGNG GTGSTGLFNA GNFNTGVANP GSYNTGSFNV 960
GDTNTGGFNP GSINTGWFNT GNANTGVANS GNVDTGALMS GNFSNGILWR GNFEGLFGLN 1020
VGITIPEFPI HWTSTGGIGP IIIPDTTILP PIHLGLTGQA NYGFAVPDIP IPAIHIDFDG 1080
AADAGFTAPA TLLLSALGIT GQFRFGPITV SNVQLNPFNV NLKLQFLHDA FPNEFPDPTI 1140
SVQIQVAIPL TSATLGGLAL PLQQTIDAIE LPAISFSQSI PIDIPPIDIP ASTINGISMS 1200
EVVPIDVSVD IPAVTITGTR IDPIPLNFDV LSSAGPINIS IIDIPALPGF GNSTELPSSG 1260
FFNTGGGGGS GIANFGAGVS GLLNQASSPM VGTLSGLGNA GSLASGVLNS GVDISGMFNV 1320
STLGSAPAVI SGFGNLGNHV SGVSIDGLLA MLTSGGSGGS GQPSIIDAAI AELRHLNPLN 1380
IVNLGNVGSY NLGFANVGDV NLGAGNLGNL NLGGGNLGGQ NLGLGNLGDG NVGFGNLGHG 1440
NVGFGNSGLG ALPGIGNIGL GNAGSNNVGF GNMGLGNIGF GNTGTNNLGI GLTGDNQTGF 1500
GGLNSGAGNL GLFNSGTGNI GFFNTGTGNW GLFNSGSYNT GIGNSGTGST GLFNAGSFNT 1560
GLANAGSYNT GSLNAGNTNT GGFNPGNVNT GWFNAGHTNT GGFNTGNVNT GAFNSGSFNN 1620
GALWTGDHHG LVGFSYSIEI TGSTLVDINE TLNLGPVHID QIDIPGMSLF DIHELVNIGP 1680
FRIEPIDVPA VVLDIHETMV IPPIVFLPSM TIGGQTYTIP LDTPPAPAPP PFRLPLLFVN 1740
ALGDNWIVGA SNSTGMSGGF VTAPTQGILI HTGPSSATTG SLALTLPTVT IPTITTSPIP 1800
LKIDVSGGLP AFTLFPGGLN IPQNAIPLTI DASGVLDPIT IFPGGFTIDP LPLSLALNIS 1860
VPDSSVPIII VPPTPGFGNA TATPSSGFFN SGAGGVSGFG NFGAGSSGWW NQAHAALAGA 1920
GSGVLNVGTL NSGVLNVGSG ISGLYNTAIV GLGTPALVSG AGNVGQQLSG VLAAGTALTQ 1980
SPIINLGLAD VGNYNLGLGN VGDFNLGAAN LGDLNLGLGN IGNANVGFGN IGHGNVGFGN 2040
SGLGAALGIG NIGLGNAGST NVGLANMGVG NIGFANTGTN NLGIGLTGDN QTGIGGLNSG 2100
AGNIGLFNSG TGNIGFFNSG TGNWGLFNSG SFNTGIGNSG TGSTGLFNAG GFTTGLANAG 2160
SYNTGSFNVG DTNTGGFNPG SINTGWFNTG NANTGIANSG NVDTGALMSG NFSNGILWRG 2220
NYEGLFSYSY SLDVPRITIL DAHFTGAFGP VVVPPIPVLA INAHLTGNAA MGAFTIPQID 2280
IPALNPNVTG SVGFGPIAVP SVTIPALTAA RAVLDMAASV GATSEIEPFI VWTSSGAIGP 2340
TWYSVGRIYN AGDLFVGGNI ISGIPTLSTT GPVHAVFNAA SQAFNTPALN IHQIPLGFQV 2400
PGSIDAITLF PGGLTFPANS LLNLDVFVGT PGATIPAITF PEIPANADGE LYVIAGDIPL 2460
INIPPTPGIG NTTTVPSSGF FNTGAGGGSG FGNFGANMSG WWNQAHTALA GAGSGIANVG 2520
TLHSGVLNLG SGLSGIYNTS TLPLGTPALV SGLGNVGDHL SGLLASNVGQ NPITIVNIGL 2580
ANVGNGNVGL GNIGNLNLGA ANIGDVNLGF GNIGDVNLGF GNIGGGNVGF GNIGDANFGF 2640
GNSGLAAGLA GMGNIGLGNA GSGNVGWANM GLGNIGFGNT GTNNLGIGLT GDNQSGIGGL 2700
NSGTGNIGLF NSGTGNIGFF NSGTANFGLF NSGSYNTGIG NSGVASTGLV NAGGFNTGVA 2760
NAGSYNTGSF NAGDTNTGGF NPGSTNTGWF NTGNANTGVA NAGNVNTGAL ITGNFSNGIL 2820
WRGNYEGLAG FSFGYPIPLF PAVGADVTGD IGPATIIPPI HIPSIPLGFA AIGHIGPISI 2880
PNIAIPSIHL GIDPTFDVGP ITVDPITLTI PGLSLDAAVS EIRMTSGSSS GFKVRPSFSF 2940
FAVGPDGMPG GEVSILQPFT VAPINLNPTT LHFPGFTIPT GPIHIGLPLS LTIPGFTIPG 3000
GTLIPQLPLG LGLSGGTPPF DLPTVVIDRI PVELHASTTI GPVSLPIFGF GGAPGFGNDT 3060

TAPSSGFFNT GGGGGSGFSN SGSGMSGVLN AISDPLLGSA SGFANFGTQL SGILNRGAGI 3120
SGVYNTGTLG LVTSAFVSGF MNVGQQLSGL LFAGTGP 3157

<212> Type : PRT
<211> Length : 3157
SequenceName : SEQ ID 142
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MSFVVMPPEI NSLLIYTGAG PGPLLAAAAA WDELAAELGS AAAAFGSVTS GLVGGIWQGP 60
SSVAMAAAAA PYAGWLSAAA ASAESAAGQA RAVVGVFEAA LAETVDPFVI AANRSRLVSL 120
ALSNLFGQNT PAIAAAEFDY ELMWAQDVAA MLGYHTGASA AAEALAPFGS PLASLAAAAE 180
PAKSLAVNLG LANVGLFNAG SGNVGSYNVG AGNVGSYNVG GGNIGGNNVG LGNVGWGNFG 240
LGNSGLTPGL MGLGNIGFGN AGSYNFGLAN MGVGNIGFAN TGSGNFGIGL TGDNLTGFGG 300
FNTGSGNVGL FNSGTGNVGF FNSGTGNWGV FNSGSYNTGI GNSGIASTGL FNAGGFNTGV 360
VNAGSYNTGS FNAGEANTGG FNPGSVNTGW LNTGDINTGV ANSGDVNTGA FISGNYSNGV 420
LWRGDYQGLL GFSSGANVLP VIPLSLDING GVGAITIEPI HILPDIPINI NETLYLGPLV 480
VPPINVPAIS LGVGIPNISI GPIKINPITL WPAQNFNQTI TLAWPVSSIT IPQIQQVALS 540
PSPIPTTLIG PIHINTGFSI PVTFSYSTPA LTLFPVGLSI PTGGPLTLTL GVTAGTEAFT 600
IPGFSIPEQP LPLAINVIGH INALSTPAIT IDNIPLNLHA IGGVGPVDIV GGNVPASPGF 660
GNSTTAPSSG FFNTGAGGVS GFGNVGAHTS GWFNQSTQAM QVLPGTVSGY FNSGTLMSGI 720
GNVGTQLSGM LSGGALGGNN FGLGNIGFDN VGFGNAGSSN FGLANMGIGN IGLANTGNGN 780
IGIGLSGDNL TGFGGFNSGS ENVGLFNSGT GNVGFFNSGT GNLGVFNSGS HNTGFFLTGN 840
NINVLAPFTP GTLFTISEIP IDLQVIGGIG PIHVQPIDIP AFDIQITGGF IGIREFTLPE 900
ITIPAIPIHV TGTVGLEGFH VNPAFVLFGQ TAMAEITADP VVLPDPFITI DHYGPPLGPP 960
GAKFPSGSFY LSISDLQING PIIGSYGGPG TIPGPFGATF NLSTSSLALF PAGLTVPDQT 1020
PVTVNLTGGL DSITLFPGGL AFPENPVVSL TNFSVGTGGF TVFPQGFTVD RIPVDLHTTL 1080
SIGPFPFRWD YIPPTPANGP IPAVPGGFGL TSGLFPFHFT LNGGIGPISI PTTTVVDALN 1140
PLLTVTGNLE VGPFTVPDIP IPAINFGLDG NVNVSFNAPA TTLLSGLGIT GSIDISGIQI 1200
TNIQTQPAQL FMSVGQTLFL FDFRDGIELN PIVIPGSSIP ITMAGLSIPL PTVSESIPLN 1260
FSFGSPASTV KSMILHEILP IDVSINLEDA VFIPATVLPA IPLNVDVTIP VGPINIPIIT 1320
EPGSGNSTTT TSDPFSGLAV PGLGVGLLGL FDGSIANNLI SGFNSAVGIV GPNVGLSNLG 1380
GGNVGLGNVG DFNLGAGNVG GFNVGGGNIG GNNVGLGNVG FGNVGLANSG LTPGLMGLGN 1440
IGFGNAGSYN FGLANMGVGN IGFANTGSGN FGIGLTGDNL TGFGGFNTGS GNVGLFNSGT 1500
GNVGFFNSGT GNWGVFNSGS YNTGIGNSGI ASTGLFNAGG FNTGVVNAGS YNTGSFNAGQ 1560
ANTGGFNPGS VNTGWLNTGD INTGVANSGD VNTGAFISGN YSNGAFWRGD YQGLLGFSYR 1620
PAVLPQTPFL DLTLTGGLGS VVIPAIDIPA IRPEFSANVA IDSFTVPSIP IPQIDLAATT 1680
VSVGLGPITV PHLDIPRVPV TLNYLFGSQP GGPLKIGPIT GLFNTPIGLT PLALSQIVIG 1740
ASSSQGTITA FLANLPFSTP VVTIDEIPLL ASITGHSEPV DIFPGGLTIP AMNPLSINLS 1800
GGTGAVTIPA ITTGEIPFDL VAHSTLGPVH ILIDLPAVPG FGNTTGAPSS GFFNSGAGGV 1860
SGFGNVGAMV SGGWNQAPSA LLGGGSGVFN AGTLHSGVLN FGSGMSGLFN TSVLGLGAPA 1920
LVSGLGSVGQ QLSGLLASGT ALHQGLVLNF GLADVGLGNV GLGNVGDFNL GAGNVGGFNV 1980
GGGNIGGNNV GLGNVGWGNF GLGNSGLTPG LMGLGNIGFG NAGSYNFGLA NMGVGNIGFA 2040
NTGSGNFGIG LTGDNLTGFG GFNTGSGNVG LFNSGTGNVG FFNSGTGNWG VFNSGSYNTG 2100
IGNSGIASTG LFNAGGFNTG VVNAGSYNTG SFNAGQANTG GFNPGSVNTG WLNTGDINTG 2160
VANSGDVNTG AFISGNYSNG AFWRGDYQGL LGFSYTSTII PEFTVANIHA SGGAGPIIVP 2220
SIQFPAIPLD LSATGHIGGF TIPPVSISPI TVRIDPVFDL GPITVQDITI PALGLDPATG 2280
VTVGPIFSSG SIIDPFSLTL LGFINVNVPA IQTAPSEILP FTVLLSSLGV THLTPEITIP 2340
GFHIPVDPIH VELPLSVTIG PFVSPEITIP QLPLGLALSG ATPAFAFPLE ITIDRIPVVL 2400
DVNALLGPIN AGLVIPPVPG FGNTTAVPSS GFFNIGGGGG LSGFHNLGAG MSGVLNAISD 2460
PLLGSASGFA NFGTQLSGIL NRGADISGVY NTGALGLITS ALVSGFGNVG QQLAGLIYTG 2520
TGP 2523

<212> Type : PRT
<211> Length : 2523
SequenceName : SEQ ID 143
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
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SYQAFGAQLS AFHAQFVQSL TNGARSYVVA EATSAAPLQD LLGVVNAPAQ ALLGRPLIGN 120
GANGADGTGA PGGPGGLLLG NGGNGGSGAP GQPGGAGGDA GLIGNGGTGG KGGDGLVGSG 180
AAGGVGGRGG WLLGNGGTGG AGGAAGATLV GGTGGVGGAT GLIGSGGFGG AGGAAAGVGT 240

TGGVGGSGGV GGVFGNGGPG GAGGLGAAGG VGGAASYFGT GGGGGVGGDG APGGDGGAGP 300
LLIGNGGVGG LGGAGAAGGN GGAGGMLLGD GGAGGQGGPA VAGVLGGMPG AGGNGGNANW 360
FGSGGAGGQG GTGLAGTNGV NPGSIANPNT GANGTDNSGN GNQTGGNGGP GPAGGVGEAG 420
GVGGQGGLGE SLDGNDGTGG KGGAGGTAGT DGGAGGAGGA GGIGETDGSA GGVATGGEGG 480
DGATGGVDGG VGGAGGKGGQ GHNTGVGDAF GGDGGIGGDG NGALGAAGGN GGTGGAGGNG 540
GRGGMLIGNG GAGGAGGTGG TGGGGAAGFA GGVGGAGGEG LTDGAGTAEG GTGGLGGLGG 600
VGGTGGMGGS GGVGGNGGAA GSLIGLGGGG GAGGVGGTGG IGGIGGAGGN GGAGGAGTTT 660
GGGATIGGGG GTGGVGGAGG TGGTGGAGGT TGGSGGAGGL IGWAGAAGGT GAGGTGGQGG 720
LGGQGGNGGN GGTGATGGQG GDFALGGNGG AGGAGGSPGG SSGIQGNMGP PGTQGADG 778

<212> Type : PRT
<211> Length : 778
SequenceName : SEQ ID 144
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
PQGADGNAGN GGDGGVGGNG GNGADNTTTA AAGTTGGAGG AGGAGGTGGT GGAAGTGTGG 60
QQGNGGNGGN GGTGGKGGTG GDGALAGSSG GAGGKGGNGG DAGKAGTGSA PGTAGTGGDG 120
GKGGNGGIGA AGTTGPVGTG ASGGTGGSGG AGGTGGDGGA ANGGTAGAGG AGGNGGKGGD 180
GGAGVTSSTA GNSGGAGGSG GKGGDAGAGG AGATPGANGI AGNGGDGGDG AAGAVGISGA 240
TGAGDGGHGG TGAAGGNGGT GGAGGSGIDG VGGGTGGTGG NGGNGAIGGA GGDAGGSGNS 300
GGNGGIGGKG GNAGAGGAAG SNGGTVGANG TGGDGGNGGA AGAATAGSNG GAGTGSAGGN 360
GGTGGRGGSG GAGGDGIGGV GGGKGGNGAD GEVGGAGGAG GSGPNTSPGG NGGQGGQGGS 420
GGAGGAAGAG GAGGGANGTA GNGGQGGAGG TGGAGAASSA TNGGSGGAGG TGGDGGSGGA 480
GGTGGAGGTG GAAGDGGQGG QGGAGGGAGG QGGAGGAGGT GGNGGNITGG TAGTAGAAGN 540
GGAAGKGGAG GQGGTGGGTG GQGGAGGDGG AGGTGGDRTV GGGTVPAGSG GQGGNAGGGG 600
AGGQGGADGG SGGDGGDAGT GGNGGNGGNR NSGNGTGGAG GNGGGGANGG AGGAGGSGGG 660
TGGNGGAGGD AGDAGNGGNG NGTGNGGNGG NGGIAGMGGN GGAGTGSGNG GNGGSGGNGG 720
NAGMGGNSGT GSGDGGAGGN GGAAGTGGTG GDGGLTGTGG TGGSGGTGGD GGNGGNGADN 780
TANMTAQAGG DGGNGGDGGF GGGAGAGGGG LTAGANGTGG QGGAGGDGGN GAIGGHGPLT 840
DDPGGNGGTG GNGGTGGTGG AGIGSLGGGT GGDGGNGGNG GTGGEGGEVG GAGGTGGAAG 900
NGGDGGTGGT GGGDGGAGGT GGTGGTGGLG DPRVGGSGGD GGTGGSGGAA GNGGNGGNAG 960
AGGNGNGGTG GAGGIGGTGG NGGDAEPGVP PGAGGAGGAG TTGGKGGTGG NGSGTGSGGT 1020
GGDGGTGGGG GNGGTGWNGG KGDTGSGGGA GDGGKAPAGG TGGAGGDGGA GGKGGSGGV 1079

<212> Type : PRT
<211> Length : 1079
SequenceName : SEQ ID 145
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MVMSLMVAPE LVAAAAADLT GIGQAISAAN AAAAGPTTQV LAAAGDEVSA AIAALFGTHA 60
QEYQALSARV ATFHEQFVRS LTAAGSAYAT AEAANASPLQ ALEQQVLGAI NAPTQLWLGR 120
PLIGDGVHGA PGTGQPGGAG GLLWGNGGNG GSGAAGQVGG PGGAAGLFGN GGSGGSGGAG 180
AAGGVGGSGG WLNGNGGAGG AGGTGANGGA GGNAWLFGAG GSGGAGTNGG VGGSGGFVYG 240
NGGAGGIGGI GGIGGNGGDA GLFGNGGAGG AGAAGLPGAA GLNGGDGSDG GNGGTGGNGG 300
RGGLLVGNGG AGGAGGVGGD GGKGGAGDPS FAVNNGAGGN GGHGGNPGVG GAGGAGGLLA 360
GAHGAAGATP TSGGNGGDGG IGATANSPLQ AGGAGGNGGH GGLVGNGGTG GAGGAGHAGS 420
TGATGTALQP TGGNGTNGGA GGHGGNGGNG GAQHGDGGVG GKGGAGGSGG AGGNGFDAAT 480
LGSPGADGGM GGNGGKGGDG GKAGDGGAGA AGDVTLAVNQ GAGGDGGNGG EVGVGGKGGA 540
GGVSANPALN GSAGANGTAP TSGGNGGNGG AGATPTVAGE NGGAGGNGGH GGSVGNGGAG 600
GAGGNGVAGT GLALNGGNGG NGGIGGNGGS AAGTGGDGGK GGNGGAGANG QDFSASANGA 660
NGGQGGNGGN GGIGGKGGDA FATFAKAGNG GAGGNGGNVG VAGQGGAGGK GAIPAMKGAT 720
GADGTAPTSG GDGGNGGNGA SPTVAGGNGG DGGKGGSGGN VGNGGNGGAG GNGAAGQAGT 780
PGPTSGDSGT SGTDGGAGGN GGAGGAGGTL AGHGGNGGKG GNGGQGGIGG AGERGADGAG 840
PNANGANGEN GGSGGNGGDG GAGGNGGAGG KAQAAGYTDG ATGTGGDGGN GGDGGKAGDG 900
GAGENGLNSG AMLPGGGTVG NPGTGGNGGN GGNAGVGGTG GKAGTGSLTG LDGTDGITPN 960
GGNGGNGGNG GKGGTAGNGS GAAGGNGGNG GSGLNGGDAG NGGNGGGALN QAGFFGTGGK 1020
GGNGGNGGAG MINGGLGGFG GAGGGAVDV AATTGGAGGN GGAGGFASTG LGGPGGAGGP 1080
GGAGDFASGV GGVGGAGGDG GAGGVGGFGG QGGIGGEGRT GGNGGSGGDG GGGISLGGNG 1140
GLGGNGGVSE TGFGGAGGNG GYGGPGGPEG NGGLGGNGGA GGNGGVSTTG GDGGAGGKGG 1200

NGGDGGNVGL GGDAGSGGAG GNGGIGTDAG GAGGAGGAGG NGGSSKSTTT GNAGSGGAGG 1260
NGGTGLNGAG GAGGAGGNAG VAGVSFGNAV GGDGGNGGNG GHGGDGTTGG AGGKGGNGSS 1320
GAASGSGVVN VTAGHGGNGG NGGNGGNGSA GAGGQGGAGG SAGNGGHGGG ATGGDGGNGG 1380
NGGNSGNSTG VAGLAGGAAG AGGNGGGTSS AAGHGGSGGS GGSGTTGGAG AAGGNGGAGA 1440
GGGSLSTGQS GGPRRQRWCR WQRRRWLGRQ RRRRWCRWQR RCRRQRWRWR CRQRRLRRQW 1500
RQGRRRCRPW LHRRRGRQGR RWRQRRFQQR QRSRWQRR 1538

<212> Type : PRT
<211> Length : 1538
SequenceName : SEQ ID 146
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MSFVVTAPPV LASAASDLGG IASMISEANA MAAVRTTALA PAAADEVSAA IAALFSSYAR 60
DYQTLSVQVT AFHVQFAQTL TNAGQLYAVV DVGNGVLLKT EQQVLGVINA PTQTLVGRPL 120
IGDGTHGAPG TGQNGGAGGI LWGNGGNGGS GAPGQPGGRG GDAGLFGHGG HGGVGGPGIA 180
GAAGTAGLPG GNGANGGSGG IGGAGGAGGN GGLLFGNGGA GGQGGSGGLG GSGGTGGAGM 240
AAGPAGGTGG IGGIGGIGGA GGVGGHGSAL FGHGGINGDG GTGGMGGQGG AGGNGWAAEG 300
ITVGIGRQGG QGGDGGAGGA GGIGGSAGGI GGSQGAGGHG GDGGQGGAGG SGGVGGGGAG 360
AGGDGGAGGI GGTGGNGSIG GAAGNGGNGG RGGAGGMATA GSDGGNGGGG GNGGVGVGSA 420
GGAGGTGGDG GAAGAGGAPG HGYFQQPAPQ GLPIGTGGTG GEGGAGGAGG DGGQGDIGFD 480
GGRGGDGGPG GGGGAGGDGS GTFNAQANNG GDGGAGGVGG AGGTGGTGGV GADGGRGGDS 540
GRGGDGGNAG HGGAAQFSGR GAYGGEGGSG GAGGNAGGAG TGGIAGSGGA GGFGGNGADG 600
GNGGNGGNGG FGGINGTFGT NGAGGTGGLG TLLGGHNGNI GLNGATGGIG STTLTNATVP 660
LQLVNTTEPV VFISLNGGQM VPVLLDTGST GLVMDSQFLT QNFGPVIGTG TAGYAGGLTY 720
NYNTYSTTVD FGNGLLTLPT SVNVVTSSSP GTLGNFLSRS GAVGVLGIGP NNGFPGTSSI 780
VTAMPGLLNN GVLIDESAGI LQFGPNTLTG GITISGAPIS TVAVQIDNGP LQQAPVMFDS 840
GGINGTIPSA LASLPSGGFV PAGTTISVYT SDGQTLLYSY TTTATNTPFV TSGGVMNTGH 900
VPFAQQPIYV SYSPTAIGTT TFN 923

<212> Type : PRT
<211> Length : 923
SequenceName : SEQ ID 147
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MIGNGGAGGS GAPGAIGGAG GPAGLIGVGG AGGAGGDSAV AGVIGGAGGA GGAALLFGAG 60
GAGGAGGSGG SGAAGGAGGA GGAGGLFASG GSGGFGGFAS TGTGGAGGTG GAGGLFASGG 120
VGGTGGGAGS GGTGGVGGTG GAGGLFASGG AGGAGGSGGT GGAGGTGGAG GLFGAGGAGG 180
LGGQGNHTGG HGGAGGSAGL LALGDGGAGG AGGAATTGTG GAGGAGGKAG LLFGSGGAGG 240
SGGAAGTFGD TGNSGGAGGA GGKAGLLFGS GGAGGSGGAG GFANGSTGGA GGAGGGAGLI 300
GNGGNGGSGG TSVATGGAGN GGAGGAGGGA GLIGNGGNGG SGGMGDAPGG TGVGGIGGLL 360
LGLDGANAPA STNPLHTAQQ QALAAVNAPI QAVTGRPLIG NGANGAPGSG APGGHGGWLF 420
GGGGTGGSGV SGGAGGDGGA GGILFGAGGA GGAGGAVTGT GATGGSGGAG GGALLFGAGG 480
AGGAGGSSGI GGFAAGGAGG PGGAGGLFNG GGAGGAGGSG VSGGAGGEGG AGGAGGLFAG 540
GGAGGAGGSG NNVGGAGGAG GVGGLFGAGG AGGSGGGGSV AGDSGAGGNA GLLAPGLAGG 600
AGGGGGQGFD TGGAGGPGGD AGLLVGSGGV GGAGGFGLTT GGPGAAGGDA GLLFGSGGAG 660
GAGGSGRTDL GGAGGAGGKA GLIGNGGNGG AGGAGGNGGG DGGPGGAAFG LGNGGNGGNG 720
GTGTSAGSPG AGGAGGSLIG AEGLPGLLP 749

<212> Type : PRT
<211> Length : 749
SequenceName : SEQ ID 148
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MSFVIAAPEA LVAVASDLAG IGSALAEANA AALAPTTALL AAGADEVSAA IAALFGAHGQ 60
AYQTVSAQAS APHAQFVQAL TGGGGAYAAA EAANVSAAQS TDQRLLDLIN GPTQALLGRP 120
LIGDGANGGP GQDGGPGGLL YGNGGNGGTS TTAGVAGGNG GAAGLIGNGG AGGGGGAGAA 180
GGNGGAGGWL YGNGGAGGAG GTSVIPGVAG GNGGAGGSAG LWGTGGAGGD GGNGRSGPVN 240
VAGSAGGNGG AGGAAGLFGD AGAGGNGGKG GAGGAAFSIN FTAGDGGAGG AGGSGGHALL 300

WGAGGAGGNG GSGGTGGAGG STAGAGGNGG AGGGGGTGGL LFGNGGAGGH GAAAGNGLAA 360
GNGVSSSGGG GAGGTGGAGG DGGAGGAGGN ARLWGVGGAG GAGGDGGAGG AGGKGGSGLS 420
GNANGGAGGD SGRGGTGGAG GEGGAAGLLV GTGGHGGDGG AGGAAVKGGD GGAAAGTGIA 480
GAGGRGGAGG SGGSGGDGGG GAAGPAGWLF GDGGAGGNGG AAAAGGAGGQ AGGGGGNGGN 540
GGNGGNGGNG GNGATGGWLY GNGGAGGQGA TAGAGGAGAN GVSSTNGGGT GGNGGIGGTG 600
GSGGAGGNAG LLGVGGAGGH GASGGAGDRG GAGGTGFISS DGGAGGDGGD GGNGGAGGTG 660
GLLFGAGGNG GPGGSGGAAD IGGNGGAGNG GGTDGNGGNG GSGGGAGSGG DGGGAGGNGA 720
WLFGNGGAGG GGGKGGNGAG GGLGGGSFGL PGLNGSGGDG GDGGNGAPGG VLYGNGGAGG 780
QGSSGGIGGP GATGGAGGKG GDGGDAQLIG DGGNGGNGGA GGTGGTPGPG GPGGSGGLGG 840
LLFGQTGTAG VSP 853

<212> Type : PRT
<211> Length : 853
SequenceName : SEQ ID 149
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MSYLVVVPEL VAAAATDLAN IGSSISAANA AAAAPTTALV AAGGDEVSAA IAALFGAHAR 60
AYQALSAQAA MFHEQFVRAL AAGGNSYAVA EAATAQSVQQ DLLNLINAPT QALLGRPLIG 120
NGANGLPGTG QNGGDGGILY GNGGNGGSGG VNQAGGNGGN AGLWGNGGSG GAGGNATTAG 180
RNGFNGGAGG SGGLLWGNGG AGGAGGNGGP APLVGGVGTT GGAGGNGGGA GLFYGFGGAG 240
GNGGMGGVAP STGPSMGILP AGGVGGPGGS GGASALAFGS GGVGGAGGLG GPTDGTVQGV 300
GGFGGQGGNG GQSGLLFGNA GAGGAGAAGG AGTGDTESFG GHGGAGGDGG AVGLIGNGGA 360
GGTGSPGAVV GGNGGVGGLG GAGSPGGLLY GTGGAGGNGG PGGDGGTGAT VGFAGSGGFG 420
GAGGIAQLFG TGGMGGSGGG IGAGTTTVVP PDVAPVGGTG GNGGRAGLLL GVGGMGGNGG 480
ATSVGGTLYA AGGNGGDGGL VWGNGGTGGS GGAGGAGSVG NGGAGGNAAL LFGNGGAGGA 540
GGAGGIGAGG AGGFGAVLFG NGGAGGSGAP GGIGAGGNGG NALLVGNGGN GGAGTGGAAG 600
GAGGSGGLLF GQNGMPGP 618

<212> Type : PRT
<211> Length : 618
SequenceName : SEQ ID 150
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MNFSVLPPEI NSALIFAGAG PEPMAAAATA WDGLAMELAS AAASFGSVTS GLVGGAWQGA 60
SSSAMAAAAA PYAAWLAAAA VQAEQTAAQA AAMIAEFEAV KTAVVQPMLV AANRADLVSL 120
VMSNLFGQNA PAIAAIEATY EQMWAADVSA MSAYHAGASA IASALSPFSK PLQNLAGLPA 180
WLASGAPAAA MTAAAGIPAL AGGPTAINLG IANVGGGNVG NANNGLANIG NANLGNYNFG 240
SGNFGNSNIG SASLGNNNIG FGNLGSNNVG VGNLGNLNTG FANTGLGNFG FGNTGNNNIG 300
IGLTGNNQIG IGGLNSGTGN FGLFNSGSGN VGFFNSGNGN FGIGNSGNFN TGGWNSGHGN 360
TGFFNAGSFN TGMLDVGNAN TGSLNTGSYN MGDFNPGSSN TGTFNTGNAN TGFLNAGNIN 420
TGVFNIGHMN NGLFNTGDMN NGVFYRGVGQ GSLQFSITTP DLTLPPLQIP GISVPAFSLP 480
AITLPSLNIP AATTPANITV GAFSLPGLTL PSLNIPAATT PANITVGAFS LPGLTLPSLN 540
IPAATTPANI TVGAFSLPGL TLPSLNIPAA TTPANITVGA FSLPGLTLPS LNIPAATTPA 600
NITVGAFSLP GLTLPSLNIP AATTPANITV SGFQLPPLSI PSVAIPPVTV PPITVGAFNL 660
PPLQIPEVTI PQLTIPAGIT IGGFSLPAIH TQPITVGQIG VGQFGLPSIG WDVFLSTPRI 720
TVPAFGIPFT LQFQTNVPAL QPPGGGLSTF TNGALIFGEF DLPQLVVHPY TLTGPIVIGS 780
FFLPAFNIPG IDVPAINVDG FTLPQITTPA ITTPEFAIPP IGVGGFTLPQ ITTQEIITPE 840
LTINSIGVGG FTLPQITTPP ITTPPLTIDP INLTGFTLPQ ITTPPITTPP LTIDPINLTG 900
FTLPQITTPP ITTPPLTIEP IGVGGFTTPP LTVPGIHLPS TTIGAFAIPG GPGYFNSSTA 960
PSSGFFNSGA GGNSGFGNNG SGLSGWFNTN PAGLLGGSGY QNFGGLSSGF SNLGSGVSGF 1020
ANRGILPFSV ASVVSGFANI GTNLAGFFQG TTS 1053

<212> Type : PRT
<211> Length : 1053
SequenceName : SEQ ID 151
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MLYVVASPDL MTAAATNLAE IGSAISTANG AAALPTVEVV AAAADEVSTQ IAALFGAHAR 60

SYQTLSTQAA AFHSRFVQAL TTAAASYASV EAANASPLQV ALDVINAPAQ TLLGRPLIGN 120
GADGSTPGQA GGPGGLLYGN GGNGAAGGPN QAGGAGGNAG LIGNGGAGGA GGVGAVGGKR 180
GTGGLLFGNG GAGGQGGLGL AGINGGSGGQ GGHGGNAILF GQGGAGGPGG TGAMGVAGTN 240
PTPIGTAAPG SDGVNQIGNG GNTDLTGGAG GDGNAGSTTV NGGNGGTGGA ARNSSGGTGN 300
SFGGAGGAGG DGANGGDGGA GGEALTEGGA TAVSGAGGKG GNAEASGGAG GNGGKGGFAQ 360
ATTSVTGGNG GNGGNGHDSN APGGAGGSGG VGGDGGRGGL LAGNGGTGGA GGNGGTGGAG 420
APGGAGGAGG KADIANSLGD NATVTGGNGG TGGDGGSALG TGGAGGAGGL GGHGGAGGLL 480
IGNGGAGGAG GLGGAGGAGG AGGEGGAGGA GGEAIPGGAS TNSAGGDGGA GGTGGNGGDG 540
GAGGAPGLGG AGGAGGWLIG QSGSTGGGGA GGAGGAGGAG GAGGSGGAGG HGDTTSGKNG 600
SSGTAGFDGN PGQPG 615

<212> Type : PRT
<211> Length : 615
SequenceName : SEQ ID 152
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MHYSVLPPEI NSALIFAGAG SGPMLAAASA WDGLATELAS AAVSFGSVTA GLVGGSWQGR 60
SSVAMAAAAA PYAGWLAAAA TQAEQAATQA QVMVAEFEAV RLAMVQPALV AANRSGLISL 120
VISNLFGQNA PAIAAAEAAY EEMWALDVSA MAAYHSGASA VAVALPAPAL PLRLPAGLAA 180
GPAAVVTALT TAVGMPTFAG RAIAASLGLA NVGGGNLGNA NNGLGNIGNA NLGNNNLGSG 240
NFGSFNIGSA NLGGNNIGIG NAGANNFGLA NLGNLNTGFA NAGIGNFGIA NTGNNNIGNG 300
LTGNNQIGIG GLNSGNGNVG LFNAGSANIG FFNSGNGNFG IGNSGNFSTG LFNPGHGNTG 360
FLNAGSFNTG MFDVGNANTG SFNVGHYNFG AFNPGPSNTG TFNTGGANTG WFNTGSINTG 420
AFNIGDMNNG LFNTGDMNNG VFYRGVGQGS LQFAITSPDL TLPSLEIPGI SVPAFSLPAI 480
TLPSLTIPAV TTPANVTVGA FDLPGLTVPS LTIPAAMTPA NITVGAFDLP GLTVPSLTIP 540
ATTTPANITV GAFNLPQLSI PSVTVPPITI PAGTALGAFN LPTLSIPSVT VPPITIPAGT 600
TVGGFTLPTI HTPLISTPQI SIGGFSTPGI ATQANSGVIN LPTFSLNGIT ITNLVVFIPN 660
NITALQTNMP GVFPQIGGFA NTPPAFINTG TITVGGGQIN GVGFSIGAIN VTPFTLPNVV 720
IQPWSLGGIS VDGFTLPEIS TQEFTTPALT ISPIGVGALS LPDITTQQFT TPELTIDPIT 780
LGGFTLPQLS IPAITTPAFT IDPIALGGFT LPQIMTPEIT TPPFAIDPIG LSGFTLPQVN 840
IPEITTPEFT IQPVGLAAFT TPALTIASIH LPSTTMGGFA IPAGPGYFNS SATPSLGFFN 900
AGIGGNSGFG NSGSGLSGWF NTSPVGLLAG SGYQNYGGLI SGFSNLGSGI SGFANTGTLP 960
FAVTSLVSGL ANIGNNLSGL FFQSTTP 987

<212> Type : PRT
<211> Length : 987
SequenceName : SEQ ID 153
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MSFVVVAPEV LAAAASDLAG IGSTLAQANA AALAPTTAVL AAGADEVSAA IASLFGAHGQ 60
AYQAVSAQMS AFHAQFMQAL TGAGGAYAAA EAVNVSAAQS VEQDLLAAIN ARFERIFGRP 120
LIGDGANGGP GQDGGPGGLL YGNGGNGGTS TTVGMAGGNG GAAGLIGNGG FGGGGGPGAA 180
GGNGGAGGWL FGNGGAGGAG GLGVAPGVPG GAGGAGGAGG VGGPAGLWGH GGAGGAGGAG 240
VAGAGGFEGT IGAGGAGGVG GAGGVGGAGG AGGWLYGDAG AGGDGGVGGA GGTGGLGNRG 300
GAGGAGGAGG VGGAGGAAGL WGGGGAGGVG GTGGGAGLGA QSVTFSSSLS GLSGGDGGAG 360
GAGGAGGAGG TGGWLYGGGG AAGSGGDGGT GGQGGAGGAG VFSLFGSGGG PGGNGGVGGV 420
GGVGGAGGRA GLFGVGGLGG AGGDAGDSGE GGFGGPGLAG GLFGNPGNGG VGGIGGDAAA 480
GGAGGAGGNG GAGGNGGWLF GNGGAGGSGG DGGAAGRGGA GNLGSAGGIN APAGNPGSGS 540
VGIGGAGGAG GTAGLFGDGG AGGAGGAGAA GGFGGISAAT PSAGSEGAMG GAGGVGGNAR 600
LLGTGGAGGV GGGGGAGGDG GRGGVATPGG QGGDAGDGGA GGAGGNGGGA SGAGGWLLGT 660
GGAGGAGGNG GNGGKAGFSP GPTNFGLNGA GGGGGVGGNG ATGPWLFGDG GPTPGSTGAG 720
AAGGHGGDAQ LIGNGGHGGA GGTGVPNGSG GAGGLSGLLF GEPGANG 767

<212> Type : PRT
<211> Length : 767
SequenceName : SEQ ID 154
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :

MSFVIANPEM LAAAATDLAG IRSAISAATA AAAAPTIQVA AAGADEVSLA ISALFGQHAQ 60
AYQALSAQAT IFHDQFVQAL TSGGNLYAAA ESHTVEQMVL NAINAPTQTL FGRPLIGDGA 120
NGTAENPDGQ NGGLLFGNGG NGFTQTTAGV AGGNGGSAGL IGNGGAGGGG GAGAAGGLGG 180
NGGWLYGNGG AGGIGGAGTG TGGHGGAGGA GGRAWLWGTG GAGGAGGDGG WLFGDGGAGG 240
TGGNGGSGFN SLTSSVGGAG GAGGHAGLFG AGGTGGTGGI GGQNTETGPA ASNGGAGGAG 300
GGGGYLVGDG GAGGTGGAGG KNSSGGATLT GGTGGTGGAG GAAGWLYGSG GAGGAGGAGG 360
LNNAGGATGG TGGTGGAGGS GAWLYGNGGA AGAGGNGGNN TSAGTGGVGA SGGTGGNAGL 420
IGAGGHGGAG GAGGNQTGGV GNGGAGGNGG AGGAGGQLYG NGGDGGNGGA GGANIAGGNG 480
SDGGAAGHGG AGGSARLIGA GGHGGDGGAG GNTAGRRADA IAGTGGDGGN GGNGGLLSGN 540
AGAGGHGGAG GSSTATTTTG TPPTGATGGN GGNGGAGGTA GFTGSGGIGG NGGAGGTGGN 600
AGVALSVGST GGLGGNGGSG GLGGGGGSLF GNGGAGGVGA TGGNGGSGIG PASVGGNGGK 660
GGVGAAGGLA GQIGNGGSGG SGGAGGNGGT GDTAGNGGNG GAGAVGGNAQ LIGNGGNGGG 720
GGNGGTGADG T 731

<212> Type : PRT
<211> Length : 731
SequenceName : SEQ ID 155
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MPGRFRNFGS QNLGSGNIGS TNVGSGNIGS TNVGSGNIGD TNFGNGNNGN FNFGSGNTGS 60
NNIGFGNTGS GNFGFGNTGN NNIGIGLTGD GQIGIGGLNS GSGNIGFGNS GTGNVGLFNS 120
GTGNVGFGNS GTANTGFGNA GNVNTGFWNG GSTNTGLANA GAGNTGFFDA GNYNFGSLNA 180
GNINSSFGNS GDGNSGFLNA GDVNSGVGNA GDVNTGLGNS GNINTGGFNP GTLNTGFFSA 240
MTQAGPNSGF FNAGTGNSGF GHNDPAGSGN SGIQNSGFGN SGYVNTSTTS MFGGNSGVLN 300
TGYGNSGFYN AAVNNTGIFV TGVMSSGFFN FGTGNSGLLV SGNGLSGFFK NLFG 354

<212> Type : PRT
<211> Length : 354
SequenceName : SEQ ID 156
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MSFVLAMPEV LGSAATDLAA LGSVLGAADA AAAATTTGIV AAAQDEVSAA IAALFSAHGR 60
AYQVASAQAA AVHAQFVEAL SAGAGAYASA EAAGAAVLAN PAQSVQQDLL AAVNAQSVAL 120
TGRPLIGNGA NGAPGTGANG APGGWLLGNG GAGGSAAAGS GLPGGAGGAA GLFGTGGAGG 180
AGGSSTVGDG EAGGAGGSGG WLLGTGGVGG VGGLGAGAGG AGGVGGAGGL LGAGGHGGAG 240
GLGAVTGGVG GTGGAGGLLA GLLAGPGGAG GTGGRGFLNN GGVGGAGGNA GLLFGAGGTG 300
GSGGAGLGGD GGAGGAGGNT GVLFGNAGSG GTGGFGDTDG GAGGAGGDAG WLGSGGVGGA 360
GGFGETGDGG VGGAGGKAGL LIGNGGAGGA GGQGAVTGGT GGAGGDGVLI GNGGNAGIGG 420
TGPTAGDTGA GGISGLLLGA DGFNTPASAS PLHTLKQQAL AAINAPTQTL TGRPLIGNGT 480
PGAVGSGATG APGGWLLGDG GAGGSGAAGS GAPGGAGGAA GLWGTGGAGG AGGSSAGGGG 540
AGGAGGAGGW LLGDGGAGGI GGASTVLGGT GGGGGVGGLW GAGGAGGAGG TGLVGGDGGA 600
GGAGGTGGLL AGLIGAGGGH GGTGGLSTNG DGGVGGAGGN AGMLAGPGGA GGAGGDGGNL 660
DTGGDGGAGG SAGLLFGSGG AGGAGGFGFL GGDGGAGGNA GLLLSSGGAG GFGGFGTAGG 720
VGGAGGNAGW LGFGGAGGVG GSAGLIGTGG NGGNGGTGAN AGSPGTGGAG GLLLGQNGLN 780
GLP 783

<212> Type : PRT
<211> Length : 783
SequenceName : SEQ ID 157
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MSLVIATPQL LATAALDLAS IGSQVSAANA AAAMPTTEVV AAAADEVSAA IAGLFGAHAR 60
QYQALSVQVA AFHEQFVQAL TAAAGRYAST EAAVERSLLG AVNAPTEALL GRPLIGNGAD 120
GTAPGQPGAA GGLLFGNGGN GAAGGFGQTG GSGGAAGLIG NGGNGGAGGT GAAGGAGGNG 180
GWLWGNGGNG GVGGTSVAAG IGGAGGNGGN AGLFGHGGAG GTGGAGLAGA NGVNPTPGPA 240
ASTGDSPADV SGIGDQTGGD GGTGGHGTAG TPTGGTGGDG ATATAGSGKA TGGAGGDGGT 300
AAAGGGGGNG GDGGVAQGDI ASAFGGDGGN GSDGVAAGSG GGSGGAGGGA FVHIATATST 360

GGSGGFGGNG AASAASGADG GAGGAGGNGG AGGLLFGDGG NGGAGGAGGI GGDGATGGPG 420
GSGGNAGIAR FDSPDPEAEP DVVGGKGGDG GKGGSGLGVG GAGGTGGAGG NGGAGGLLFG 480
NGGNGGNAGA GGDGGAGVAG GVGGNGGGGG TATFHEDPVA GVWAVGGVGG DGGSGGSSLG 540
VGGVGGAGGV GGKGGASGML IGNGGNGGSG GVGGAGGVGG AGGDGGNGGS GGNASTFGDE 600
NSIGGAGGTG GNGGNGANGG NGGAGGIAGG AGGSGGFLSG AAGVSGADGI GGAGGAGGAG 660
GAGGSGGEAG AGGLTNGPGS PGVSGTEGMA GAPG 694
<212> Type : PRT
<211> Length : 694
SequenceName : SEQ ID 158
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MSFVIAAPEV IAAAATDLAS LESSIAAANA AAAANTTALL AAGADEVSTA VAALFGAHGQ 60
AYQALSAQAQ AFHAQFVQAL TSGGGAYAAA EAAATSPLLA PINEFFLANT GRPLIGNGTN 120
GAPGTGANGG DGGWLIGNGG AGGSGAAGVN GGAGGNGGAG GLIGNGGAGG AGGRASTGTG 180
GAGGAGGAAG MLFGAAGVGG PGGFAAAFGA TGGAGGAGGN GGLFADGGVG GAGGATDAGT 240
GGAGGSGGNG GLFGAGGTGG PGGFGIFGGG AGGDGGSGGL FGAGGTGGSG GTSIINVGGN 300
GGAGGDAGML SLGAAGGAGG SGGSNPDGGG GAGGIGGDGG TLFGSGGAGG VGGLGFDAGG 360
AGGAGGKAGL LIGAGGAGGA GGGSFAGAGG TGGAGGAPGL VGNAGNGGNG GASANGAGAA 420
GGAGGSGVLI GNGGNGGSGG TGAPAGTAGA GGLGGQLLGR DGFNAPASTP LHTLQQQILN 480
AINEPTQALT GRPLIGNGAN GTPGTGADGG AGGWLFGNGG NGGHGATGAD GGDGGSGGAG 540
GILSGIGGTG GSGGIGTTGQ GGTGGTGGAA LLIGSGGTGG SGGFGLDTGG AGGRGGDAGL 600
FLGAAGTGGQ AALSQNFIGA GGTAGAGGTG GLFANGGAGG AGGFGANGGT GGNGLLFGAG 660
GTGGAGTLGA DGGAGGHGGL FGAGGTGGAG GSSGGTFGGN GGSGGNAGLL ALGASGGAGG 720
SGGSALNVGG TGGVGGNGGS GGSLFGFGGA GGTGGSSGIG SSGGTGGDGG TAGVFGNGGD 780
GGAGGFGADT GGNSSSVPNA VLIGNGGNGG NGGKAGGTPG AGGTSGLIIG ENGLNGL 837

<212> Type : PRT
<211> Length : 837
SequenceName : SEQ ID 159
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MSFVIAVPET IAAAATDLAD LGSTIAGANA AAAANTTSLL AAGADEISAA IAALFGAHGR 60
AYQAASAEAA AFHGRFVQAL TTGGGAYAAA EAAAVTPLLN SINAPVLAAT GRPLIGNGAN 120
GAPGTGANGG DAGWLIGNGG AGGSGAKGAN GGAGGPGGAA GLFGNGGAGG AGGTATANNG 180
IGGAGGAGGS AMLFGAGGAG GAGGAATSLV GGIGGTGGTG GNAGMLAGAA GAGGAGGFSF 240
STAGGAGGAG GAGGLFTTGG VGGAGGQGHT GGAGGAGGAG GLFGAGGMGG AGGFGDHGTL 300
GTGGAGGDGG GGGLFGAGGD GGAGGSGLTT GGAAGNGGNA GTLSLGAAGG AGGTGGAGGT 360
VFGGGKGGAG GAGGNAGMLF GSGGGGGTGG FGFAAGGQGG VGGSAGMLSG SGGSGGAGGS 420
GGPAGTAAGG AGGAGGAPGL IGNGGNGGNG GESGGTGGVG GAGGNAVLIG NGGEGGIGAL 480
AGKSGFGGFG GLLLGADGYN APESTSPWHN LQQDILSFIN EPTEALTGRP LIGNGDSGTP 540
GTGDDGGAGG WLFGNGGNGG AGAAGTNGSA GGAGGAGGIL FGTGGAGGAG GVGTAGAGGA 600
GGAGGSAFLI GSGGTGGVGG AATTTGGVGG AGGNAGLLIG AAGLGGCGGG AFTAGVTTGG 660
AGGTGGAAGL FANGGAGGAG GTGSTAGGAG GAGGAGGLYA HGGTGGPGGN GGSTGAGGTG 720
GAGGPGGLYG AGGSGGAGGH GGMAGGGGGV GGNAGSLTLN ASGGAGGSGG SSLSGKAGAG 780
GAGGSAGLFY GSGGAGGNGG YSLNGTGGDG GTGGAGQITG LRSGFGGAGG AGGASDTGAG 840
GNGGAGGKAG LYGNGGDGGA GGDGATSGKG GAGGNAVVIG NGGNGGNAGK AGGTAGAGGA 900
GGLVLGRDGQ HGLT 914
<212> Type : PRT
<211> Length : 914
SequenceName : SEQ ID 160
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MSLVIVTPET VAAAASDVAR IGSSIGVANS AAAGSTTSVL AAGADEVSAA IATLFGSHAR 60
EYQAISTQVA AFHDRFAQTL SAAVGSYVSA EATNAAPLAT LEHNVLNALN APTQALLGRP 120
LIGDGAAGAP GTGQAGGAGG ILWGNGGAGG SGAPGQVGGA GGAAGLFGTG GAGGAGGAGA 180

AGGAGGSGGW LLGNGGVGGA GGQSLLGGAT GGAGGNAGLF GVGGTGGPGG PGGPGGVGGT 240
GGAGGLGGTL YGAGGHGGAG GPGPIGGVGG HGGVGGAAGL LGVGGHGGAG GHGAEGVAGA 300
AGEDLSPHGT SGGVGGDAGD GGTGGRGGWL AGAGGAGGAG GVGGTGGAGG AGFSRALIVA 360
GDNGGDGGNG GMGGAGGAGG PGGAGGLISL LGGQGAGGAG GTGGAGGVGG DRGAGGPGNQ 420
AFNAGAGGAG GHGGDPGAGG AGGTGGAGSI TGAQGAIGAT PTSGGNGGAG GNGANATTAG 480
TNGANGGPGG HGGLVGNGGA GGNGANGAAG TNASDSGAVG GKGNSGGNGG QGGAGGDGGT 540
LAGNGGAGGT GGRGADGGLG GSGAEGANAT TAGERGQDGG KGGNGGVGGT GGNAVAPGAN 600
GGHGGNGGNP GPSGAGGLGG LSGDGVTRAA QGATPDFADT GGKGGNGGNG ANAVAPGGTG 660
ASGGAGGNAG AGGKGGENII GDGGGGNGGA GGKGGAGTLL GLTVFGDNGG AGVLGDSTDP 720
DGSGGAGGAG GAGGAGGDPT I 741

<212> Type : PRT
<211> Length : 741
SequenceName : SEQ ID 161
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MSFVTAAPEM LATAAQNVAN IGTSLSAANA TAAASTTSVL AAGADEVSQA IARLFSDYAT 60
HYQSLNAQAA AFHHSFVQTL NAAGGAYSSA EAANASAQAL EQNLLAVINA PAQALFGRPL 120
IGNGANGTAA SPNGGDGGIL YGNGGNGFSQ TTAGVAGGAG GSAGLIGNGG NGGAGGAGAA 180
GGAGGAGGWL LGNGGAGGPG GPTDVPAGTG GAGGAGGDAP LIGWGGNGGP GGFAAFGNGG 240
AGGNGGASGS LFGVGGAGGV GGSSEDVGGT GGAGGAGRGL FLGLGGDGGA GGTSNNNGGD 300
GGAGGTAGGR LFSLGGDGGN GGAGTAIGSN AGDGGAGGDS SALIGYAQGG SGGLGGFGES 360
TGGDGGLGGA GAVLIGTGVG GFGGLGGGSN GTGGAGGAGG TGATLIGLGA GGGGGIGGFA 420
VNVGNGVGGL GGQGGQGAAL IGLGAGGAGG AGGATVVGLG GNGGDGGDGG GLFSIGVGGD 480
GGNAGNGAMP ANGGNGGNAG VIANGSFAPS FVGFGGNGGN GVNGGTGGSG GILFGANGAN 540
GPS 543

<212> Type : PRT
<211> Length : 543
SequenceName : SEQ ID 162
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MSYVLATPEM VAAAANNLAQ IGSTLSAANA AALAPTTGVL AAGADEVSAA VASLFSGHAQ 60
AYQTLGTQAA AFHERFIQAL STAAGAYGSA EAANASPLQQ ALNVINAPTQ TLLGRPLIGN 120
GTNGAPGTGQ AGGPGGLLYG NGGNGGSGGV GQAGGAGGSA GLIGIGGTGG AGGAGAVGGV 180
GGNGGWLYGN GGAGGLGGTG VAGVNGGMGA AGGAGGNAYL FGSGGAGGQG GMGAAGADGV 240
NPTPTGTADA GSTGTDQTLG GNAIGGNGGP GDAGDAMTSG GAGGSGGNAV STVNGDAVGG 300
EGGKGGEGAY GGAGGAGGSA ASIGNAAIGG NGGAGGNAQA PGGVGGAGGE GGDAQVGTNS 360
PSNAEAGNGG SGGNGFDSFA SGGTGGAGGT GGAGGRGGLL IGDGGAGGAG GVGGTGGSGA 420
PGGGGGAGGD GGAANTDSAG SSRKAFGGDG GVGGDGASAL GTGGEGGIGG QGGNGGAGGL 480
LIGNGGAGGV GGTAGAGGTG GSGGAGGAGG AGGGGTNSGP GAAFGGNGNT GGNGGNGGAP 540
GALGGKGGSG GLIGRAGSDG GVGAGGAGGA GGAGGTGGEG GTGGDGKTTD GNPGMGGSPG 600
SAGQPG 606

<212> Type : PRT
<211> Length : 606
SequenceName : SEQ ID 163
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MSFLFAQPEM LGAAATDLAS IGSAISTANA AAAAATTRVL AAGADEVSAA VAALFSGHAQ 60
TYQALRTQAA AFHQQIVQTL TSTAGAYASA EAANVEQQLL GAINAPTMAL LGRPLIGHGA 120
DGAPGTGQAG GAGGILYGNG GNGGSGATGQ AGGAGGAAGL IGHGGAGGLG GTGASGGAGG 180
AGGWLWGNGG AGGNGGVGVA GDPGGVGGAG GAGGAAGLWG SGGSGGTGGQ GGVGGGKSGD 240
GGTGGIGGAG GGGGWLHGDG GAGGHGGQGG TGVSSGGNGG AGGTGGDGRG LSGSGGAGGR 300
GGQTGVGGKV GENNFGGAGG AGGTGGLIGN GGAGGNGGQG AISGAGGAGG NAWLIGDGGA 360
GGNGGDIRGQ GGGAGGAGGA GGQLIGNGGT GGAGGTVTSP NGLGGAGGAG GSAGLIGHGG 420
TGGAGGHSAQ GPDGNGGIGG AGGAGGNGGQ LYGTGGTGGT GGKGGDGFGV FGKGGAGGTG 480
GRGGAAGLIG DAGTGGTGGK GGTAGEDGTG GNGGTGGNGG AAVLIGNGGG GGAGGNGGAG 540

NDGTPGNGGG GGVGGTGGTL FGQPGQPGPP GQPGPA 576

<212> Type : PRT
<211> Length : 576
SequenceName : SEQ ID 164
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MWTSQMIVAP AFVDAAAKDL ATIGSAISRA NAEALVPITA LLPAGADDVS AAIAALFATH 60
GQAYQELSAH AVAFHEQFVQ LMSAGAAQYA SAEAANSSPL QIVGQTALDA INSPVQTLTG 120
RPLIGNGANG VAGTGQNGGD GGWLYGNGGN GGSGGTGQNG GNGGSAGLWG SGGNGGQGGA 180
GANGAAGQPG KAGGSGGNGG AGGWIYGHGG HGGAGGNGGN ATAPGGASAG FDGGAGGNGG 240
SGGRGGLLFG NGGNGSVGGM GGQGTNDTAG DSAGSGGLGG NGGNGAQGGW LIGNGGQGGD 300
SGAGGGTDST QTGVMNGASG GSAGIAGNGG DAGLVGNGGA GGNGGNGAAG SALGTTIFGG 360
SGGVGGSGGD GGNGGWLFGS GASGGNGGQG GDAGTNGFAG FGGSAGGGGW VGAVNFGPIS 420
VQGFGLFGHG GDGGNGGDVG AGSLSIQFGA SGGDGGQGGV LYGNGGNGGN AGSGGGTGFE 480
GSAGQGGAAI LIGNGGAGGN GATGGTGVGN IIQEAGGDGS DGGAGGSGGL LFGSGGAGGI 540
GGAGGVGGSG NDGGNGGDGG QGGASGLGIG NGGPGGSGGT GGAGGTGGSA GTGGAGGDGG 600
NAALLIGTGG DGGDGVPPAP GGQGGKGGLI GLPGQNGQP 639

<212> Type : PRT
<211> Length : 639
SequenceName : SEQ ID 165
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MSWVMVSPEL VVAAAADLAG IGSAISSANA AAAVNTTGLL TAGADEVSTA IAALFGAQGQ 60
AYQAASAQAA AFYAQFVQAL SAGGGAYAAA EAAAVSPLLA PINAQFVAAT GRPLIGNGAN 120
GAPGTGANGG PGGWLIGNGG AGGSGAPGAG AGGNGGAGGL FGSGGAGGAS TDVAGGAGGA 180
GGAGGNAGML FGAAGVGGVG GFSNGGATGG AGGAGGAGGL FGAGRERGSG GSGNLTGGAG 240
GAGGNAGTLA TGDGGAGGTG GASRSGGPGG AGGAGGDAGM FFGSGGSGGA GGISKSVGDS 300
AAGGAGGAPG LIGNGGNGGN GGASTGGGDG GPGGAGGTGV LIGNGGNGGS GGTGATLGKA 360
GIGGTGGVLL GLDGFTAPAS TSPLHTLQQD VINMVNDPFQ TLTGRPLIGN GANGTPGTGA 420
DGGAGGWLFG NGGNGGQGTI GGVNGGAGGA GGAGGILFGT GGTGGSGGPG ATGLGGIGGA 480
GGAALLFGSG GAGGSGGAGA VGGNGGAGGN AGALLGAAGA GGAGGAGAVG GNGGAGGNGG 540
LFANGGAGGP GGFGSPAGAG GIGGAGGNGG LFGAGGTGGA GGGSTLAGGA GGAGGNGGLF 600
GAGGTGGAGS HSTAAGVSGG AGGAGGDAGL LSLGASGGAG GSGGSSLTAA GVVGGIGGAG 660
GLLFGSGGAG GSGGFSNSGN GGAGGAGGDA GLLVGSGGAG GAGASATGAA TGGDGGAGGK 720
SGAFGLGGDG GAGGATGLSG AFHIGGKGGV GGSAVLIGNG GNGGNGGNSG NAGKSGGAPG 780
PSGAGGAGGL LLGENGLNGL M 801

<212> Type : PRT
<211> Length : 801
SequenceName : SEQ ID 166
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
GQSYQAVSAQ AAAFHDRFVQ LLNAGGGSYA SAEIANAQQN LLNAVNAPTQ TLLGRPLVGD 60
GADGASGPVG QPGGDGGILW GNGGNGGDST SPGVAGGAGG SAGLIGNGGR GGNGAPGGAG 120
GNGGLGGLLL GNGGAGGVGG TGDNGVGDLG AGGGGGDGGL GGRAGLIGHG GAGGNGGDGG 180
HGGSGKAGGS GGSGGFGQFG GAGGLLYGNG GAAGSGGNGG DAGTGVSSDG FAGLGGSGGR 240
GGDAGLIGVG GGGGGNGGDP GLGARLFQVG SRGGDGGVGG WLYGDGGGGG DGGNGGLPFI 300
GSTNAGNGGS ARLIGNGGAG GSGGSGAPGS VSSGGVGGAG NPGGSGGNGG VWYGNGGAGG 360
AAGQGGPGMN TTSPGGPGGV GGHGGTAILF GDGGAGGAGA AGGPGTPDGA AGPGGSGGTG 420
GLLFGVPGPS GPDG 434

<212> Type : PRT
<211> Length : 434
SequenceName : SEQ ID 167
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MAHFSVLPPE INSLRMYLGA GSAPMLQAAA AWDGLAAELG TAASSFSSVT TGLTGQAWQG 60
PASAAMAAAA APYAGFLTTA SAQAQLAAGQ AKAVASVFEA AKAAIVPPAA VAANREAFLA 120
LIRSNWLGLN APWIAAVESL YEEYWAADVA AMTGYHAGAS QAAAQLPLPA GLQQFLNTLP 180
NLGIGNQGNA NLGGGNTGSG NIGNGNKGSS NLGGGNIGNN NIGSGNRGSD NFGAGNVGTG 240
NIGFGNQGPI DVNLLATPGQ NNVGLGNIGN NNMGFGNTGD ANTGGGNTGN GNIGGGNTGN 300
NNFGFGNTGN NNIGIGLTGN NQMGINLAGL LNSGSGNIGI GNSGTNNIGL FNSGSGNIGV 360
FNTGANTLVP GDLNNLGVGN SGNANIGFGN AGVLNTGFGN ASILNTGLGN AGELNTGFGN 420
AGFVNTGFDN SGNVNTGNGN SGNINTGSWN AGNVNTGFGI ITDSGLTNSG FGNTGTDVSG 480
FFNTPTGPLA VDVSGFFNTA SGGTVINGQT SGIGNIGVPG TLFGSVRSGL NTGLFNMGTA 540
ISGLFNLRQL LG 552
<212> Type : PRT
<211> Length : 552
SequenceName : SEQ ID 168
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MSFLIASPEA LAATATYLTG IGSAISAANA VAAAPTTEIL AAGTDEVSTA ISALFGAHAQ 60
AYQALSAHVA AFHDQFVHTL TAGAGSYMAA EAAAASPLQA LQLELLNAIN APTLALLGRP 120
LIGDGTDAAP GSGGAGGAGG ILIGNGGTGG ASDLAGTGRG GVGGAGGAGG LFGIGGAGGG 180
CGSAVAIGGD GGAGGAGGVF SGGGAGGAGD AIGGSGGAGG TGGLLGGGGG AGGAGGAGGN 240
GGGASNSASI GGDGGSGGAG GMLYGAGGVG GNGGAAVAIG GDGGAGGRAG AIGNGGDGGN 300
GGTSNTPGGS GGDGGNGGNA GLIGNGGNGG NAEIVISGGS VAGTGGNGGL LLGFNGTNGL 360
P 361
<212> Type : PRT
<211> Length : 361
SequenceName : SEQ ID 169
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
AQASPAAHGG SGGAGGNGGA GSAGNGGAGG AGGNGGAGGN GGGGDAGNAG SGGNGGKGGD 60
GVGPGSTGGA GGKGGAGANG GSSNGNARGG NAGNGGHGGA GGSGDTGGAG GAGGQGGFGG 120
TGGSGSGIGG GAGGNGGNGG AGGTGVVLGG KGGDGGNGDH GGPATNPGSG SRGGAGGSGG 180
NGGAGGNATG SGGKGGAGGN GGDGSFGATS GPASIGVTGA PGGNGGKGGA GGSNPNGSGG 240
DGGKGGNGGA GGNGGSIGAN SGIVGGSGGA GGAGGAGGNG SLSSGEGGKG GDGGHGGDGV 300
GGNSSVTQGG SGGGGGAGGA GGSGFFGGKG GFGGDGGQGG PNGGGTVGTV AGGGGNGGVG 360
GRGGDGVFAG AGGQGGLGGQ GGNGGGSTGG NGGLGGAGGG GGNAPDGGFG GNGGKGGQGG 420
IGGGTQSATG LGGDGGDGGD GGNGGNSGAK AGGAGGKGQA GQPNSGTEPG FGGDGGLGGA 480
GATP 484
<212> Type : PRT
<211> Length : 484
SequenceName : SEQ ID 170
SequenceDescription :

Sequence

<213> OrganismName : Rickettsia prowazekii
<400> PreSequenceString :
MKKSKILRKF LATASLCGTL FTNSNATGTI IPNNGSVSLN TDAGLVGGVF NNGDIIQIVN 60
GGREIKISAD KANAIIGGIN TLKELPDFGG VEVSQNVSIG PLNAGEDLNT NFGPLKFISN 120
NVTSIITGVG TKTFSNIDFA GKNATLQINK DLNITTKIDN TVAGNNGSIT FEGSGIISNH 180
IGYTNSLLGI NVGNGEAKIY APEANNITIN AKNINLTHNN SILTLCDGNI TTLKGNINNT 240
TEIDGQGILN LAYDLGSSSI ITGDIGNIGS LDTINVLLGS ATFNSTILKA TNINLKHNTS 300
TLNLDDNIIV IGNIKGNNNK DILNFKVHGT NLDNEMIIPA PQKTHGTLNF KGNATLNGNI 360
NNLNILKFSG GHGKTLNLQG NTKVDNLVFA DSVLDSGTIS VNGLLDTDCV TFNNSNVNGG 420
TLIINAKNTI SAKLLNATKA KIQINANLTM NHPSAGDISD IRIADNTIYT IDAKNGNVNL 480
LNNNAKIIFE GADSMLALIN TGVTADRTFT IYNNLNQSGN DEYGIVKIEA IKKVITIANQ 540
SGPYTIGQDN THRLKELIVE GAGDIIIDDT IFTKLLSINS TGQITFNRTL DLGAGGNIAF 600
GKHGTLVVNG VTGSITTSEN NQGILTINSG NITGVIGTNE LGLKLVNIGA DPVTCSANVF 660

ASVALTNPSS VLILADGVTL TGEVTTHNNT KGVLSLGTGS NITGQIGTNS AALEKINIGA 720
GASNIDSNIY AGSTVLTDQT SELTLNNIDVV VNSNIITTAG NNSGKLIFTG NGGITGNIGA 780
NGAALQEVVF NGTTNIGGTA NSQNFTVAHS AANVVITGLT TGALKYKDTG TIIAHGGLVG 840
DIDFNNKAGK FILGDGAMID GSVLCNGGVA GTLDFIGDGN VTQNIGADNA NSISTINIQG 900
DNTKNVTIAN DIFVDNIHFT NGGILQLGGN LTTHNIDFGA NGGTLEFNGN NTYNLNAIIV 960
NGQNGILNAF TNLKASDDTI GTVKIINIGQ IGTPQNFTIQ VNNKNLTLVS SVNSSINFGD 1020
ANSQLILSAP VDQTIKFINN LNETGGGIIT LDSNGNNLTI SGNNGIKLGS KGNELSSLNI 1080
KGKVTVTNDL DIQNIHQLNI NNGALFDDQS LTSAKIKNIN IGTVAGGATY TLDAINDNFD 1140
LNTSGMVFKH QDSILELKNS SNTNDHTITL TSALDPGNNQ FGIIKLITDT NKLTIDNNGN 1200
VAYTLGTANH MLKQLTFASI DNGAIALKVG INVENVTLNI KDIELNEVNA NVLFNKNTTY 1260
TATGNINGHV DFQGNAGVIN LNDDIEIDGS VTSTGNVNGT LNFNGSGKVT GLINNIVMLQ 1320
AGAGDVSLSA SGNYSITEIQ GNGNNNLTFA ANSHLTTDIN KTGGQDLNLV FINGGSVSGS 1380
IGANAAVGDI IINAGSVNFS NTLKSGNIVI SDGATMQVNN NVTATDISGK NANNGTLKLN 1440
NHTPINITST LGNNNAIGTI EVANNDVTIT GTLQAQNIHF SNATQAATLT LGAASQVTNI 1500
TTAGNNIHTL EVTDFDTGND GIIGDANNRL KSIELTGNGT VTINSPHVYS SITTANNAQG 1560
NVKLNIEGGI TYDLGSKIKS LANVQISEDT TIRGDVYSKY LNIDAGKTIN FDRGDNNMNP 1620
KNLDIPDALI DLDVLPRSLS LFNYFTDIKA DNLNFADDTA TANFKDAVVI DAHIDNGGIL 1680
KFNDNAWLTQ EIKNANIIEI ASDKFMLLQK NIKAATLIAD NANLVLLDNV EVNTNLNVRD 1740
IVLDLANYEL KYTGNVTHNG LLTIITYFDT ALQKGGHILV SQGSNVDMSD LDNLIIKIKA 1800
HSDITNITSD TKHQIVKLET GAIYTPVPQT KVIIDASEEQ NKFVKWVADA NGLVLLTDTG 1860
GRDDTGGRDD TRGRGNTDNG CRDNCDVGNI SNNSSNEAGG SSSDKNYGIT DVVPIFDPSP 1920
ILDYTKNNYV ASGIANQLIN HVKDFGNTTD AGKLLNDLGF MSPNRVTETL DRLSNRINVN 1980
GLNEGVVGLN GIEVENFLTD IAINMDNFTA KEIGNRLEEL SDANTVNGLN KTNTLLNNKI 2040
NLKRLNTNNQ AIIAAGDEDN IVTGIWGMSF YGKIKQNSKN SASGYQSNTG GGIIGFDYNI 2100
DNSIVIGAAY TMADSKVKHK NDKNGDRTKA KSNIYSIYGL YNWLTNNFFV EAIGVYGRNK 2160
IKNYEKRITT ITDQIAIGKF INTFYSYELL GGYNYLISHR TTITPMFGMR YATPKNNGYK 2220
ENNTTFQNLS IKKNYYDKFE TILGLNSVTH YLSQDIIIKP ELHWFINYQC KNKLPNIDAR 2280
LDGIDEPLTT IRFKPAKITY NLGGGISTKN NMIEFGIRYN LSLAKKYTAH QGSLKIKVNL 2340

<212> Type : PRT
<211> Length : 2340
SequenceName : SEQ ID 171
SequenceDescription :

Sequence

<213> OrganismName : Rickettsia prowazekii
<400> PreSequenceString :
MAQKPNFLKK IISAGLVTAS TATIVAGFSG VAMGAAMQYN RTTNAAATTF DGIGFDQAAG 60
ANIPVAPNSV ITANANNPIT FNTPNGHLNS LFLDTANDLA VTINEDTTLG FITNIAQQAK 120
FFNFTVAAGK ILNITGQGIT VQEASNTINA QNALTKVHGG AAINANDLSG LGSITFAAAP 180
SVLEFNLINP TTQEAPLTLG ANSKIVNGGN GTLNITNGFI QVSDNTFAGI KTINIDDCQG 240
LMFNSTPDAA NTLNLQVGGN TINFNGIDGT GKLVLVSKNG AATEFNVTGT LGGNLKGIIE 300
LNTAAVAGKL ISQGGAANAV IGTDNGAGRA AGFIVSVDNG NAATISGQVY AKNMVIQSAN 360
AGGQVTFEHI VDVGLGGTTN FKTADSKVII TENSNFGSTN FGNLDTQIVV PDTKILKGNF 420
IGDVKNNGNT AGVITFNANG ALVSASTDPN IAVTNINAIE AEGAGVVELS GIHIAELRLG 480
NGGSIFKLAD GTVINGPVNQ NALMNNNALA AGSIQLDGSA IITGDIGNGG VNAALQHITL 540
ANDASKILAL DGANIIGANV GGAIHFQANG GTIKLTNTQN NIVVNFDLDI TTDKTGVVDA 600
SSLTNNQTLT INGSIGTVVA NTKTLAQLNI GSSKTILNAG DVAINELVIE NNGSVQLNHN 660
TYLITKTINA ANQGQIIVAA DPLNTNTTLA DGTNLGSAEN PLSTIHFATK AANADSILNV 720
GKGVNLYANN ITTNDANVGS LHFRSGGTSI VSGTVGGQQG HKLNNLILDN GTTVKFLGDT 780
TFNGGTKIEG KSILQISNNY TTDHVESADN TGTLEFVNTD PITVTLNKQG AYFGVLKQVI 840
ISGPGNIVFN EIGNVGIVHG IAANSISFEN ASLGTSLFLP SGTPLDVLTI KSTVGNGTVD 900
NFNAPIVVVS GIDSMINNGQ IIGDKKNIIA LSLGSDNSIT VNANTLYSGI RTTKNNQGTV 960
TLSGGMPNNP GTIYGLGLEN GSPKLKQVTF TTDYNNLGSI IANNVTINDY VTLTTGGIAG 1020
TDFDAKITLG SVNGNANVRF VDSTFSDPRS MIVATQANKG TVTYLGNALV SNIGSLDTPV 1080
ASVRFTGNDS GAGLQGNIYS QNIDFGTYNL TILNSNVILG GGTTAINGEI DLLTNNLIFA 1140
NGTSTWGDNT SISTTLNVSS GNIGQVVIAE DAQVNATTTG TTTIKIQDNA NANFSGTQAY 1200
TLIQGGARFN GTLGAPNFAV TGSNIFVKYE LIRDSNQDYV LTRTNDVLNV VTTAVGNSAI 1260
ANAPGVSQNI SRCLESTNTA AYNNMLLAKD PSDVATFVGA IATDTSAAVT TVNLNDTQKT 1320
QDLLSNRLGT LRYLSNAETS DVAGSATGAV SSGDEAEVSY GVWAKPFYNI AEQDKKGGIA 1380
GYKAKTTGVV VGLDTLASDN LMIGAAIGIT KTDIKHQDYK KGDKTDINGL SFSLYGSQQL 1440
VKNFFAQGNA IFTLNKVKSK SQRYFFESNG KMSKQIAAGN YDNMTFGGNL IFGYDYNAMP 1500
NVLVTPMAGL SYLKSSNENY KETGTTVANK RINSKFSDRV DLIVGAKVAG STVNITDIVI 1560
YPEIHSFVVH KVNGKLSNSQ SMLDGQTAPF ISQPDRTAKT SYNIGLSANI KSDAKMEYGI 1620
GYDFNSASKY TAHQGTLKVR VNF 1643
<212> Type : PRT

<211> Length : 1643
SequenceName : SEQ ID 172
SequenceDescription :

Sequence

<213> OrganismName : Porphyromonas gingivalis W83
<400> PreSequenceString :

MARIILEAHD VWEDGTGYQM LWDADHNQYG ASIPEESFWF ANGTIPAGLY DPFEYKVPVN 60
ADASFSPTNF VLDGTASADI PAGTYDYVII NPNPGIIYIV GEGVSKGNDY VVEAGKTYHF 120
TVQRQGPGDA ASVVVTGEGG NEFAPVQNLQ WSVSGQTVTL TWQAPASDKR TYVLNESFDT 180
QTLPNGWIMI DADGDGHNWL STINVYNTAT HTGDGAMFSK SWTASSGAKI DLSPDNYLVT 240
PKFTVPENGK LSYWVSSQEP WTNEHYGVFL STTGNEAANF TIKLLEETLG SGKPAPMNLV 300
KSEGVKAPAP YQERTIDLSA YAGQQVYLAF RHPGCTGIFR LYLDDVAVSG EGSSNDYTYT 360
VYRDNVVIAQ NLTATTFNQE NVAPGQYNYC VEVKYTAGVS PKVCKDVTVE GSNEFAPVQN 420
LTGSAVGQKV TLKWDAPNGT PNPNPGTTTL SESFENGIPA SWKTIDADGD GNNWTTTPPP 480
GGSSFAGHNS AICVSSASYI NFEGPQNPDN YLVTPELSLP NGGTLTFWVC AQDANYASEH 540
YAVYASSTGN DASNFANALL EEVLTAKTVV TAPEAIRGTR VQGTWYQKTV QLPAGTKYVA 600
FRHFGCTDFF WINLDDVEIK ANGKRADFTE TFESSTHGEA PAEWTTIDAD GDGQGWLCLS 660
SGQLGWLTAH GGTNVVASFS WNGMALNPDN YLISKDVTGA TKVKYYYAVN DGFPGDHYAV 720
MISKTGTNAG DFTVVFEETP NGINKGGARF GLSTEANGAK PQSVWIERTV DLPAGTKYVA 780
FRHYNCSDLN YILLDDIQFT MGGSPTPTDY TYTVYRDGTK IKEGLTETTF EEDGVATGNH 840
EYCVEVKYTA GVSPKECVNV TVDPVQFNPV QNLTGSAVGQ KVTLKWDAPN GTPNPNPGTT 900
TLSESFENGI PASWKTIDAD GDGNNWTTTP PPGGTSFAGH NSAICVSSAS YINFEGPQNP 960
DNYLVTPELS LPNGGTLTFW VCAQDANYAS EHYAVYASST GNDASNFANA LLEEVLTAKT 1020
VVTAPEAIRG TRVQGTWYQK TVQLPAGTKY VAFRHFGCTD FFWINLDDVE IKANGKRADF 1080
TETFESSTHG EAPAEWTTID ADGDGQGWLC LSSGQLDWLT AHGGTNVVAS FSWNGMALNP 1140
DNYLISKDVT GATKVKYYYA VNDGFPGDHY AVMISKTGTN AGDFTVVFEE TPNGINKGGA 1200
RFGLSTEANG AKPQSVWIER TVDLPAGTKY VAFRHYNCSD LNYILLDDIQ FTMGGSPTPT 1260
DYTYTVYRDG TKIKEGLTET TFEEDGVATG NHEYCVEVKY TAGVSPKECV NVTVDPVQFN 1320
PVQNLTGSAV GQKVTLKWDA PNGTPNPNPG TTTLSESFEN GIPASWKTID ADGDGNNWTT 1380
TPPPGGTSFA GHNSAICVSS ASYINFEGPQ NPDNYLVTPE LSLPNGGTLT FWVCAQDANY 1440
ASEHYAVYAS STGNDASNFA NALLEEVLTA KTVVTAPEAI RGTRVQGTWY QKTVQLPAGT 1500
KYVAFRHFGC TDFFWINLDD VEIKANGKRA DFTETFESST HGEAPAEWTT IDADGDGQGW 1560
LCLSSGQLGW LTAHGGTNVV ASFSWNGMAL NPDNYLISKD VTGATKVKYY YAVNDGFPGD 1620
HYAVMISKTG TNAGDFTVVF EETPNGINKG GARPGLSTEA NGAKPQSVWI ERTVDLPAGT 1680
KYVAFRHYNC SDLNYILLDD IQFTMGGSPT PTDYTYTVYR DGTKIKEGLT ETTFEEDGVA 1740
TGNHEYCVEV KYTAGVSPKE CVNVTINPTQ FNPVQNLTAE QAPNSMDAIL KWNAPASKRA 1800
EVLNEDFENG IPASWKTIDA DGDGNNWTTT PPPGGSSFAG HNSAICVSSA SYINFEGPQN 1860
PDNYLVTPEL SLPGGGTLTF WVCAQDANYA SEHYAVYASS TGNDASNFAN ALLEEVLTAK 1920
TVVTAPEAIR GTRVQGTWYQ KTVQLPAGTK YVAFRHFGCT DFFWINLDDV VITSGNAPSY 1980
TYTIYRNNTQ IASGVTETTY RDPDLATGFY TYGVKVVYPN GESAIETATL NITSLADVTA 2040
QKPYTLTVVG KTITVTCQGE AMIYDMNGRR LAAGRNTVVY TAQGGHYAVM VVVDGKSYVE 2100
KLAVK 2105

<212> Type : PRT
<211> Length : 2105
SequenceName : SEQ ID 173
SequenceDescription :

Sequence

<213> OrganismName : Porphyromonas gingivalis W83
<400> PreSequenceString :

MKTSERILSY FFLLCAVFSL GSCEGLYAQV TFPNYSPTAA SSIAVCSGEE TLIIDFTVVQ 60
EDSNGIKVNV KLADGVEYVV GTAVVSVTQG NAVTVAETNV SNPNEPVFTV KSADGNNVVE 120
LGTIVKLTIK RRAVCTAWSN AINAAETGFV FKDKVTVTIG DHSDSKESNS YSVNYPNLTI 180
KQPAPQVNKQ IGETIVREFS ITNGSQNPTQ TVYLSIEYPD EAYLTGVGAM TLQAKLGASG 240
TYADLTPTVT NGKVRIYTLS GSSLGPDHLL TNGEIIYLKE TFKLKTCAPV TVYRVGWGCS 300
IDSQCEIKTT AATITMAAGA ANITGYSVTG PDYRSPTFSL CQPFELTIKF SNSGAGGSMG 360
AAFNINTIGR NDYYRPRGFV LHEFIDVKVN GKPVTNFKTD GSELDLRFDG QFTEDPDGPG 420
VGLDDVDGDG FYDDLPVGAT ITITVTVRLK CDQFTACNNA PNDLSDRGLI LKTLYQTSCD 480
RTSWIDPNTW FNLSSTHLYL SRESVQDASH MPTVIEKDTP FDLKIMTSYY SILSSYNNIW 540
YANPNTRYVV EIVFPQGMTM PPKSDIEWTN IKNHPIDGSL VFTPPINLPD ANITTSGNTM 600
TIVSPSQERG FVTLHGVKYD CTNNHEMVVE YKIREVFNYL HFPDCLCPVG PIMCNTAKRY 660
VLGCDPPCGR GAETSVPKIE RADNSLGWTD YTMRTRQSRS NISAYDLAKA LYMDEVNITA 720
TSIQHGTASS LGARFVLATG VDRVETLTPL SADIKIFRDG VQIVSVDGYT TFRSIRRNNN 780
AEQVIDWDFT SILPAGGLLD RDKVDVVTRY RVTSQNAHRV DTQVGREWFF YNSTANVSPI 840

WDEANPLTCL ILVPEIYIMG TFVVNGTDPH VISQCTPTDL GRVANHYARR FGSGAFEYAN 900
EYRPGVKIRN IYLKVPKSYT LNRVEYSNHR NHSSLGTTMP FEEINHTDVT SQGEYNIYKY 960
QLADNEKAHF NITVKNAYGA ALKVNVSPTC ASSAVATNYD KISYYVDYID YYYYAATQPT 1020
VPNSLDIVAD QSAGSNGIYS VSALNVYNRP ILYTNKPSIA LVNQSGEVEL VGKTGEWKLR 1080
ISNPSSATAP YVWLALPTTS GLTIEKVTDA AGTEMAFTTY SGGKMYRLSE AGVPVGSALD 1140
YTIHFTYSGC SPIALKAMGG WNCSAYPLSL DEYVCSSQVI DLKLKPLPAA MELTEIAVPD 1200
PTAAATLCST LEYIYSIQST DNANVYSPTF SIFPEEGLVV TPNQVQVEYP AGSGNWAALN 1260
VVNNSVNLLQ HPALTTIGYL KGLKEGESND NQRKILVKFY IKTECSFVSG KNFRVRADGR 1320
NACNQNAKGS GLAISTPPIR INGAIEPYTT SASTQLVTTT TSQSDCKAPK RVKVVQTVVG 1380
GETTPKAYLE ITLPLGFKYV TGSYAPDNTH PGGVNASPAG TEEVTLTANG EDKIKINVKA 1440
GLTSGQSFAY TLEMKEDDDN VPACGNHTIE IVNVEEIEGL WCEGVQCAET LVVTGANKFE 1500
FELDKPYLDI TVISAVSTFS GGKENLTIEY KVSNTSTTQP LKPGAVVTLF SDKDNNQVFS 1560
GGDVAVATQE LVAEITNTTP LTQIMKVKGV SSSHTGNLVL TILPKDGCYC EIKSPMVTLN 1620
HLPSNYWIGG TVGKPNEWKE PNNWTNDQVP DAAEDVEFAT EVNNPTDPNN PKSGPAKENL 1680
HLDDIHQNGT AGRVIGNLIN DSDKDLVITT GNQLTINGVV EDNNPNVGTI VVKSSKDNPT 1740
GTLLFANPGN NQNVGGTVEF YNQGYDCADC GMYRRSWQYF GIPVNESDFP YDHVDGNATV 1800
NQWVEPFNGD KWRPAPYAPD TKLQKFKGYQ ITNDVQAQPT GVYSFKGTLC VCDAFLNLTR 1860
TSGVNYSGAN LIGNSYTGAI DIKQGIVFPP EVEQTVYLFN TGTRDQWRKL NGSTVSGYRA 1920
GQYLSVPKNT AGQDNLPDRI PSMHISFLVKM QNGASCTLQI LYDKLLKNTT VNNGNGTQIT 1980
WRSGNSGSAN MPSLVMDVLG NESADRLWIF TDGGLSFGFD NGWDGRKLTE KGLSQLYAMS 2040
DIGNDKFQVA GVPELNNLLI GFDADKDGQY TLEFALSDHF AKGGVFLEDL SRGVTRRVVD 2100
GGSYSFDAKR GDSGARFRLS YDEEWVESAE VSVLVGTAGK RIVITNNSEH ACQANVYTTD 2160
GKLLIRLDVK PGSKSMTEPL VDGVYVVSLQ SPATSSNVRK VVVN 2204

<212> Type : PRT
<211> Length : 2204
SequenceName : SEQ ID 174
SequenceDescription :

Sequence

<213> OrganismName : Porphyromonas gingivalis W83
<400> PreSequenceString :
MNKFYKSLLQ SGLAAFVSMA TALTASAQIS FGGEPLSFSS RSAGTHSFDD AMTIRLTPDF 60
NPEDLIAQSR WQSQRDGRPV RIGQVIPVDV DFASKASHIS SIGDVDVYRL QFKLEGAKAI 120
TLYYDAFNIP EGGRLYIYTP DHEIVLGAYT NATHRRNGAF ATEPVPGSEL IMDYEVSRGG 180
TLPDIKISGA GYIFDKVGGR PVTDNHYGIG EDDSDSDCEI NINCPEGADW QAEKNGVVQM 240
IMVKGQYISM CSGNLLNNTK GDFTPLIISA GHCASITTNF GVTQSELDKW IFTFHYEKRG 300
CSNGTLAIFR GNSIIGASMK AFLPIKGKSD GLLLQLNDEV PLRYRVYYNG WDSTPDIPSS 360
GAGIHHPAGD AMKISILKKT PALNTWISSS GSGGTDDHFY FKYDQGGTEG GSSGSSLFNQ 420
NKHVVGTLTG GAGNCGGTEF YGRLNSHWNE YASDGNTSRM DIYLDPQNNG QTTILNGTYR 480
DGYKPLPSVP RLLLQSTGDQ VELNWTAVPA DQYPSSYQVE YHIFRNGKEI ATTKELSYSD 540
AIDESIIGSG IIRYEVSARF IYPSPLDGVE SYKDTDKTSA DLAIGDIQTK LKPDVTPLPG 600
GGVSLSWKVP FLSQLVSRFG ESPNPVFKTF EVPYVSAAAA QTPNPPVGVV IADKFMAGTY 660
PEKAAIAAVY VMPSAPDSTF HLFLKSNTNR RLQKVTTPSD WQAGTWLRIN LDKPFPVNND 720
HMLFAGIRMP NKYKLNRAIR YVRNPDNLFS ITGKKISYNN GVSFEGYGIP SLLGYMAIKY 780
LVVNTDAPKI DMSLVQEPYA KGTNVAPFPE LVGIYVYKNG TFIGTQDPSV TTYSVSDGTE 840
SDEYEIKLVY KGSGISNGVA QIENNNAVVA YPSVVTDRFS IKNAHMVHAA ALYSLDGKQV 900
RSWNNLRNGV TFSVQGLTAG TYMLVMQTAN GPVSQKIVKQ 940

<212> Type : PRT
<211> Length : 940
SequenceName : SEQ ID 175
SequenceDescription :

Sequence

<213> OrganismName : Porphyromonas gingivalis W83
<400> PreSequenceString :
MKNLNKFVSI ALCSSLLGGM AFAQQTELGR NPNVRLLEST QQSVTKVQFR MDNLKFTEVQ 60
TPKGMAQVPT YTEGVNLSEK GMPTLPILSR SLAVSDTREM KVEVVSSKFI EKKNVLIAPS 120
KGMIMRNEDP KKIPYVYGKS YSQNKFFPGE IATLDDPFIL RDVRGQVVNF APLQYNPVTK 180
TLRIYTEITV AVSETSEQGK NILNKKGTFA GFEDTYKRMF MNYEPGRYTP VEEKQNGRMI 240
VIVAKKYEGD IKDFVDWKNQ RGLRTEVKVA EDIASPVTAN AIQQFVKQEY EKEGNDLTYV 300
LLIGDHKDIP AKITPGIKSD QVYGQIVGND HYNEVFIGRF SCESKEDLKT QIDRTIHYER 360
NITTEDKWLG QALCIASAEG GPSADNGESD IQHENVIANL LTQYGYTKII KCYDPGVTPK 420
NIIDAFNGGI SLANYTGHGS ETAWGTSHFG TTHVKQLTNS NQLPFIFDVA CVNGDFLFSM 480
PCFAEALMRA QKDGKPTGTV AIIASTINQS WASPMRGQDE MNEILCEKHP NNIKRTFGGV 540
TMNGMFAMVE KYKKDGEKML DTWTVFGDPS LLVRTLVPTK MQVTAPAQIN LTDASVNVSC 600

DYNGAIATIS ANGKMFGSAV VENGTATINL TGLTNESTLT LTVVGYNKET VIKTINTNGE 660
PNPYQPVSNL TATTQGQKVT LKWDAPSTKT NATTNTARSV DGIRELVLLS VSDAPELLRS 720
GQAEIVLEAH DVWNDGSGYQ ILLDADHDQY GQVIPSDTHT LWPNCSVPAN LFAPFEYTVP 780
ENADPSCSPT NMIMDGTASV NIPAGTYDFA IAAPQANAKI WIAGQGPTKE DDYVFEAGKK 840
YHFLMKKMGS GDGTELTISE GGGSDYTYTV YRDGTKIKEG LTATTFEEDG VAAGNHEYCV 900
EVKYTAGVSP KVCKDVTVEG SNEFAPVQNL TGSAVGQKVT LKWDAPNGTP NPNPNPNPNP 960
NPGTTTLSES FENGIPASWK TIDADGDGHG WKPGNAPGIA GYNSNGCVYS ESFGLGGIGV 1020
LTPDNYLITP ALDLPNGGKL TFWVCAQDAN YASEHYAVYA SSTGNDASNF TNALLEETIT 1080
AKGVRSPEAI RGRIQGTWRQ KTVDLPAGTK YVAFRHFQST DMFYIDLDEV EIKANGKRAD 1140
FTETFESSTH GEAPAEWTTI DADGDGQGWL CLSSGQLDWL TAHGGTNVVS SFSWNGMAIN 1200
PDNYLISKDV TGATKVKYYY AVNDGFPGDH YAVMISKTGT NAGDFTVVFE ETPNGINKGG 1260
ARFGLSTEAD GAKPQSVWIE RTVDLPAGTK YVAFRHYNCS DLNYILLDDI QFTMGGSPTP 1320
TDYTYTVYRD GTKIKEGLTE TTFEEDGVAT GNHEYCVEVK YTAGVSPKKC VNVTVNSTQF 1380
NPVKNLKAQP DGGDVVLKWE APSAKKTEGS REVKRIGDGL FVTIEPANDV RANEAKVVLA 1440
ADNVWGDNTG YQFLLDADHN TFGSVIPATG PLFTGTASSD LYSANFEYLI PANADPVVTT 1500
QNIIVTGQGE VVIPGGVYDY CITNPEPASG KMWIAGDGGN QPARYDDFTF EAGKKYTFTM 1560
RRAGMGDGTD MEVEDDSPAS YTYTVYRDGT KIKEGLTETT YRDAGMSAQS HEYCVEVKYT 1620
AGVSPKVCVD YIPDGVADVT AQKPYTLTVV GKTITVTCQG EAMIYDMNGR RLAAGRNTVV 1680
YTAQGGYYAV MVVVDGKSYV EKLAIK 1706

<212> Type : PRT
<211> Length : 1706
SequenceName : SEQ ID 176
SequenceDescription :

Sequence

<213> OrganismName : Porphyromonas gingivalis W83
<400> PreSequenceString :
MKRKPLFSAL VILSGFFGSV HPASAQKVPA PVDGERIIME LSEADVECTI KIEAEDGYAN 60
DIWADLNGNG KYDSGERLDS GEFRDVEFRQ TKAIVYGKMA KFLFRGSSAG DYGATFIDIS 120
NCTGLTAFDC FANLLTELDL SKANGLTFVN CGKNQLTKLD LPANADIETL NCSKNKITSL 180
NLSTYTKLKE LYVGDNGLTA LDLSANTLLE ELVYSNNEVT TINLSANTNL KSLYCINNKM 240
TGLDVAANKE LKILHCNNNQ LTALNLSANT KLTTLSFFNN ELTNIDLSDN TALEWLFCNG 300
NKLTKLDVSA NANLIALQCS NNQLTALDLS KTPKLTTLNC YSNRIKDTAM RALIESLPTI 360
TEGEGRFVPY NDDEGGEEEN VCTTEHVEMA KAKNWKVLTS WGEPFPGITA LISIEGESEY 420
SVYAQDGILY LSGMEQGLPV QVYTVGGSMM YSSVASGSAM EIQLPRGAAY VVRIGSHAIK 480
TAMP 484

<212> Type : PRT
<211> Length : 484
SequenceName : SEQ ID 177
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MKRAITLFAV LLMGWSVNAW SFACKTANGT AIPIGGGSAN VYVNLAPVVN VGQNLVVDLS 60
TQIFCHNDYP ETITDYVTLQ RGSAYGGVLS NFSGTVKYSG SSYPFPTTSE TPRVVYNSRT 120
DKPWPVALYL TPVSSAGGVA IKAGSLIAVL ILRQTNNYNS DDFQFVWNIY ANNDVVVPTG 180
GCDVSARDVT VTLPDYPGSV PIPLTVYCAK SQNLGYYLSG TTADAGNSIF TNTASFSPAQ 240
GVGVQLTRNG TIIPANNTVS LGAVGTSAVS LGLTANYART GGQVTAGNVQ SIIGVTFVYQ 300

<212> Type : PRT
<211> Length : 300
SequenceName : SEQ ID 178
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MGIKQHNGNT KADRLAELKI RSPSIQLIKF GAIGLNAIIP SPLLIAADTG SQYGTNITIN 60
DGDRITGDTA DPSGNLYGVM TPAGNTPGNI NLGNDVTVNV NDASGYAKGI IIQGKNSSLT 120
ANRLTVDVVG QTSAIGINLI GDYTHADLGT GSTIKSNDDG IIIGHSSTLT ATQFTIENSN 180
GIGLTINDYG TSVDLGSGSK IKTDGSTGVY IGGLNGNNAN GAARFTATDL TIDVQGYSAM 240
GINVQKNSVV DLGTNSTIKT NGDNAHGLWS FGQVSANALT VDVTGAAANG VEVRGGTTTI 300
GADSHISSAQ GGGLVTSSSD ATINFSGTAA QRNSIFSGGS YGASAQTATA VINMQNTDIT 360

VDRNGSLALG LWALSGGRIT GDSLAITGAA GARGIYAMTN SQIDLTSDLV IDMSTPDQMA 420
IATQHDDGYA ASRINASGRM LINGSVLSKG GLINLDMHPG SVWTGSSLSD NVNGGKLDVA 480
MNNSVWNVTS NSNLDTLALS HSTVDFASHG STAGTFTTLN VENLSGNSTF IMRADVVGEG 540
NGVNNRGDLL NISGSSAGNH VLAIRNQGSE ATTGNEVLTV VKTTDGAASF SASSQVELGG 600
YLYDVRKNGT NWELYASGTV PEPTPNPEPT PAPAQPPIVN PDPTPEPAPT PKPTTTADAG 660
GNYLNVGYLL NYVENRTLMQ RMGDLRNQSK DGNIWLRSYG GSLDSFASGK LSGFDMGYSG 720
IQFGGDKRLS DVMPLYVGLY IDSTHASPDY SGGDGTARSD YMGMYASYMA QNGFYSDLVI 780
KASRQKNSFH VLDSQMNGVN ANGTANGMSI SLEAGQRFNL SPTGYGFYIE PQTQLTYSHQ 840
NEMAMKASNG LNIHLNHYES LLGRASMILG YDITAGNSQL NVYVKTGAIR EFSGDTEYLL 900
NDSREKYSFK GNGWNNGVGV SAQYNKQHTF YLEADYTQGN LFDQKQVNGG YRFSF 955

<212> Type : PRT
<211> Length : 955
SequenceName : SEQ ID 179
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MSKFVKTAIA AAMVMGVFTS TATIAAGNNG TARFYGTIED SVCSIVPDDH KLEVDMGDIG 60
AEKLKNNGTT TPKSFQIRLQ DCVFDTQETM TTTFTGTVSS ANSGNYYTIF NTDTGAAFNN 120
VSLAIGDSLG TSYKSGMGID QKIVKDTSTN KGKAKQTLNF NAWLVGAADA PDLGNFEANT 180
TFQITYL 187
<212> Type : PRT
<211> Length : 187
SequenceName : SEQ ID 180
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MKIKTLAIVV LSALSLSSAA ALADTITVNG GTIHFKGEVV NAACAVDAGS VDQTVQLGQV 60
RTASLKQAGA TSSAVGFNIQ LNDCDTTVAT KAAVAFLGTA IDATRTDVLA LQSSAAGSAT 120
NVGVQILDRT GNALTLDGAT FSAQTTLNNG TNTIPFQARY YAIGEATPGA ANADATFKVQ 180
YQ 182
<212> Type : PRT
<211> Length : 182
SequenceName : SEQ ID 181
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MASISSLGVG SGLDLSSILD SLTAAQKATL TPISNQQSSF TAKLSAYGTL KSALTTFQTA 60
NTALSKADLF SATSTTSSTT AFSATTAGNA IAGKYTISVT HLAQAQTLTT RTTRDDTKTA 120
IATSDSKLTI QQGDDKDPIT IDISAANSSL SGIRDAINNA KAGVSASIIN VGNGEYRLSV 180
TSNDTGLDNA MTLSVSGDDA LQSFMGYDAS ASSNGMEVSV AAQNAQLTVN NVAIENSSNT 240
ISDALENITL NLNDVTTGNQ TLTITQDTSK VQTAIKDWVN AYNSLIDTFS SLTKYTAVDA 300
GADSQSSSNG ALLGDSTLRT IQTQLKSMLS NTVSSSSYKT LAQIGITTDP SDGKLELDAD 360
KLTAALKKDA SGVGALIVGD GKKTGITTTI GSNLTSWLST TGIIKAATDG VSKTLNKLTK 420
DYNAASDRID AQVARYKEQF TQLDVLMTSL NSTSSYLTQQ FENNSNSK 468
<212> Type : PRT
<211> Length : 468
SequenceName : SEQ ID 182
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MEGKADNVVL ENGGRLDVLT GHTATNTRVD DGGTLDVRNG GTATTVSMGN GGVLLADSGA 60
AVSGTRSDGK AFSIGGGQAD ALMLEKGSSF TLNAGDTATD TTVNGGLFTA RGGTLAGTTT 120
LNNGAILTLS GKTVNNDTLT IREGDALLQG GALTGNGSVE KSGSGTLTVS NTTLTQKAVN 180
LNEGTLTLND STVTTDVIAQ RGTALKLTGS TVLNGAIDPT NVTLASGATW NIPDNATVQS 240

VVDDLSHAGQ IHFTSTRTGK FVPATLKVKN LNGQNGTISL RVRPDMAQNN ADRLVIDGGR 300
ATGKTILNLV NAGNSASGLA TSGKGIQVVE AINGATTEEG AFIQGNKLQA GAFNYSLNRD 360
SDESWYLRSE NAYRAEVPLY ASMLTQAMDY DRILAGSRSH QTGVSGENNS VRLSIQGGHL 420
GHDNNGGIAR GATPESSGSY GFVRLEGDLL RTEVAGMSVT AGVYGAAGHS SVDVKDDDGS 480
RAGTVRDDAG SLGGYLNLIH NASGLWADIV AQGTRHSMKA SSDNNDFRVR GWGWLGSLET 540
GLPFSITDNL MLEPQLQYTW QGLSLDDGQD NASYVKFGHG SAQHVRAGFR LGSHHDMNFG 600
KGTSSRDTLR GSAKHSVREL PVNWWVQPSV IRTFSSRGDM SMGTAAAGSN MTFSPSQNGT 660
SLDLQAGLEA RVRENITLGV QASYAHSING SSAEGYNSQA TLNVTF 706
<212> Type : PRT
<211> Length : 706
SequenceName : SEQ ID 183
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MAFSQAVSGL NAAATNLDVI GNNIANSATY GFKSGTASFA DMFAGSKVGL GVKVAGITQD 60
FTDGTTTNTG RGLDVAISQN GFFRLVDSNG SVFYSRNGQF KLDENRNLLN TQGLQLTGYP 120
VTGTPPTIQQ GANPTNISIP NTLMAAKTTT TASMQINLNS SDPLPTVTPF SASNADSYNK 180
KGSVTVFDSQ GNAHDMSVYF VKTGDNNWQV YTQDSSDPNS IAKTATTLEF NANGTLVDGA 240
MANNIATGAI NGAEPATFSL SFLNSMQQNT GANNIVATTQ NGYKPGDLVS YQINDDGTVV 300
GNNSNEQTQL LGQIVLANFA NNEGLASEGD NVWSATQSSG VALLGTAGTG NFGTLTNGAL 360
EASNVDLSKE LVNMIVAQRN YKSNAQTIKT QDQILNTRVN LR 402
<212> Type : PRT
<211> Length : 402
SequenceName : SEQ ID 184
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MKLVHMASGL AVAIALAACA DKSADIQTPA PAANTSISAT QQPAIQQPNV SGTVWIRQKV 60
ALPPDAVLTV TLSDASLADA PSKVLAQKAV RTEGKQSPFS FVLPFNPADV QPNARILLSA 120
AITVNDKLVF ITDTVQPVIN QGGTKADLTL VPVQQTAVPV QASGGATTTV PSTSPTQVNP 180
SSAVPAPTQY 190
<212> Type : PRT
<211> Length : 190
SequenceName : SEQ ID 185
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MIIKKSGGRW QLSLLASVVI SAFFLNTAYA WQQEYIVDTQ PGHSTERYTW DSDHQPDYND 60
ILSQRIQSSQ RALGLEVNLA EETPVDVTSS MSMGWNFPLY EQVTTGPVAA LHYDGTTTSM 120
YNEFGDSTTT LTDPLWHASV SSLGWRVDSR LGDLRPWAQI SYNQQFGENI WKAQSGLSRM 180
TATNQNGNWL DVTVGADMLL NQNIAAYAAL TQAENTTNNS DYLYTMGVSA RF 232

<212> Type : PRT
<211> Length : 232
SequenceName : SEQ ID 186
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MKWCKRGYVL AAMLALASAT IQAADVTITV NGKVVAKPCT VSTTNATVDL GDLYSFSLMS 60
AGAASAWHDV ALELTNCPVG TSRVTASFSG AADSTGYYKN QGTAQNIQLE LQDDSGNTLN 120
TGATKTVQVD DSSQSAHFPL QVRALTVNGG ATQGTIQAVI SITYTYS 167
<212> Type : PRT
<211> Length : 167
SequenceName : SEQ ID 187
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MKRAPLITGL LLISTSCAYA SSGGCGADST SGATNYSSVV DDVTVNQTDN VTGREFTSAT 60
LSSTNWQYAC SCSAGKAVKL VYMVSPVLTT TGHQTGYYKL NDSLDIKTTL QANDIPGLTT 120
DQVVSVNTRF TQIKSSTVYS AATQTGVCQG DTSRYGPVNI GANTTFTLYV TKPFLGSMTI 180
PKTDIAVIKG AWVDGMGSPS TGDFHDLVKL SIQGNLTAPQ SCKINQGDVI KVNFGFINGQ 240
KFTTRNAMPD GFTPVDFDIT YDCGDTSKIK NSLQMRIDGT TGVVDQYNLV ARRRSSDNVP 300
DVGIRIENLG GGVANIPFQN GILPVDPSGH GTVNMRAWPV NLVGGELETG KFQGTATITV 360
MVR 363
<212> Type : PRT
<211> Length : 363
SequenceName : SEQ ID 188
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MQKNAAHTYA ISSLLVLSLT GCAWIPSTPL VQGATSAQPV PGPTPVANGS IFQSAQPINY 60
GYQPLFEDRR PRNIGDTLTI VLQENVSASK SSSANASRDG KTNFGFDTVP RYLQGLFGNA 120
RADVEASGGN TFNGKGGANA SNTFSGTLTV TVDQVLVNGN LHVVGEKQIA INQGTEFIRF 180
SGVVNPRTIS GSNTVPSTQV ADARIEYVGN GYINEAQNMG WLQRFFLNLS PM 232

<212> Type : PRT
<211> Length : 232
SequenceName : SEQ ID 189
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MKRHLNTCYR LVWNHITGAF VVASELARAQ GKRGGVAVAL SLAAVTSLPV LAADIVVHPG 60
ETVNGGTLVN HDNQFVSGTA DGVTVSTGLE LGPDSDENTG GQWIKAGGTG RNTTVTANGR 120
QIVQAGGTAS DTVIRDGGGQ SLNGLAVNTT LDNRGEQWVH GGGKAAGTII NQDGYQTIKH 180
GGLATGTIVN TGAEGGPESE NVSSGQMVGG TAESTTINKN GRQVIWSSGM ARDTLIYAGG 240
DQTVHGEAHN TRLEGGNQYV HNGGTATETL INRDGWQVIK EGGTAAHTTI NQKESCR 297

<212> Type : PRT
<211> Length : 297
SequenceName : SEQ ID 190
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MMMKTIKHLL CCAIAASALI STGVHAASWK DALSSAASEL GNQNSTTQEG GWSLASLTNL 60
LSSGNQALSA DNMNNAAGIL QYCAKQKLAS VTDAENIKNQ VLEKLGLNSE EQKEDTNYLD 120
GIQGLLKTKD GQQLNLDNIG TTPLAEKVKT KACDLVLKQG LNFIS 165
<212> Type : PRT
<211> Length : 165
SequenceName : SEQ ID 191
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MFKGQKTLAA LAVSLLFTAP VYAADEGSGE IHFKGEVIEA PCEIHQDDID KEVELGQVTT 60
SHINQSHHSD AVAVDLLLVN CDLENSSNGS GGKISKVAVT FDSSAKTTGA DPILNNTSTG 120
EATGVGVRLM NKDQSNIVLG TATPDIDLAP TSSEQTLNFF AWMEQIDQAT PVTPGAVTAN 180
ATYVLDYK 188
<212> Type : PRT

<211> Length : 188
SequenceName : SEQ ID 192
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MSAGSPKFTV RRIAALSLVS LWLAGCSDTS NPPAPVSSVN GNAPANTNSG MLITPPPKMG 60
TTSTAQQPQI QPVQQPQIQA TQQPQIQPVQ PVAQQPVQME NGRIVYNRQY GNIPKGSYSG 120
STYTVKKGDT LFYIAWITGN DFRDLAQRNN IQAPYALNVG QTLQVGNASG TPITGGNAIT 180
QADAAEQGVV IKPAQNSTVA VASQPTITYS ESSGEQSANK MLPNNKPTAT TVTAPVTVPT 240
ASTTEPTVSS TSTSTPISTW RWPTEGKVIE TPGASEGGNK GIDIAGSKGQ AIIATADGRV 300
VYAGNALRGY GNLIIIKHND DYLSAYAHND TMLVREQQEV KAGQKIATMG STGTSSTRLH 360
FEIRYKGKSV NPLRYLPQR 379
<212> Type : PRT
<211> Length : 379
SequenceName : SEQ ID 193
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MIKFLSALIL LLVITAAQAE RIRDLTSVQG VRQNSLIGYG LVVGLDGTGD QTTQTPFTTQ 60
TLNNMLSQLG ITVPTGTNMQ LKNVAAVMVT ASLPPFGRQG QTIDVVVSSM GNAKSLRGGT 120
LLMTPLKGVD SQVYALAQGN ILVGGAGASA GGSSVQVNQL NGGRITNGAV IERELPSQFG 180
VGNTLNLQLN DEDFSMAQQI ADTINRVRGY GSATALDART IQVRVPSGNS SQVRFLADIQ 240
NMQVNVTPQD AKVVINSRTG SVVMNREVTL DSCAVAQGNL SVTVNRQANV SQPDTPFGGG 300
QTVVTPQTQI DLRQSGGSLQ SVRSSASLNN VVRALNALGA TPMDLMSILQ SMQSAGCLRA 360
KLEII 365
<212> Type : PRT
<211> Length : 365
SequenceName : SEQ ID 194
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MKRSIIAAAV FSSFFMSAGV FAADVDTGTL TIKGNIAESP CKFEAGGDSV SINMPTVPTT 60
VPEGKAKYST YDDAVGVTSS MLKISCPKEV AGVKLSLITN DKITGNDKAI ASSNDTVGDN 120
SDVLDVSAPF NIESYKTAEG QYAIPFKAKY LKLTDNSVQS GDVLSSLVMR VAQD 174

<212> Type : PRT
<211> Length : 174
SequenceName : SEQ ID 195
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MAVQKNVIKG ILAGTFALML SGCVTVPDAI KGSSTTPQQD LVRVMSAPQL YVGQEARFGG 60
KVVAVQNQQG KTRLEIATVP LDSGARPTLG EPSRGRIYAD VNGFLDPVDF RGQLVTVVGP 120
ITGAVDGKIG NTPYKFMVMQ VTGYKRWHLT QQVIMPPQPI DPWFYGGRGW PYGYGGWGWY 180
NPGPARVQTV VTE 193
<212> Type : PRT
<211> Length : 193
SequenceName : SEQ ID 196
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MRNKPFYLLC AFLWLAVSRV LAADSTITIR GYVRDNGCSV AAESTNFTVD LMENAAKQFN 60

NIGATTPVVP FRILLSPCGN AVSAVKVGFT GVADSHNANL LALENTVSAA AGLGIQLLNE 120
QQNQIPLNAP SSAISWTTLT PGKPNTLNFY ARLMATQVPV TAGHINATAT FTLEYQ 176

<212> Type : PRT
<211> Length : 176
SequenceName : SEQ ID 197
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MKKLTVAALA VTTLLSGSAF AHEAGEFFMR AGSATVRPTE GAGGTLGSLG GFSVTNNTQL 60
GLTFTYMATD NIGVELLAAT PFRHKIGTRA TGDIATVHHL PPTLMAQWYF GDASSKFRPY 120
VGAGINYTTF FDNGFNDHGK EAGLSDLSLK DSWGAAGQVG VDYLINRDWL VNMSVWYMDI 180
DTTANYKLGG AQQHDSVRLD PWVFMFSAGY RF 212
<212> Type : PRT
<211> Length : 212
SequenceName : SEQ ID 198
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MFFKRGKILS AGRLNKKSLG IVMFLSVGLL LAGCSGSKSS DTGTYSGSVY TVKRGDTLYR 60
ISRTTGTSVK ELARLNGISP PYTIEVGQKL KLGGAKSSSS TRKSTAKSTT KTASVTPSSA 120
VPKSSWPPVG QRCWLWPTTG KVIMPYSTAD GGNKGIDISA PRGTPIYAAG AGKVVYVGNQ 180
LRGYGNLIMI KHSEDYITAY AHNDTMLVNN GQSVKAGQKI ATMGSTDAAS VRLHFQIRYR 240
ATAIDPLRYL PPQGSKPKC 259
<212> Type : PRT
<211> Length : 259
SequenceName : SEQ ID 199
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MAQVINTNSL SLITQNNINK NQSALSSSIE RLSSGLRINS AKDDAAGQAI ANRFTSNIKG 60
LTQAARNAND GISVAQTTEG ALSEINNNLQ RIRELTVQAS TGTNSDSDLD SIQDEIKSRL 120
DEIDRVSGQT QFNGVNVLAK DGSMKIQVGA NDGQTITIDL KKIDSDTLGL NGFNVNGGGA 180
VANTAASKAD LVAANATVVG NKYTVSAGYD AAKASDLLAG VSDGDTVQAT INNGFGTAAS 240
ATNYKYDSAS KSYSFDTTTA SAADVQKYLT PGVGDTAKGT ITIDGSAQDV QISSDGKITA 300
SNGDKLYIDT TGRLTKNGSG ASLTEASLST LAANNTKATT IDIGGTSISF TGNSTTPDTI 360
TYSVTGAKVD QAAFDKAVST SGNNVDFTTA GYSVNGTTGA VTKGVDSVYV DNNEALTTSD 420
TVDFYLQDDG SVTNGSGKAV YKDADGKLTT DAETKAATTA DPLKALDEAI SSIDKFRSSL 480
GAVQNRLDSA VTNLNNTTTN LSEAQSRIQD ADYATEVSNM SKAQIIQQAG NSVLAKANQV 540
PQQVLSLLQG 550
<212> Type : PRT
<211> Length : 550
SequenceName : SEQ ID 200
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MKKIACLSAL AAVLAFTAGT SVAATSTVTG GYAQSDAQGQ MNKMGGFNLK YRYEEDNSPL 60
GVIGSFTYTE KSRTASSGDY NKNQYYGITA GPAYRINDWA SIYGVVGVGY GKFQTTEYPT 120
YKHDTSDYGF SYGAGLQFNP MENVALDFSY EQSRIRSVDV GTWIAGVGYR F 171

<212> Type : PRT
<211> Length : 171
SequenceName : SEQ ID 201
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MKRNIIGGAF TLASLMLAGH ALAEDGVVNF VGEIVDTTCE VTSDTADQIV PLGKVSKNAF 60
SGVGSLASPQ KFSIKLENCP ATYTQAAVRF DGTEAPGGDG DLKVGTPLTA GNPGDFTGTG 120
QAIAATGVGI RIFNQSDNSQ VKLYNDSAYT AIDAEGKAEM KFIARYVATN ATVTAGTANA 180
DSQFTVEYKK 190
<212> Type : PRT
<211> Length : 190
SequenceName : SEQ ID 202
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MKKSTLALVV MGIVASASVQ AAEIYNKDGN KLDVYGKVKA MHYMSDNASK DGDQSYIRFG 60
FKGETQINDQ LTGYGRWEAE FAGNKAESDT AQQKTRLAFA GLKYKDLGSF DYGRNLGALY 120
DVEAWTDMFP EFGGDSSAQT DNFMTKRASG LATYRNTDFF GVIDGLNLTL QYQGKNENRD 180
VKKQNGDGFG TSLTYDFGGS DFAISGAYTN SDRTNEQNLQ SRGTGKRAEA WATGLKYDAN 240
NIYLATFYSE TRKMTPITGG FANKTQNFEA VAQYQFDFGL RPSLGYVLSK GKDIEGIGDE 300
DLVNYIDVGA TYYFNKNMSA FVDYKINQLD SDNKLNINND DTVAVGMTYQ F 351

<212> Type : PRT
<211> Length : 351
SequenceName : SEQ ID 203
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MRKQWLGICI AAGMLAACTS DDGQQQTVSV PQPAVCNGPI VEISGADPRF EPLNATANQD 60
YQRDGKSYKI VQDPSRFSQA GLAAIYDAEP GSNLTASGEA FDPTKLTAAH PTLPIPSYAR 120
ITNLANGRMI VVRINDRGPY GNDRVISLSR AAADRLNTSN NTKVRIDPII VAQDGSLSGP 180
GMACTTVAKQ TYALPAPPDL SGGAGTSSVS GPQGDILPVS NSTLKSEDPT GAPVTSSGFL 240
GAPTTLAPGV LEGSEPTPAP QPVVTASSTT PATSPAMVTP QAASQSASGN FMVQVGAVSD 300
QARAQQYQQQ LGQKFGVPGR VTQNGAVWRI QLGPFASKAE ASTLQQRLQT EAQLQSFITT 360
AQ 362
<212> Type : PRT
<211> Length : 362
SequenceName : SEQ ID 204
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MKKKTIYQCV ILFFSLLNIH VGMAGPEQVS MHIYGNVVDQ GCDVATKSAL QNIHIGDFNI 60
SDFQAANTVS TAADLNIDIT GCAAGITGAD VLFSGEADTL APTLLKLTDT GGSGGMATGI 120
AVQILDAQSQ QEIPLNQVQP LTPLKAGDNT LKYQLRYKST KAGATGGNAT AVLYFDLVYQ 180

<212> Type : PRT
<211> Length : 180
SequenceName : SEQ ID 205
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MKNKLLFMML TILGAPGIAA AAGYDLANSE YNFAVNELSK SSFNQAAIIG QAGTNNSAQL 60
RQGGSKLLAV VAQEGSSNRA KIDQTGDYNL AYIDQAGSAN DASISQGAYG NTAMIIQKGS 120
GNKANITQYG TQKTAVVVQR QSQMAIRVTQ R 151
<212> Type : PRT
<211> Length : 151

SequenceName : SEQ ID 206
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MMKFKKCLLP VAMLASFTLA GCQSNADDHA ADVYQTDQLN TKQETKTVNI ISILPAKVAV 60
DNSQNKRNAQ AFGALIGAVA GGVIGHNVGS GSNSGTTAGA VGGGAVGAAA GSMVNDKTLV 120
EGVSLTYKEG TKVYTSTQEG KECQFTTGLA VVITTTYNET RIQPNTKCPE KS 172

<212> Type : PRT
<211> Length : 172
SequenceName : SEQ ID 207
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MQTKKNEIWV GIFLLAALLA ALFVCLKAAN VTSIRTESTY TLYATFDNIG GLKARSPVSI 60
GGVVVGRVAD ITLDPKTYLP RVTLEIEQRY NHIPDTSSLS IRTSGLLGEQ YLALNVGFED 120
PELGTAILKD GDTIQDTKSA MVLEDLIGQF LYGSKGDDNK NSGDAPAAAP GNNETTEPVG 180
TTK 183
<212> Type : PRT
<211> Length : 183
SequenceName : SEQ ID 208
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MAPLAFSAQS LAESLTVEQR LELLEKALRE TQSELKKYKD EEKKKYTPAT VNRSVSTNDQ 60
GYAANPFPTS SAAKPDAVLV KNEEKNASET GSIYSSMTLK DFSKFVKDEI GFSYNGYYRS 120
GWGTASHGSP KSWAIGSLGR FGNEYSGWFD LQLKQRVYNE NGKRVDAVVM IDGNVGQQYS 180
TGWFGDNAGG ENPMQFSDMY VTTKGFLPFA PEADFWVGKH GAPKIEIQML DWKTQRTDAA 240
AGVGLENWKV GPGKIDIALV REDVDDYDRS LQNKQQINTH TIDLRYKDIP LWDKATLMVS 300
GRYVTANESA SEKDNQDNNG YYDWKDIWMF GTSLTQKFDK GGFNEFSFLV ANNSIARNFG 360
RYAGASPFTT FNGRYYGDHT GGTAVRLTSQ GEAYIGDHFI VANAIVYSFG NNIYSYETGA 420
HSDFESIRAV VRPAYIWDQY NQTGVELGYF TQQNKDANSN KFNESGYKTT LFHTFKVNTS 480
MLTSRLEIRF YATYIKALEN ELDGFTFEDN KDAQFAVGAQ AEIWW 525
<212> Type : PRT
<211> Length : 525
SequenceName : SEQ ID 209
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
MKKRILSAVL VSGVTLSSAT TLSAVKADDF DAQIASQDSK INNLTAQQQA AQAQVNTIQG 60
QVSALQTQQA ELQAENQRLE AQSATLGQQI QTLSSKIVAR NESLKQQARS AQKSNAATSY 120
INAIINSKSV SDAINRVSAI REVVSANEKM LQQQEQDKAA VEQKQQENQA AINTVAANQE 180
TIAQNTNALN TQQAQLEAAQ LNLQAELTTA QDQKATLVAQ KAAAEEAARQ AAAAQAAAEA 240
KAAAEAKALQ EQAAQAQAAA NNNTQATDVS DQQAAAADNT QAAQTGDSTE QSAAQAVNNS 300
DQESTTATEA QPSASSASTA AVAANTSSAN TYPAGQCTWG VKSLAPWVGN YWGNGGQWAA 360
SAAAAGYRVG STPSAGAVAV WNDGGYGHVA YVTGVQGGQI QVQEANYAGN QSIGNYRGWF 420
NPGSVSYIYP N 431
<212> Type : PRT
<211> Length : 431
SequenceName : SEQ ID 210
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159

<400> PreSequenceString :
MKVKKTYGFR KSKISKTLCG AVLGTVAAVS VAGQKVFADE TTTTSDVDTK VVGTQTGNPA 60
TNLPEAQGSA SKEAEQSQNQ AGETNGSIPV EVPKTDLDQA AKDAKSAGVN VVQDADVNKG 120
TVKTAEEAVQ KETEIKEDYT KQAEDIKKTT DQYKSDVAAH EAEVAKIKAK NQATKEQYEK 180
DMAAHKAEVE RINAANAASK TAYEAKLAQY QADLAAVQKT NAANQAAYQK ALAAYQAELK 240
RVQEANAAAK AAYDTAVAAN NAKNTEIAAA NEEIRKRNAT AKAEYETKLA QYQAELKRVQ 300
EANAANEADY QAKLTAYQTE LARVQKANAD AKAAYEAAVA ANNAKNAALT AENTAIKQRN 360
ENAKATYEAA LKQYEADLAA VKKANAANEA DYQAKLTAYQ TELARVQKAN ADAKAAYEAA 420
VAANNAANAA LTAENTAIKK RNADAKADYE AKLAKYQADL AKYQKDLADY PVKLKAYEDE 480
QASIKAALAE LEKHKNEDGN LTEPSAQNLV YDLEPNANLS LTTDGKPLKA SAVDDAFSKS 540
TSKAKYDQKI LQLDDLDITN LEQSNDVASS MELYGNFGDK AGWSTTVSNN SQVKWGSVLL 600
ERGQSATATY TNLQNSYYNG KKISKIVYKY TVDPKSKFQG QKVWLGIFTD PTLGVFASAY 660
TGQVEKNTSI FIKNEFTFYD EDGKPINFDN ALLSVASLNR ENNSIEMAKD YTGKFVKISG 720
SSIGEKNGMI YATDTLNFRQ GQGGARWTMY TRASEPGSGW DSSDAPNSWY GAGAIRMSGP 780
NNSVTLGAIS STLVVPADPT MAIETGKKPN IWYSLNGKIR AVNVPKVTKE KPTPPVKPTA 840
PTKPTYETEK PLKPAPVAPN YEKEPTPPTR TPDQAEPNKP TPPTYETEKP LEPAPVEPSY 900
EAEPTPPTRT PDQAEPNKPT PPTYETEKPL EPAPVEPSYE AEPTPPTPTP DQPEPNKPVE 960
PTYEVIPTPP TDPVYQDLPT PPSVPTVHFH YFKLAVQPQV NKEIRNNNDI NIDRTLVAKQ 1020
SVVKFQLKTA DLPAGRDETT SFVLVDPLPS GYQFNPEATK AASPGFDVTY DNATNTVTFK 1080
ATAATLATFN ADLTKSVATI YPTVVGQVLN DGATYKNNFT LTVNDAYGIK SNVVRVTTPG 1140
KPNDPDNPNN NYIKPTKVNK NENGVVIDGK TVLAGSTNYY ELTWDLDQYK NDRSSADTIQ 1200
KGFYYVDDYP EEALELRQDL VKITDANGNE VTGVSVDNYT NLEAAPQEIR DVLSKAGIRP 1260
KGAFQIFRAD NPREFYDTYV KTGIDLKIVS PMVVKKQMGQ TGGSYENQAY QIDFGNGYAS 1320
NIIINNVPKI NPKKDVTLTL DPADTNNVDG QTIPLNTVFN YRLIGGIIPA DHSEELFEYN 1380
FYDDYDQTGD HYTGQYKVFA KVDITFKDGS IIKSGAELTQ YTTAEVDTAK GAITIKFKEA 1440
FLRSVSIDSA FQAESYIQMK RIAVGTFENT YINTVNGVTY SSNTVKTTTP EDPTDPTDPQ 1500
DPSSPRTSTV INYKPQSTAY QPSSVQETLP NTGVTNNAYM PLLGIIGLVT SFSLLGLKAK 1560
KD 1562
<212> Type : PRT
<211> Length : 1562
SequenceName : SEQ ID 211
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
MLTELKAVLK KPMLWITMVG VALVPALYNI IFLSSMWDPY GKVSDLPVAV VNKDKTATYE 60
GKKMTIGKDM TDNMVRNKSL DYHFVDSEKA QKGLEKGDYY MIITLPEDLS QNAASVLTDE 120
PKKLTIPYQT SKGHSFVASK MSETAAKTLK ESVSKNITSS YTKSLFKNMS TLKTGLGSAA 180
NASQKIATGS KQLANGSQVM TDNLNLLSNS SQSFAQGTNT LYSGLTAYTG GVGQLSAGLN 240
NLNNGLTAYT NGVGQLANGS SQLSNQSQKL LGGVAQLANG SASIQQLVNA SSQLNQGLIK 300
LSTATGLSEE QVQQFSSLIN QLGTLNQSIQ NYSDNGTATT ANSPDLSTYL SAITTAAQAI 360
VNSGNTSQQT TTNQSNALAA VQATGAYQRL SAEDQSEIAA ALANTGSSTT TTGADANAVS 420
QAQAILNNVQ SIQSALSTLQ TTTANTPTSP SASLTQIKNT ANSVLPSAAT SLTTLSSGLT 480
QAKTALDSQV VPVSTALANG TAQLGSTFST GANSLMTGVG QYTNAVDILN AGANTLAAKN 540
NQLTDGTSQL VNGANQLNSN SGQLTKGTAQ LANGANQIET GAGKLAAGGE SLTAGLTTLS 600
SGSGELSKAL STAKNKLSLV AVDNDNAKTL SSPVTIKHTD KDNVKTNGVG MAPYMMSAAL 660
MVMAISTNTI FRVALSGKQA KTLREWIDQK LAVNGLIAVT GAILILYFGVH IIGLSANFEL 720
KTLGLIILTS ITFMVLVTTL VTWHDKFGSF AALILLLLQL GSSAGTYPLA VTDKFFQVVN 780
PYLPMSYSVS GLRETISMAG TIGNQLLALS LFFLTFAALG LLIARRRIRS VKVA 834

<212> Type : PRT
<211> Length : 834
SequenceName : SEQ ID 212
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
MVSQKNKSKK GQSKTFTLIS NRINLLFFLI VALFTVLLLR LAQMQLYDAK FYKSKLTEST 60
TYTIKTSSPR GQIYDAKGVA LVENEVKEVV AFTRSNTMTA KDIKANAKKL ADMVTLTESK 120
VTKRQKKDYY LADPKNYQKI VKKLPNNKKY DNFGNNLTES KIYANAVKAV PNSAIDYSED 180
EKKIIHIFSQ MNATSVFNTA SLTTGDLTAE QIAVLATSKS DLKGISVKTD WERKTDKNSI 240
TSIIGKVSSQ KTGLPAEEAN NYVKKGYSLN DRVGTSYLEK QYENDLQGSR TVQAIKVNKE 300
GKIISDKTTA KGTKGKNLKL TLDLEFQKGV EQILNQYFNS ELASGNTKYS EGVYAVVLNP 360

NTGAVLSMAG LEHDLKTGEV SSNALGAVTE VFTPGSVVKG ATLTAGWENG VLSGNQVLND 420
QPIQFAGSSP INSWFTNGST PLTASQSLEY SSNTYMVQLA LKLMGQDYHS GMTLSTDGYK 480
EAMEKLRATY AQYGLGVSTG IDLPGESKGY TPEHYDPSNV LTESFGQFDN YTAMQLAQYA 540
AAVANGGKRI APHLVEGIYD NNKTGGLGNL VQSIDTKVLN NVSISSDDMG IIKEGFYNVV 600
NGGSYATGKT LAKGASVPIS AKTGTAEAYV TGDDGKSVYT SNLNVVAYAP SSNPQIAVAV 660
VLPHETDLHG TTSHAITRDI INLYQKMYPM NQ 692
<212> Type : PRT
<211> Length : 692
SequenceName : SEQ ID 213
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
MTVLKYGLGI LLSAIILAII IGGLLFTYYV SSTPKLSEAK LKATNSSLVY DSNNNLIADL 60
GAEKRESISS DSIPMKLVNA VTSIEDHRFF KHRGVDIYRI IGAAWSNLLH KSTQGGSTLD 120
QQLIKLAYFS TKESDQTLKR KAQEVWLSLQ MEKKYTKEEI LTFYVNKVYM GNGNYGMRTA 180
AKSYYGKDLK DLSIAQLATL AGIPQAPTQY DPYAQPKAAT SRRNTVLSQM YKHKKITKRE 240
YDAAVATPIS DGLQELKRSS SYPKYMDNYL KQVISEVKKR TGQDIFSAGM KVYTNVNADA 300
QQYLWNIYNT DEYIAYPDDN FQVASTVMDV TNGKVIAQLG GRHQDTNVSF GTNQAVLTDR 360
DWGSTMKPIS AYGPALESEA FTTTAQMLND SVYYYPGTTT QVYDWDHRYN GWMTIQTAIQ 420
QSRNVPAVRA IDAAGLDTAK GFLSGLGIDY PEMRYSNAIS SNTSSSEQKY GASSEKMAAA 480
YAAFSNGGTY YEPQYVNKIE FKDGTSETYD AKGNRAMKET TAYMMTDMLK TVLTYGTGTE 540
AAIPGLYQAG KTGTSNYDDN ELVEMSEKLG INPYGLGTIA PDENFVGYTP QYSMAVWTGY 600
KNRLMPVYGD SMKIAAQVYR TMMAYLSSSG NSDWTMPDGL YRSGGYLYLN GSSGSNSRYG 660
AAPATSSSSS SSSSSDSNNN DQNNNQTTEA SSDSSSSSSD ATTSSNP 707
<212> Type : PRT
<211> Length : 707
SequenceName : SEQ ID 214
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
MKSKTAKITL LSSLALAAFG ATNVFADEAS TQLNSDTVAA PTADTQASEP AATEKEQSPV 60
VAVVESHTQG NTTTTTSQVT SKELEDAKAN ANQEGLEVTE TEAQKQPSVE AADADNKAQA 120
QTINTAVADY QKAKAEFPQK QEQYNKDFEK YQSDVKEYEA QKAAYEQYKK EVAQGLASGR 180
VEKAQGLVFI NEPEAKLSIE GVNQYLTKEA RQKHATEDIL QQYNTDNYTA SDFTQANPYD 240
PKEDTWFKMK VGDQISVTYD NIVNSKYNDK KISKVKINYT LNSSTNNEGS ALVNLFHDPT 300
KTIFIGAQTS NAGRNDKISV TMQIIFYDEN GNEIDLSGNN AIMSLSSLNH WTTKYGDHVE 360
KVNLGDNEFV KIPGSSVDLH GNEIYSAKDN QYKANGATFN GDGADGWDAV NADGTPRAAT 420
AYYGAGAMTY KGEPFTFTVG GNDQNLPTTI WFATNSAVAV PKDPGAKPTP PEKPELKKPT 480
VTWHKNLVVE TKTEEVPPVT PPTTPDEPTP EKPKTPEDPQ SPVVAKSVSF RTARKGEMRV 540
RERDYQPTLP HAGAAKQNGL ATLGAISTAF AAATLIAARK KEN 583
<212> Type : PRT
<211> Length : 583
SequenceName : SEQ ID 215
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
MEQKIFSKRK SKIAGLCGAI LTTTVVALAS GTVIEADETI EQPVAAETVS QADGDNPEQT 60
TSVQQETAPQ QTKTSQSSDA TVDSEESATS PSDEQTVSQN DSNSSSQIDQ TIADTNRSDS 120
DHISKTSAAT TEDQEEKVNS AKAQTAAATN NQDTRYSAKD AYGNSNFNKT LTEFGKNANV 180
ADVTYNGVRD EYIVVNDPSA PYVPNANEIA KYLKEYLTEL RNINNIAIPV PSVDQVMQKY 240
AQDRANEEAN EKNGLDHDIN LPIPNNLTWV AEDGHLDMDS SIQSKSQEGY TLASDKATAY 300
YLALNWFSDY FNIYDDPNDG LKSFGHAVSI LSDGGTGMGL GLASGQDNEK GMWYAQLEFG 360
GNDNEDNTND FSSLKNGKGE WVLYYKGSPV KFLPNTTFWY VKKGTSPDAA STPHNSDKPS 420
FQSSKDLDPN FKADNRFQEG KEASVHQAIP ATFKSHRDEV GNKDQNSLSA QLPDTGVQKN 480
NQLALIALGT GLILLSGLLL SKRKSLK 507
<212> Type : PRT
<211> Length : 507
SequenceName : SEQ ID 216

SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
MTFEKQKHFS LRKLKFGLVS VAIIAFLFAV TKTAEADETV ITEQRQTSKI NASSQKVENQ 60
TSNQVEAKTD SANKDPQEKT GSVATDAPSM NSANNMSQSD KQNTVNEISS DSQQTKTDEQ 120
TDLPQNSFKQ QSAHVKMTTE AEKTPSHSIN TFVNDGNGNW YYLGADGRNV TGSHTIGGKT 180
MYFAQDGKQV KGAFAQDSDG NKHYYDRDSG EMWTNRFVND QGNWYYLNND GVPVTGSITV 240
NGQSLYFNSD GSQVKGNFVE EDGSLRYYDK NSGDLLRKTS RTINGVNYQF DNDGNARAID 300
KIEVVKTSLV VDSYEFGPSV SKIILEFNHK VTPAVVHAGA MVTTAGVQRK ILNSYVSNAS 360
GHVVYFDSSH YVTLELDIPY DPNDSSRNAS PFIFDSAAFR NNWVNSYTVK VDNLQVQADG 420
SNSSQIISSE QDAINNRFLP TTDRFSERGS YGNFNYAAYQ PEAAIGGEKN PLIVWLHGIG 480
EVGTDINIPL LASNVARLTE DPIQSHFTST GSGGQKGAYV LVPQSSIPWS QNQTASLMAL 540
IKAYVASHPD IDSRRIYLAG VSNGGGMTLD MGVAYPNYFA ALVPIAASYS NQLTDNQITA 600
AALKALKGQP MWLIHTRTDK TISADSSVLP FYKELLQAGA QNKWLSYYET NVGKHHSGVT 660
YNGHWSWIYF LNDQVTGTQN TDNAKNWSGL SGMVATNPTY GGDAKATVNG RTYSNVFDWL 720
NGQRRR 726
<212> Type : PRT
<211> Length : 726
SequenceName : SEQ ID 217
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
MKIFIKKHQQ SILYYSLSFL LPSFIMFLVL FSKNIYWGSS TTILASDGFH QYVIFDALFR 60
NILHGTDSLF YSFKAGLGFN IFALTSYYLG SFLTPFTYFF NVKNMADAFY LFTLIKFGLI 120
GLSAFYSLGQ IYTKISKSLV LMLSTSYALM SFTSSQLELN NWLDVFILLP LIMLGLQRLV 180
EKRGIFLYFL TLTCLFIQNY YFGFMTAIFL TLWFFTQVSW DIRNRMKRLS DFVLVSIFAT 240
LTSAFMLLPT FLDLKSHGEV LTEQISLFSS DIWYFDFFAK SLLGSYDTTK YGSIPTIYIG 300
LLPLIFAITF FFVKSIKWQV KVAYFLLLAI IIASFIFQPL DLFWQGMHSP NMFLHRYSWA 360
FSLVIVIMAA ETLTRIKDIK LKNFYPAFTF LGVGLLATFL FKDYYNYLTQ VNFILTTIFL 420
VSYFIILFTF FNQLVSYKVI ISFTLIFTSF EIALNTFYQI EGIQTDWNFP SREVYEDNVK 480
EIDNYVKKTK KDNLEFFRTE KQIPQTYNDG MKFNYNSISQ FSSVKNNLSA QLLNSLGYYS 540
QGNHSTISYP NNTILMDSLF SIKYNINNQN PHKPGFHLKQ KNNKLQLYKN FYSLPLALMS 600
NHIYKDVKFD SYPLDNQQKF VNELTDLNLT LFKEIPIISS VGMQVLDNRV TINGSKGNKA 660
QVYYTVKCPA NSQLYISLPN LTVNNKDENV FITTNKHTSS YIIDESYYLF NLGNYKKTQT 720
LIFKLSFPKN KTVSYDLPHI YALDLTAYQK SIKQLKSQTV KTTTKKNKIF TTYVAKKRTS 780
LIYTLPYDKG WFAKQNGKAI KISKAQNGLM KIDVSKGSGK IIMTFVPQGL YQGILLTCLG 840
IFLFVFYQLY YKKFNLK 857
<212> Type : PRT
<211> Length : 857
SequenceName : SEQ ID 218
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
MKLKHILRIG AVAFASILLL TACGSKTSKK TVTLATVGTT NPFSYEKKGK LTGYDIEVAK 60
EVFKASDKYD VKYQKTEWTS IFSGLDSDKY QIGANNISYT KERANKYLYS NPTASNPLVL 120
VVPKDSDIKS YNDIAGHSTQ VVQGNTTVSM LQKFNKNHEN NQVKLNFTSE DLAHQIRNVS 180
DGKYDFKIFE KISAETIIKE QGLDNLKVID LPSDQKPYVY FIPAQDQKDL QKFVNKRLKK 240
LYENGTLEKL SKKYLGGSYL PDKKDMK 267
<212> Type : PRT
<211> Length : 267
SequenceName : SEQ ID 219
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
MRFLVFLIAF FAAFYKFIET ERIDSNTVAV NPDSLILKRF LKTNQLNGIM IVTGPDGKAQ 60

VFSNQSKVDG SPVSIKDYFP LASLQKLITG VAIQQLIDKG KLSLNTPLSK YYPQIENSEN 120
ITIQNLLTHT SGLADRKEVP QQVLTTQEQQ LDFSLTNYRV TYRKKWKYAN INYALLAGII 180
SQISGQNYAT YVRQHFLTAG KGWHFKKYIQ IKDKSKLAAL SVMDQSTIWD KLSKEVTSTF 240
GAGDYASRPV DYWKFMMAFI NDQFVPVSEY QRSMKMTSKS YYGGLYISQK MLHANGGGFD 300
TYSCFAYSNP KTKQVMVLFI TNGKYKRVKS LAAKAFKLYA DSYALRKNET SK 352

<212> Type : PRT
<211> Length : 352
SequenceName : SEQ ID 220
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
MKKKIALAAL SFVSAAVLAA CSSAPGGSSD AAGNKIGDTV KIGYNLELSG DVAAYGQAEK 60
NGANLAVEEI NKAGGIDGKK IKVISKDNKS DNGEASTIST NLATQSKVNA ILGPATSGAT 120
AAAAPNANDA AVPLVTPSGT QDNLTYSKGK VQDYIFRTTP QDSFQGKIIA KYATDNLKAK 180
KVALYYDKSS DYAQGIADAF KKAYKGKITV EDTFQAKDQD FQAALTKFKN KDFDAIVIPG 240
YYTETGLITK QARDMGLTQP ILGPDGFNDE KYVEGAGAAN TNNVHYVSGY STKVALTNKA 300
EKFLKDYKAK YGEEPNMFAA LAYDSVYMIA DAAKDAKTSK DIATNLAKLK NFKGVTGKMT 360
IDKKHNPVKS AVMVGLKDGK EDTATAVEAK 390

<212> Type : PRT
<211> Length : 390
SequenceName : SEQ ID 221
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
MKKLSLLLLV CLSLLGLFAC TSKKTADKKL TVVATNSIIA DITKNIAGNK VVLHSIVPVG 60
RDPHEYEPLP EDVKKTSQAD VIFYNGINLE NGGNAWFTKL VKNAHKKTDK DYPAVSDSVK 120
TIYLENAKEK GKEDPHAWLD LKNGIIYAKN IMKRLSEKDP KNKSYYQKNF QAYSAKLEKL 180
HKVAKEKISR IPTEKKMIVT SEGCFKYFSK AYDIPSAYIW EINTEEEGTP NQIKALVKKL 240
RKSRVSALFV ESSVDDRPMK TVSKDTGIPI AAKIFTDSVA KKGQAGDSYY AMMKWNLDKI 300
ANGLSQ 306

<212> Type : PRT
<211> Length : 306
SequenceName : SEQ ID 222
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
MFVHTKTKKK RKWQRKVFLL LLLFLLPIVS VLAFIVLFIG GGTAESHDVE ATTGGVKLSA 60
KQFADKTKLG ISEEEAKNAL AFADRLMSRH HFTAQATAGV LAVGFRESGF DVKAVNNSGG 120
VAGFFQWSGW GSSVNGDRWK VASKRELTLE VEVDLMSTEL DGRYADVVKK VGSATDEKQA 180
AKDWSQYYEG VAVSDGQTKA DKIESWATTI CEALKSGGTN YAKVNNTGTS STAIPQGWEN 240
ISAFDGHAYE GSENYPQGQC TWYVYNRAKQ LGVSFSPYMG NGGQWYQVQG YHSSHTPKAH 300
TALSFVNGQA GSDPTYGHVA FVEAVKDDGS ILISEMNVYG QPAMTVAYRT FDAETAKQFW 360
YVEGK 365

<212> Type : PRT
<211> Length : 365
SequenceName : SEQ ID 223
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
MKMKRKLLSL VSVLTILLGA FWVTKIVKAD QVTNYTNTAS ITKSDGTALS NDPSKAVNYW 60
EPLSFSNSIT FPDEVSIKAG DTLTIKLPEQ LQFTTALTFD VMHTNGQLAG KATTDPNTGE 120
VTVTFTDIFE KLPNDKAMTL NFNAQLNHNN ISIPGVVNFN YNNVAYSSYV KDKDITPISP 180
DVNKVGYQDK SNPGLIHWKV LINNKQGAID NLTLTDVVGE DQEIVKDSLV AARLQYLAGD 240
DVDSLDEAAS RPYAEDFSKN VTYQTNDLGL TTGFTYTIPG SSNNAIFISY TTRLTSSQSA 300

GKDVSNTIAI SGNNINYSNQ TGYARIESAY GRASSRVKRQ AETTTVTETT TSSSSETTTS 360
EATTETSSTT NNNSTTTETA TSTTGASTTQ TKTTASQTNV PTTTNITTTS KQVTKQKAKF 420
VLPSTGEQAG LLLTTVGLVI VAVAGVYFYR TRR 453
<212> Type : PRT
<211> Length : 453
SequenceName : SEQ ID 224
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
MTFKKLVLGL LSFVAVFTLV ACSSSNSKNL QDDIKEKKKL VVAVSPDYAP FEFKALVNGK 60
DTVVGADIDL AKAIAKELGV KLELSSMSFD NVLSSLKTGK ADIAISGLSY TKERAQAYDF 120
SEAYYKTENA ILIKKSDLNK YTMISSFNNK TKVAVQKGTI EEGLAKNQLK QSNITSLTSM 180
GEAVNELKSG QVDAIDLEKP VAEGYVSQNS DLVLAKVALK TGEGDAKAVA LPKDSGQLVK 240
TVNKVIKKLK KEDKYKQFIS DAVKLTGQQV D 271
<212> Type : PRT
<211> Length : 271
SequenceName : SEQ ID 225
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
MKKHFFMTFS LLLAAVFLVA CSNLSDSGQR NWDKINKRGM LKIATAGTLY PQSYHDDHNK 60
LTGYDVEILK EIGKRLGLKV QFTEMGVDGM LTAIKSGQID VANYSLEDGN KNISKFLRTS 120
PYKYSFTSMV VRSKDDSGIH SWSDLKGKKA AGAASTNYMK IAKKLGAKLV VYDNVTNDVY 180
MKDLVNGRTD VIINDYYLQK IAVAAVKDKY AIKINQGLYA NPYSTSFTLS LKNKVLQKKI 240
NKAVKDMRKD GTLTKLSKKF FQGEDVTKKH YNSYKKIDIS DVD 283
<212> Type : PRT
<211> Length : 283
SequenceName : SEQ ID 226
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pneumoniae R6
<400> PreSequenceString :
MKLLKKMMQV ALATFFFGLL GTSTVFADDS EGWQFVQENG RTYYKKGALK ETYWRVIDGK 60
YYYFDPLSGE MVVGWQYIPA PHKGVTIGPS PRIEIALRPD WFYFGQDGVL QEFVGKQVLE 120
AKTATNTNKH HGEEYDSQAE KRVYYFEDQR SYHTLKTGWI YEEGYWYYLQ KDGGFDSRIN 180
RLTVGELARG WVKDYPLTYD EEKLKAAPWY YLDPATGWQN LGNKWYYLRS SGAMATGWYQ 240
EGSTWYYLNA SNGDMKTGWF QVNGNWYYAY DSGALAVNTT VGGYYLNYNG EWVK 294

<212> Type : PRT
<211> Length : 294
SequenceName : SEQ ID 227
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pneumoniae R6
<400> PreSequenceString :
MKLLKKMMQV LLAVFFFGLL ATNTVFANTT GGRFVDKDNR KYYVKDDHKA IYWHKIDGKT 60
YYFGDIGEMV VGWQYLEIPG TGYRDNLFDN QPVNEIGLQE KWYYFGQDGA LLEQTDKQVL 120
EAKTSENTGK VYGEQYPLSA EKRTYYFDNN YAVKTGWIYE DGNWYYLNKL GNFGDDSYNP 180
LPIGEVAKGW TQDFHVTIDI DRSKPAPWYY LDASGKMLTD WQKVNGKWYY FGSSGSMATG 240
WKYVRGKWYY LDNKNGDMKT GWQYLGNKWY YLRSSGAMVT GWYQDGLTWY YLNAGNGDMK 300
TGWFQVNGKW YYAYSSGALA VNTTVDGYSV NYNGEWVQ 338
<212> Type : PRT
<211> Length : 338
SequenceName : SEQ ID 228
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pneumoniae R6
<400> PreSequenceString :
MNKKKMILTS LASVAILGAG FVASQPTVVR AEESPVASQS KAEKDYDAAK KDAKNAKKAV 60
EDAQKALDDA KAAQKKYDED QKKTEEKAAL EKAASEEMDK AVAAVQQAYL AYQQATDKAA 120
KDAADKMIDE AKKREEEAKT KFNTVRAMVV PEPEQLAETK KKSEEAKQKA PELTKKLEEA 180
KAKLEEAEKK ATEAKQKVDA EEVAPQAKIA ELENQVHRLE QELKEIDESE SEDYAKEGFR 240
APLQSKLDAK KAKLSKLEEL SDKIDELDAE IAKLEDQLKA AEENNNVEDY FKEGLEKTIA 300
AKKAELEKTE ADLKKAVNEP EKPAPAPETP APEAPAEQPK PAPAPQPAPA PKPEKPAEQP 360
KPEKTDDQQA EEDYARRSEE EYNRLTQQQP PKAEKPAPAP KTGWKQENGM WYFYNTDGSM 420
ATGWLQNNGS WYYLNSNGAM ATGWLQYNGS WYYLNANGAM ATGWAKVNGS WYYLNANGAM 480
ATGWLQYNGS WYYLNANGAM ATGWAKVNGS WYYLNANGAM ATGWLQYNGS WYYLNANGAM 540
ATGWAKVNGS WYYLNANGAM ATGWVKDGDT WYYLEASGAM KASQWFKVSD KWYYVNGLGA 600
LAVNTTVDGY KVNANGEWV 619
<212> Type : PRT
<211> Length : 619
SequenceName : SEQ ID 229
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pneumoniae R6
<400> PreSequenceString :
MKILPFIARG TSYYLKMSVK KLVPFLVVGL MLAAGDSVYA YSRGNGSIAR GDDYPAYYKN 60
GSQEIDQWRM YSRQCTSFVA FRLSNVNGFE IPAAYGNANE WGHRARREGY RVDNTPTIGS 120
ITWSTAGTYG HVAWVSNVMG DQIEIEEYNY GYTESYNKRV IKANTMTGFI HFKDLDSGSV 180
GNSQSSASTG GTHYFKTKSA IKTEPLVSAT VIDYYYPGEK VHYDQILEKD GYKWLSYTAY 240
NGSYRYVQLE AVNKNPLGNS VLSSTGGTHY FKIKSAIKTE PLVSATVIDY YYPGEKVHYD 300
QILEKDGYKW LSYTAYNGSR RYIQLEGVTS SQNYQNQSGN ISSYGSNNSS TVGWKKINGS 360
WYHFKSNGSK STGWLKDGSS WYYLKLSGEM QTGWLKENGS WYYLGSSGAM KTGWYQVSGE 420
WYYSYSSGAL AINTTVDGYR VNSDGERV 448
<212> Type : PRT
<211> Length : 448
SequenceName : SEQ ID 230
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pneumoniae R6
<400> PreSequenceString :
MFASKSERKV HYSIRKFSIG VASVAVASLV MGSVVHATEN EGSTQAATSS NMAKTEHRKA 60
AKQVVDEYIE KMLREIQLDR RKHTQNVALN IKLSAIKTKY LRELNVLEEK SKDELPSEIK 120
AKLDAAFEKF KKDTLKPGEK VAEAKKKVEE AKKKAEDQKE EDRRNYPTNT YKTLELEIAE 180
FDVKVKEAEL ELVKEEAKES RNEGTIKQAK EKVESKKAEA TRLENIKTDR KKAEEEAKRK 240
ADAKLKEANV ATSDQGKPKG RAKRGVPGEL ATPDKKENDA KSSDSSVGEE TLPSSSLKSG 300
KKVAEAEKKV EEAEKKAKDQ KEEDRRNYPT NTYKTLDLEI AESDVKVKEA ELELVKEEAK 360
EPRDEEKIKQ AKAKVESKKA EATRLENIKT DRKKAEEEAK RKAAEEDKVK EKPAEQPQPA 420
PATQPEKPAP KPEKPAEQPK AEKTDDQQAE EDYARRSEEE YNRLTQQQPP KTEKPAQPST 480
PKTGWKQENG MWYFYNTDGS MATGWLQNNG SWYYLNANGA MATGWLQNNG SWYYLNANGS 540
MATGWLQNNG SWYYLNANGA MATGWLQYNG SWYYLNSNGA MATGWLQYNG SWYYLNANGD 600
MATGWLQNNG SWYYLNANGD MATGWLQYNG SWYYLNANGD MATGWVKDGD TWYYLEASGA 660
MKASQWFKVS DKWYYVNGSG ALAVNTTVDG YGVNANGEWV N 701
<212> Type : PRT
<211> Length : 701
SequenceName : SEQ ID 231
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pneumoniae R6
<400> PreSequenceString :
MKKTTILSLT TAAVILAAYV PNEPILAAYV PNEPILADTP SSEVIKETKV GSIIQQNNIK 60
YKVLTVEGNI GTVQVGNGVT PVEFEAGQDG KPFTIPTKIT VGDKVFTVTE VASQAFSYYP 120
DETGRIVYYP SSITIPSSIK KIQKKGFHGS KAKTIIFDKG SQLEKIEDRA FDFSELEEIE 180
LPASLEYIGT SAFSFSQKLK KLTFSSSSKL ELISHEAFAN LSNLEKLTLP KSVKTLGSNL 240
FRLTTSLKHV DVEEGNESFA SVDGVLFSKD KTQLIYYPSQ KNDESYKTPK ETKELASYSF 300
NKNSYLKKLE LNEGLEKIGT FAFADAIKLE EISLPNSLET IERLAFYGNL ELKELILPDN 360

VKNFGKHVMN GLPKFLTLSG NNINSLPSFF LSGVLDSLKE IHIKNKSTEF SVKKDTFAIP 420
ETVKFYVTSE HIKDVLKSNL STSNDIIVEK VDNIKQETDV AKPKKNSNQG VVGWVKDKGL 480
WYYLNESGSM ATGWVKDKGL WYYLNESGSM ATGWVKDKGL WYYLNESGSM ATGWVKDKGL 540
WYYLNESGSM ATGWVKDKGL WYYLNESGSM ATGWVKDKGL WYYLNESGSM ATGWVKDKGL 600
WYYLNESGSM ATGWVKDKGL WYYLNESGSM ATGWVKDKGL WYYLNESGSM ATGWVKVSGK 660
WYYTYNSGDL LVNTTTPDGY RVNANGEWVG 690

<212> Type : PRT
<211> Length : 690
SequenceName : SEQ ID 232
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pneumoniae R6
<400> PreSequenceString :
MEINVSKLRT DLPQVGVQPY RQVHAHSTGN PHSTVQNEAD YHWRKDPELG FFSHIVGNGC 60
IMQVGPVDNG AWDVGGGWNA ETYAAVELIE SHSTKEEFMT DYRLYIELLR NLADEAGLPK 120
TLDTGSLAGI KTHEYCTNNQ PNNHSDHVDP YPYLAKWGIS REQFKHDIEN GLTIETGWQK 180
NDTGYWYVHS DGSYPKDKFE KINGTWYYFD SSGYMLADRW RKHTDGNWYW FDNSGEMATG 240
WKKIADKWYY FNEEGAMKTG WVKYKDTWYY LDAKEGAMVS NAFIQSADGT GWYYLKPDGT 300
LADRPEFTVE PDGLITVK 318

<212> Type : PRT
<211> Length : 318
SequenceName : SEQ ID 233
SequenceDescription :

Sequence

<213> OrganismName : Neisseria meningitidis Z2491
<400> PreSequenceString :
MTFAYWCILI AYLLPLFCAA YAKKAGGFRF KDNHNPRDFL ARTQGTAARA HAAQQNGFEA 60
FAPFAAAVLT AHATGNAGQA TVNTLAGLFI LFRLAFIWCY IADKAALRSL MWVGGFVCTV 120
GLFVVAA 127

<212> Type : PRT
<211> Length : 127
SequenceName : SEQ ID 234
SequenceDescription :

Sequence

<213> OrganismName : Neisseria meningitidis Z2491
<400> PreSequenceString :
MNKIYRIIWN SALNAWVAVS ELTRNHTKRA SATVKTAVLA TLLFATVQAN ATDEDEEEEL 60
ESVQRSVVGS IQASMEGSGE LETISLSMTN DSKEFVDPYI VVTLKAGDNL KIKQNTNENT 120
NASSFTYSLK KDLTGLINVE TEKLSFGANG KKVNIISDTK GLNFAKETAG TNGDTTVHLN 180
GIGSTLTDTL AGSSASHVDA GNQSTHYTRA ASIKDVLNAG WNIKGVKTGS TTGQSENVDF 240
VRTYDTVEFL SADTKTTTVN VESKDNGKRT EVKIGAKTSV IKEKDGKLVT GKGKGENGSS 300
TDEGEGLVTA KEVIDAVNKA GWRMKTTTAN GQTGQADKFE TVTSGTNVTF ASGKGTTATV 360
SKDDQGNITV MYDVNVGDAL NVNQLQNSGW NLDSKAVAGS SGKVISGNVS PSKGKMDETV 420
NINAGNNIEI SRNGKNIDIA TSMAPQFSSV SLGAGADAPT LSVDDEGALN VGSKDANKPV 480
RITNVAPGVK EGDVTNVAQL KGVAQNLNNR IDNVDGNARA GIAQAIATAG LVQAYLPGKS 540
MMAIGGGTYR GEAGYAIGYS SISDGGNWII KGTASGNSRG HFGASASVGY QW 592

<212> Type : PRT
<211> Length : 592
SequenceName : SEQ ID 235
SequenceDescription :

Sequence

<213> OrganismName : Neisseria meningitidis Z2491
<400> PreSequenceString :
MLLAEGQKSA VTEYYLNHGT WPSNNSDAGV ASTATDIKGK YVKEVKVEKG VITATMLSSG 60
VNNEIKGKKL SLWAKRQAGS VKWFCGQPVE RAANNAANDA VTAATANGNG KIDTKHLPST 120
CRDAASAVCI ETPPTAFYKN T 141

<212> Type : PRT
<211> Length : 141

SequenceName : SEQ ID 236
SequenceDescription :

Sequence

<213> OrganismName : Neisseria meningitidis Z2491
<400> PreSequenceString :
MKTTDKRTTE THRKAPKTGR IRFSPAYLAI CLSFGILPQA WAGHTYFGIN YQYYRDFAEN 60
KGKFAVGAKD IEVYNKKGEL VGKSMTKAPM IDFSVVSRNG VAALVGDQYI VSVAHNGGYN 120
NVDFGAEGRN PDQHRFSYQI VKRNNYKPDN SHPYNGDYHM PRLHKFVTDA EPVEMTSDMR 180
GNTYSDKEKY PERVRIGSGH HYWRYDDDKH GDLSYSGAWL IGGNTHMQGW GNNGVVSLSG 240
DVRHANDYGP MPIAGAAGDS GSPMFIYDKT NNKWLLNGVL QTGYPYSGRE NGFQLIRKDW 300
FYDDIYRGDT HTVFFEPRSN GHFSFTSNNN GTGTVTETNE KVSNPKLKVQ TVRLFDESLN 360
ETDKEPVYAA GGVNQYRPRL NNGENLSFID YGNGKLILSN NINQGAGGLY FEGDFTVSPE ... 420
NNETWQGAGV HISEDSTVTW KVNGVANDRL SKIGKGTLHV QAKGENQGSI SVGDGTVILD 480
QQADDKGKKQ AFSEIGLVSG RGTVQLNADN QFNPDKLYFG FRGGRLDLNG HSLSFHRIQN 540
TDEGAMIVNH NATTTSTVTI TGNESITQPS GKNINRLNYS KEIAYNGWFG EKDTTKTNGR 600
LNLVYQPAAE DRTLLLSGGT NLNGNITQTN GKLFFSGRPT PHAYNHLGSG WSKMEGIPQG 660
EIVWDNDWIN RTFKAENFHI QGGQAVISRN VAKVEGDWHL SNHAQAVFGV APHQSHTICT 720
RSDWTGLTNC VEKTITDDKV IASLTKTDIS GNVSLADHAH LNLTGLATLN GNLSANGDTR 780
YTVSHNATQN GNLSLVGNAQ ATFNQATLNG NTSASGNASF NLSNNAAQNG SLTLSDNAKA 840
NVSHSALNGN VSLADKAVFH FENSRFTGQL SGSKDTALHL KDSEWTLPSG TELGNLNLDN 900
ATITLNSAYR HDAAGAQTGS VSDTPRRRSR RSLLSVTPPT SVESRFNTLT VNGKLNGQGT 960
FRFMSELFGY RSDKLKLAES SEGTYTLAVN NTGNEPVSLD QLTVVEGKDN KPLSENLNFT 1020
LQNEHVDAGA WRYQLIRKDG EFRLHNPVKE QELSDKLGKA EAKKQAEKDN AQSLDALIAA 1080
GRDAAEKTES VAEPARQAGG ENVGIMQAEE EKKRVQADKD SALAKQREAE TRPATTAFPR 1140
ARRARRDLPQ PQPQPQPQPQ PQRDLISRYA NSGLSEFSAT LNSVFAVQDE LDRVFAEDRR 1200
NAVWTSGIRD TKHYRSQDFR AYRQQTDLRQ IGMQKNLGSG RVGILFSHNR TENTFDDGIG 1260
NSARLAHGAV FGQYGIGRFD IGISTGAGFS SGSLSDGIGG KIRRRVLHYG IQARYRAGFG 1320
GFGIEPYIGA TRYFVQKADY RYENVNIATP GLAFNRYRAG IKADYSFKPA QHISITPYLS 1380
LSYTDAASGK VRTRVNTAVL AQDFGKTRSA EWGVNAEIKG FTLSLHAAAA KGPQLEAQHS 1440
AGIKLGYRW 1449
<212> Type : PRT
<211> Length : 1449
SequenceName : SEQ ID 237
SequenceDescription :

Sequence

<213> OrganismName : Neisseria meningitidis Z2491
<400> PreSequenceString :
MNTLQKGFTL IELMIVIAIV GILAAVALPA YQDYTARAQV SEAILLAEGQ KSAVTEYYLN 60
HGEWPSNNTS AGVASSTDIK GKYVQSVEVK NGVVTATMAS SNVNNEIKGK KLSLWAKRQD 120
GSVKWFCGQP VKRNDTATTN DDVKADTAAN GKQIDTKHLP STCRDAASAG 170
<212> Type : PRT
<211> Length : 170
SequenceName : SEQ ID 238
SequenceDescription :

Sequence

<213> OrganismName : Neisseria meningitidis Z2491
<400> PreSequenceString :
MQARLLIPIL FSVFILSACG TLTGIPSHGG GKRFAVEQEL VAASARAAVK DMDLQALHGR 60
KVALYIATMG DQGSGSLTGG RYSIDALIRG EYINSPAVRT DYTYPRYETT AETTSGGLTG 120
LTTSLSTLNA PALSRTQSDG SGSKSSLGLN IGGMGDYRNE TLTTNPRDTA FLSHLVQTVF 180
FLRGIDVVSP ANADTDVFIN IDVFGTIRNR TEMHLYNAET LKAQTKLEYF AVDRTNKKLL 240
IKPKTNAFEA AYKENYALWM GPYKVSKGIK PTEGLMVDFS DIQPYGNHMG NSAPSVEADN 300
SHEGYGYSDE AVRRHRQGQP 320
<212> Type : PRT
<211> Length : 320
SequenceName : SEQ ID 239
SequenceDescription :

Sequence

<213> OrganismName : Neisseria meningitidis Z2491

<400> PreSequenceString :
MRPIFLSFVL FPILITACST PDKSARWENI GTISNGNIHT YINKDSVRKN GNLMIFQDKK 60
VVTNLKQERF ANTPAYKTAI AEWEIHCNNK TYRLSSLQLF DTKNTEISTQ NYTASSLRPM 120
SILSGTLTEK QYETVCGKKL 140
<212> Type : PRT
<211> Length : 140
SequenceName : SEQ ID 240
SequenceDescription :

Sequence

<213> OrganismName : Neisseria meningitidis Z2491
<400> PreSequenceString :
MNKLFITALS ALALSACAGT WEGAKQDTAE NLDKTQAAAE RAAEQTGNAV EKGWDKTKEA 60
VKKGGNAVGR GISHLGGKIE NATE 84
<212> Type : PRT
<211> Length : 84
SequenceName : SEQ ID 241
SequenceDescription :

Sequence

<213> OrganismName : Neisseria meningitidis Z2491
<400> PreSequenceString :
MKLLFIPLVL FVAVEHFYIA WLEMTQIPSE KAAETFKLPY EFMEQNRVQT LFGNQGLYNG 60
FLGIGLVWSR FAAPDNAVYG ATVLFLGFVL IAAAWGAFSS GNKGILVKQG LPAFLAAAAV 120
LAV 123
<212> Type : PRT
<211> Length : 123
SequenceName : SEQ ID 242
SequenceDescription :

Sequence

<213> OrganismName : Neisseria meningitidis Z2491
<400> PreSequenceString :
MASSNVNNEI KDKKLSLWAK RQDGSVKWFC GQPVKRDAAT DADVTADSGN EIDTKHLPST 60
CRDAASAVCT KTPEYYPNHG EWPKNFVIPA QAGIQVCRHG NLSGKKVSPV LSSRFPLSWE 120

<212> Type : PRT
<211> Length : 120
SequenceName : SEQ ID 243
SequenceDescription :

Sequence

<213> OrganismName : Neisseria meningitidis Z2491
<400> PreSequenceString :
MLLAEGQKSA VTEYYLNHGE WPSNNTSAGV ATSTDIKGKY VQSVEVKNGV VTATMASSNV 60
NNEIKGKKLS LWAKRQDGSV KWFCGQPVKR NDTATTNDDV KADTAANGKQ IDTKHLPSTA 120
STRKSTPN 128
<212> Type : PRT
<211> Length : 128
SequenceName : SEQ ID 244
SequenceDescription :

Sequence

<213> OrganismName : Neisseria meningitidis Z2491
<400> PreSequenceString :
MPIPFKPVLA AAAIAQAFPA FAADPAPQSA QTLNEITVTG THKTQKLGEE KIRRKTLDKL 60
LVNDEHDLVR YDPGISVVEG GRAGSNGFTI RGVDKDRVAI NVDGLAQAES RSSEAFQELF 120
GAYGNFNANR NTSEPENFSE VTITKGADSL KSGSGALGGA VNYQTKSASD YVSEDKPYHL 180
GIKGGSVGKN SQKFSSITAA GRLFGLDALL VYTRRFGKET KNRSTEGDIE IKNDGYVYNP 240
TDTGGPSKYL TYVATGVARS QPDPQEWVNK STLFKLGYNF NDQNRIGWIF EDSRTDRFTN 300
ELSNLWTGTT TSAATGDYRH RQDVSYRRRS GVEYKNELEH GPWDSLKLRY DKQRIDMNTW 360
TWDIPKNYDK RGINGEVYHS FRHIRQNTAQ WTADFEKQLD FSKAVWAAQY GLGGGKGDNA 420

NSDYSYFAKL YDPKILASNQ AKITMLIENR SKYKFAYWNN AFHLGGNDRF RLNAGIRYDK 480
NSSSAKDDPK YTTAIRGQIP HLGSERAHAG FSYGTGFDWR FTKHLHLLAK YSTGFRAPTS 540
DETWLLFPHP DFYLKANPNL KAEKAKNWEL GLAGSGKAGN FKLSGFKTKY RDFIELTYMG 600
VSSDDKNNPR YAPLSDGTAL VSSPVWQNQN RSAAWVKGIE FNGTWNLDSI GLPKGLHTGL 660
NVSYIKGKAT QNNGKETPIN ALSPWTAVYS LGYDAPSKRW GINAYATRTA AKKPSDTVHS 720
NDDLNNPWPY AKHSKAYTLF DLSAYLNIGK QVTLRAAAYN ITNKQYYTWE SLRSIREFGT 780
VNRVDNKTHA GIQRFTSPGR SYNFTIEAKF 810

<212> Type : PRT
<211> Length : 810
SequenceName : SEQ ID 245
SequenceDescription :

Sequence

<213> OrganismName : Neisseria meningitidis Z2491
<400> PreSequenceString :
MKKSLIALTL AALPVAAMAD VTLYGTIKTG VETSRSVEHN GGQVVSVETG TGIVDLGSKI 60
GFKGQEDLGN GLKAIWQVEQ KASIAGTDSG WGNRQSFIGL KGGFGKLRVG RLNSVLKDTG 120
DINPWDSKSD YLGVNKIAEP EARLISVRYD SPEFAGLSGS VQYALNDNVG RHNSESYHAG 180
FNYKNGGFFV QYGGAYKRHQ DVDDVKIEKY QIHRLVSGYD NDALYASVAV QQQDAKLVED 240
NSHNSQTEVA ATLAYRFGNV TPRVSYAHGF KGSVDDAKRD NTYDQVVVGA EYDFSKRTSA 300
LVSAGWLQEG KGENKFVATA GGVGLRHKF 329

<212> Type : PRT
<211> Length : 329
SequenceName : SEQ ID 246
SequenceDescription :

Sequence

<213> OrganismName : Neisseria meningitidis Z2491
<400> PreSequenceString :
MKTLLLLIPL VLTACGFLTG IPAHGGGKRF AVEQELVAAS SRAAVKEMDL SALKGRKAAL 60
YVSVMGDQGS GNISGGRYSI DALIRGGYHN NPESATQYSY PAYDTTATTK SDALSSVTTS 120
TSLLNAPAAA LTKNSGRKGE RSAGLSVNGT GDYRNETLLA NPRDVSFLTN LIQTVFYLRG 180
IEVVPPEYAD TDVFVTVDVF GTVRSRTELH LYNAETLKAQ TKLEYFAVDR DSRKLLIAPK 240
TAAYESQYQE QYALWMGPYS VGKTVKASDR LMVDFSDITP YGDTTAQNRP DFKQNNGKKP 300
DVGNEVIRRR KGG 313

<212> Type : PRT
<211> Length : 313
SequenceName : SEQ ID 247
SequenceDescription :

Sequence

<213> OrganismName : Neisseria meningitidis Z2491
<400> PreSequenceString :
MNKTLSILPV AILLGGCAAG GGNTFGSLDG GTGMGGSIVK MAVESQCRAE LNKRSEWRLT 60
ALAMSAEKQA EWENKICACV AQEAPNQLTG NDVMQMLDPS TRNQALAALT AKTVSACFKH 120
LYR 123

<212> Type : PRT
<211> Length : 123
SequenceName : SEQ ID 248
SequenceDescription :

Sequence

<213> OrganismName : Neisseria meningitidis Z2491
<400> PreSequenceString :
MNPLIHQAKE SSMQTRILSA VLLAFSTAAF AGGAFTLQFD NPSEDGGFTQ NQILSAPYGF 60
GCSGGNASPA LSWKNPPAGT KSFVLTVYDK DAPTGLGWMH WVVADIPADV RRRNATSLQL 120
SRCASIADDQ SAAISAVISL QICRIRLTPS YTAKPMPSCC NHANTPQSAA SAALCGTSSS 180
VSTAAA 186

<212> Type : PRT
<211> Length : 186
SequenceName : SEQ ID 249
SequenceDescription :

Sequence

<213> OrganismName : Neisseria meningitidis Z2491
<400> PreSequenceString :
MNKTLKRRVF RHTALYAAIL MFSHTGGGGG AMAQTRQYAI IMNERNQPEV QWNGSYSIKD 60
KDRKREYTHH NHQQGGSSVS FNNSDELVSR QSGTAVFGTA TYLPPYGKVS GFDAAALKER 120
NNAVDWIHTT HPGLIGYSYD GVVCRSATDC PKLVYKTRFS FDNPDLAKTG GGLDKHTEPS 180
RDNSPIYKLK DHPWLGVSFN LGAEGIAKNG KTINKLVSSF NEKNSNNNLV YTTEGRDISL 240
GNWQRETTAM AYYLNAKLHL LDKKQIQNIT DKTVQLGVLK PSIDVRTRNT GTAGILSYWA 300
KWDIKDTGQI PVKLSLTQVK AGRCVNKDNP NKNTKTSSPA LTAPALWFGA GQDGKAEMYS 360
ASVSTYPDSS SSRIFLQNLK RKTDTSRPGR YSLATLNKSD IESREPSFTS RQTVIRLDGG 420
VQQIKLDRNN TEVTGFNGND GKNDTFGIVS EGSFMPDASE WKKVLLPWTV RAFNYDGRFN 480
TVNKEENNGK PKYSQKYRSR NNGKHERNLG DIVNSPIVAV GEYLATSAND GMVHIFKQSG 540
GDKRSYNLKL SYIPGTMPRK DIESKDSTLA KELRAFAEKG YVGDRYGVDG GFVLRRITDD 600
QDKQKHFFMF GAMGLGGRGA YALDLTKADD NDPTKASLFD VKDNGNNGNN GNNRVELGYT 660
VGTPQIGKTH NGKYAAFLAS GYATKQIDSG ENKTALYVYD LESNNGTLIR KIEVTDGKGG 720
LSSPTLVDKD LDGTVDIAYA GDRGGKMYRF DLSGNNPNSW TVRTIFQGTK PITSAPAISQ 780
LKDKRVVIFG TGSDLSEDDV LSTDEQHIYG IFDNDINTGT AQEGLGKGLL EQKLSEENKT 840
LFLTDYKRSD GSGDKGNVVK LKDGQRVTVK PTVVLRTAFV TIHKYTGNDK CGAETAILGI 900
NTADGGKLTK KSARPIVPAA NSKVAQYSGD KKTSSGKSIP IGCMEKDGGT VCPNGYVYDK 960
PVNVRYLDEK KTDGFSTTAD GDAGGSGTFK EGKKPARNNR CFSGKGVRTL LMNDLDSLDI 1020
TGPMCGMKRI SWREVFY 1037
<212> Type : PRT
<211> Length : 1037
SequenceName : SEQ ID 250
SequenceDescription :

Sequence

<213> OrganismName : Neisseria meningitidis Z2491
<400> PreSequenceString :
MKHPKLTLIA ALLTTAATAA PLPVVTSFSI LGDVAKQIGG ERVSIQSLVG ANQDTHAYHM 60
TSGDIKKIRS AKLVLINGLG LEAADIQRAV KQSKVSYAEA TKGIQPLKAE EEGGHHHDHD 120
HDHDHDHEGH HHDHGEYDPH VWNDPVLMSA YAQNVAEALI KADPEGKVYY QQRLGNYQMQ 180
LKKLHSDAQA AFNAVPAAKR KVLTGHDAFS YMGKRYHIEF IAPQGVSSEA EPSAKQVAAI 240
IRQIKREGIK AVFTENIKDT RMVDRIAKET GVNVSGKLYS DALGNAPADT YIGMYRHNIK 300
ALTNAMKQ 308
<212> Type : PRT
<211> Length : 308
SequenceName : SEQ ID 251
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pyogenes MGAS8232
<400> PreSequenceString :
MKKRILSAVL VSGVTLGAAT TVGAEDLSTK IAKQDSIISN LTTEQKAAQN QVSALQAQVS 60
SLQSEQDKLT ARNTELEALS KRFEQEIKAL TSQIVARNEK LKNQARSAYK NNETSGYINA 120
LLNSKSISDV VNRLVAINRA VSANAKLLEQ QKADKVSLEE KQAANQTAIN TIAANMAMAE 180
ENQNTLRTQQ ANLEAATANL ALQLASATED KANLVAQKEA AEKAAAEALA QEQAAKVKAQ 240
EQAAQQAASV EAAKSAITPA PQATPAAQSS NAIEPAALTA PAAPSARPQT SYDSSNTYPV 300
GQCTWGAKSL APWAGNNWGN GGQWAYSAQA AGYRTGSTPM VGAIAVWNDG GYGHVAVVVE 360
VQSASSIRVM ESNYSGRQYI ADHRGWFNPT GVTFIYPH 398
<212> Type : PRT
<211> Length : 398
SequenceName : SEQ ID 252
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pyogenes MGAS8232
<400> PreSequenceString :
MITIKNPKIL KWLKYVLSAI LSLIILVIII GGLLFTFYIS SAPKLSEAQL KSTNSSLVYD 60
GNNNLIADLG SEKRENVTAD SIPINLVNAI TSIEDKRFFN HRGVDLYRIF GAAFHNLTSQ 120
TTQGGSTLDQ QLIKLAYFST NESDQTLKRK AQEVWLALQM ERKYTKQEIL TFYINKVYMG 180
NGNYGMLTAA KSYYGKDLKD LSYAQLALLA GIPQAPSQYD PYLHPEAAQN RRNVVLQQMY 240
MEKHLTKAEY ETAIATPVAE GLQSLQQRST YPKYMDNYLK QVIEEVKKET NKDIFTAGLK 300

VYTNIIPDAQ QTLYNIYHSG DYVYYPDQDF QVASTIVDVT NGHVIAQLGG RNQDENVSFG 360
TNQAVLTDRD WGSTMKPITA YAPAIESGVY TSTAQSTNDS VYYWPGTTTQ LFNWDLRYNG 420
WMTIQAAIML SRNVPAVRAL EAAGLDYARS FLSSLGINYP EMHYSNAISS NNSSSDKKYG 480
ASSEKMAAAY AAFANGGIYH KPRYVNKVEF SDGTSKTFDE KGKRAMKETT AYMMTDMLKT 540
VLTYGTGTAA AIPGVAQAGK TGTSNYTDEE LAKIGEKYGL YPDYVGTLAP DENFVGFTKR 600
YAMAVWTGYK NRLTPVYGSS LEIASDVYRS MMTYLTNGYS EDWTMPNGLY RSGGFLYLSG 660
TYASNTDYTN SVYNNLYSNN TTTASSQTTS DDTSSSNDTS NSTNTDNNGS HPSTDDKKTT 720
H 721

<212> Type : PRT
<211> Length : 721
SequenceName : SEQ ID 253
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pyogenes MGAS8232
<400> PreSequenceString :
MIITKKSLFV TSVALSLAPL VTAQAQEWTP RSVTEIKSEL VLVDNVFTYT VKYGDTLSTI 60
AEAMGIDVHV LGDINHIANI DLIFPDTILT ANYNQHGQAT TLTVQAPASS PASVSHVPSS 120
EPLPQASATS QSTVPMAPSA TPSDVPTTPL ASAKPDSFVT ASSELTSSTN DVSTELSSES 180
QKQPEVSQEA VPTPKAAETT EVEPKTDISE DPTSANRPVP NESASEEASS AAPAQAPAEK 240
EETSQMLTAP AAQKAVADTT SVATSNGLSY APNHAYNPMN AGLQPQTAAF KEEVASAFGI 300
TSFSGYRPGD PGDHGKGLAI DFMVPVSSTL GDQVAQYAID HMAERGISYV IWKQRFYAPF 360
ASIYGPAYTW NPMPDRGSIT ENHYDHVHVS FNA 393

<212> Type : PRT
<211> Length : 393
SequenceName : SEQ ID 254
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pyogenes MGAS8232
<400> PreSequenceString :
MKKKILLMMS LISVFFAWQL TQAKQVLAEG KVKVVTTFYP VYEFTKGVIG NDGDVSMLMK 60
AGTEPHDFEP STKDIKKIQD ADAFVYMDDN METWVSDVKK SLTSKKVTIV KGTGNMLLVA 120
GAGHDHHHED ADKKHEHNKH SEEGHNHAFD PHVWLSPYRS ITVVENIRDS LSKAYPEKAE 180
NFKANAATYI EKLKELDKDY TAALSDAKQK SFVTQHAAFG YMALDYGLNQ ISINGVTPDA 240
EPSAKRIATL SKYVKKYGIK YIYFEENASS KVAKTLAKEA GVKAAVLSPL EGLTKKEMKA 300
GQDYFTVMRK NLETLRLTTD VAGKEILPEK DTTKTVYNGY FKDKEVKDRQ LSDWSGSWQS 360
VYPYLQDGTL DQVWDYKAKK SKGKMTAABY KDYYTTGYKT DVEQIKINGK KKTMTFVRNG 420
EKKTFTYTYA GKEILTYPKG NRGVRFMFEA KEPNAGEFKY VQFSDHAIAP EKAEHFHLYW 480
GGDSQEKLHK ELEHWPTYYG SDLSGREIAQ EINAH 515

<212> Type : PRT
<211> Length : 515
SequenceName : SEQ ID 255
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pyogenes MGAS8232
<400> PreSequenceString :
MKKFHRFLVS GVILLGFNGL VPTMPSTLIS QQENLVHAAV LGDNYPSKWK KGNGIDSWNM 60
YIRQCISFAA FRLSSANGFQ LPKGYGNACT WGHIAKNQGY PVNKTPSIGA IAWFDKNAYQ 120
SNAAYDHVAW VADIRGDTVT IEEYNYNAGQ GPERYHKRQI PKSQVSGYIH FKDLSSQTSH 180
SYPRQLKHIS QASFDPSGTY HFTTRLPVKG QTSIDSPDLA YYEAGQSVYY DKVVTAGGYT 240
WLSYLSFSGN RRYIPIKEPA QSVVQNDNTK PSIKVGDTVT FPGVFRVDQL VNNLIVNKEL 300
AGGDPTPLNW IDPTPLDETD NQGKVLGNQI LRVGEYFTVT GSYKVLKIDQ PSNGIYVQIG 360
SRGTWVNADK ANKL 374

<212> Type : PRT
<211> Length : 374
SequenceName : SEQ ID 256
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pyogenes MGAS8232
<400> PreSequenceString :

MLKPTSNILA TSVAETTQVA PGGCCCCCTT CCFSIATGSG NSQGGSGSYT PGK

<212> Type : PRT
<211> Length : 53
SequenceName : SEQ ID 257
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pyogenes MGAS8232
<400> PreSequenceString :
MGESYSVEAV LTAVDKTFGK TLQSAIRSIE GLEKRSTGFS SVSQKASSMF KSMLGANLAG 60
QAISAMTRTV SSGLGSMLGE MNSSAKAWKT FDANLADIGF GKKQILAVKT AMQDYATKTI 120
YSASDMASTY AQLAAVGVKD TGKLVKAFGG LAASAENPKQ AMKSISQQMT QAVGRPTVAN 180
QDFRIMLEQT PAGMAKVAKS MGKNLDELVA DIQAGRVKTS DFLEAVKKAG NDKSFQKMAT 240
EFKTVDQAID GMREGLSNKL QPAFEKVNQF GIRAIEAIGK QLDKVDFSKF ASNLGKFLEG 300
INIDKIVSNI SSAVSSVTSK VKEFWDGFKQ TGAISAFSGA LQSVWGALKN VASAMSGGNW 360
KTFGATVGGI VKHVSNFAKA VSDVLGKMDP GRLRSWIATF AAVAGGFKLF EKLTGQSVIG 420
SFLDKIGSKF GLFGNKAKEG TDKASNGARR SGGIISQIFS GLGNIVKSAG TAISTAAKGI 480
GVGIKTALSG IPPYH 495

<212> Type : PRT
<211> Length : 495
SequenceName : SEQ ID 258
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pyogenes MGAS8232
<400> PreSequenceString :
MKKGFFLMVM VVSLVMIAGC DKSANPKQPT QGMSVVTSFY PMYAMTKEVS GDLNDVRMIQ 60
SGAGIHSFEP SVNDVAAIYD ADLFVYHSHT LEAWARDLDP NLKKSKVDVF EASKPLTLDR 120
VKGLEDMEVT QGIDPATLYD PHTWTDPVLA GEEAVNIAKE LGRLDPKHKD SYTKNAKAFK 180
KEAEQLTEEY TQKFKKVRSK TFVTQHTAFS YLAKRFGLKQ LGISGISPEQ EPSPRQLKEI 240
QDFVKEYNVK TIFAEDNVNP KIAHAIAKST GAKVKTLSPL EAAPSGNKTY LENLRANLEV 300
LYQQLK 306

<212> Type : PRT
<211> Length : 306
SequenceName : SEQ ID 259
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pyogenes MGAS8232
<400> PreSequenceString :
MEKKQRFSLR KYKSGTFSVL IGSVFLMMTT TVAADELSTM SEPTITNHTQ QQAQHLTNTE 60
LSSAESKSQD TSQITPKTNR EKEQPQGLVS EPTTTELADT DAAPMANTGP DATQKSASLP 120
PVNTDVHDWV KTKGAWDKGY KGQGKVVAVI DTGIDPAHQS MRISDVSTAK VKSKEDMLAR 180
QKAAGINYGS WINDKVVFAH NYVENSDNIK ENQFEDFDED WENFEFDAEA EPKAIKKHKI 240
YRPQSTQAPK ETVIKTEETD GSHDIDWTQT DDDTKYESHG MHVTGIVAGN SKEAAATGER 300
FLGIAPEAQV MFMRVFANDV MGSAESLFIK AIEDAVALGA DVINLSLGTA NGAQLSGSKP 360
LMEAIEKAKK AGVSVVVAAG NERVYGSDHD DPLAINPDYG LVGSPSTGRT PTSVAAINSK 420
WVIQRLMTVK ELENRADLNH GKAIYSESVD FKNIKDSLGY DKSEQFAYVK ESTDAGYKAQ 480
DVKDKIALIE RDPNKTYDEM IALAKKHGAL GVLIFNNKPG QSNRSMRLTA NGMGIPSAFI 540
SHEFGKAMSQ LNGNGTGSLE FDSVVSKAPS QKGNEMNHFS NWGLTSDGYL KPDITAPGGD 600
IYSTYNDNHY GSQTGTSMAS PQIAGASLLV KQYLEKTQPN LPKEKIADIV KNLLMSNAQI 660
HVNPETKTTT SPRQQGAGLL NIDGAVTSGL YVTGKDNYGS ISLGNITDTM TFDVTVHNLS 720
NKDKTLRYDT ELLTDHVDPQ KGRFTLTSRS LKTYQGGEVT VPANGKVTVR VTMDVSQFTK 780
ELTKQMSNGY YLEGFVRFRD SQDDQLNRVN IPFVGFKGQF ENLAVAEESI YRLKSQGKTG 840
FYFDESGPKD DIYVGKHFTG LVTLGSETNV STKTISDNGL HTLGTFKNAD GKFILEKNAQ 900
GNPVLAISPN GDNNQDFAAF KGVFLRKYQG LKASVYHASD KEHKNPLWVS PESFKGDKNF 960
NSDIRFAKST TLLGTAFSGK SLTGAELPDG YYHYVVSYYP DVVGAKRQEM TFDMILDRQK 1020
PVLSQATFDP ETNRFKPEPL KDRGLAGVRK DSVFYLERKD NKPYTVTIND SYKYVSVEDN 1080
KTFVERQADG SFILPLDKAK LGDFYYMVED FAGNVAIAKL GDHLPQTLGK TPIKLKLTDG 1140
NYQTKETLKD NLEMTQSDTG LVTNQAQLAV VHRNQPQSQL TKMNQDFFIS PNEDGNKDFV 1200
AFKGLKNNVY NDLTVNVYAK DDHQKQTPIW SSQAGASASA IESTAWYGIT ARGSKVMPGD 1260
YQYVVTYRDE HGKEHQKQYT ISVNDKKPMI TQGRFDTING VDHFTPDKTK ALGSSGIVRE 1320
EVFYLAKKNG RKFDVTEGKD GITVSDNKMY IPKNPDGSYT ISKRDGVTLS DYYYLVEDRA 1380

GNVSFATLRD LKAVGKDKAV VNFGLDLPVP EDKQIVNFTY LVRDADGKPI ENLEYYNNSG 1440
NSLILPYGKY TVELLTYDTN AAKLESDKIV SFTLSADNNF QQVTFKMTML ATSQITAHFD 1500
HLLPEGSRVS LKTAQGQLIP LEQSLYVPKA YGKTVQEGTY EVVVSLPKGY RIEGNTKVNT 1560
LPNEVHELSL RLVKVGDASD STGDHKVMSK NNSQALTAFA TPTKTTTSAT AKALPSAGEK 1620
MGLKLRIVGL VLLGLTCVFS RKKSTKD 1647
<212> Type : PRT
<211> Length : 1647
SequenceName : SEQ ID 260
SequenceDescription :

Sequence

<213> OrganismName : Treponema pallidum subsp. pallidum str. Nichols
<400> PreSequenceString :
MMRSLPSGVS GMQNEQTRMD VIGNNVANVN TTGFKRGRVN FQDLISQQLS AAARPNEEVG 60
GVNPKEVGLG VLIASIDTVH TQGALQTTGI NTDVSIQGSG FFVLKSGEKT FFTRAGAFGV 120
DNAGTLVNPA NGMRVQGWMA QDVAGERLIN SSAQTQDLVI PIGQKIDAQQ TSTVHYACNL 180
DKRLPELAAD ANEADVRKST WTTDFQVYDS FGQQHTLQIN FSRVPGTNNQ WQATVAVDPG 240
TEVDTQTRVG VGTSDGAANT FIVNFDNFGH LASVTDTAGN VTGPTGQVIL EASYDVVGAN 300
PDDAGQVTRH AFTLNLGEIG TARNTITQFA ERSTTKAYRQ DGYAMGYLEN FKIDQSGVIT 360
GVYSNGVSQD IGQLALAGFA NQGGLEKAGE NTYVQSNNSG IANISTSGVM GKGKLIAGTL 420
EMSNVDLTDQ FTDMIITQKG FQAGAKTIQT SDTMLDTVLS LKR 463
<212> Type : PRT
<211> Length : 463
SequenceName : SEQ ID 261
SequenceDescription :

Sequence

<213> OrganismName : Treponema pallidum subsp. pallidum str. Nichols
<400> PreSequenceString :
MGCMRWGSVL CVVVGVGASG GVLGQEFSPK LTGSATLEWG ISYGKGVGSH GQAPGAVMGT 60
GPYNLKHGFR TTNTVGVSFP LVMRTTHTRR GQHPALYAEL KVADLQADLS QGKAGFAVKR 120
KGKVEATLHC YGAYLTIGKN PTFLTNFARL WKPWVTAQYQ EDAVQYAPGF GGLGGKVGYR 180
AQDIGGSGVS LDVGPLSFAS NGAWDSTDPT HSKYGFGADL KLMYARAGHP LCTVELASNV 240
TLEDGYLIGA QKDANNQNKD KLLWNVGGRL TLEPGAGFRF SFALDAGNQH QSAQDFQNRT 300
QRAQSELTAL SNNLFQGESQ KQEAWVTQVV QQATQTVTAG VRSALESRGT TYINALEAVQ 360
PNPAKPTGKV VQNLHTPQGS PPNLPPLPAL PAFSLMGQVL LQYDAEQVVK GFEQVQTQIV 420
TEINQKVQAA VAKNNANMQA VGGSLGDTAR MVGEALIKQQ LSRKQNSILT MVSVQDEVKQ 480
DLADLVPMMR TEITAFFASV QQHITEEVKK KTDALNAGQQ IRQAIQNLRA SAWRAFLMGV 540
SAVCLYLDTY NVAFDALFTA QWKWLSSGIY FATAPANVFG TRVLDNTIAS CGDFAGFLKL 600
ETKSGDPYTH LLTGLDAGVE TRVYIPLTHD LYKNNNGNPL PSGGSSGHIG LPVVGKAWCS 660
YRIPVQDYGW VKPSVTVHAS TNRAHLNAPA AGGAVGATYL TKEYCAQLRA GISASLIEKT 720
VFSLDWEQGM LSDVPYLLVS ECLTQGIGRI VCGVTLSW 758
<212> Type : PRT
<211> Length : 758
SequenceName : SEQ ID 262
SequenceDescription :

Sequence

<213> OrganismName : Treponema pallidum subsp. pallidum str. Nichols
<400> PreSequenceString :
MGRQVMQAGV LAGMVCAASG YAGVLTPQVS GTAQLQWGIA FQKNPRTGPG KHTHGFRTTN 60
SLTISLPLVS KHTHTRRGEA RSGVWAQLQL KDLAVELASS KSSTALSFTK PTASFQATLH 120
CYGAYLTVGT SPSCVVNFAQ LWKPFVTRAY SEKDTRYAPG FSGSGAKLGY QAHNVGNSGV 180
DVDIGFLSFL SNGAWDSTDT THSKYGFGAD ATLSYGVDRQ RLLTLELAGN ATLDQNYVKG 240
TEDSKNENKT ALLWGVGGRL TLEPGAGFRF SFALDAGNQH QSNAHAQTQE RAILKAREVF 300
RRVEGKLVQN LPNIMMPPGI TEQTTLIEMV GLAALIAEGT LGSAIQTVLA AGALAALVSQ 360
LVPNIEQGVR DVFRSSDPRV VTAKLLAPLE RAPMNALNID ALLRMQWKWL SSGIYFATAG 420
TNIFGKRVFA TTRAHYFDFA GFLKLETKSG DPYTHLLTGL NAGVEARVYL PLTYIRYRNN 480
GGYELNGAVP PGTINMPILG KAWCSYRIPL GSHAWLAPHT SVLGTTNRFN IINPAGNLLN 540
ERALQYQVGL TFSPFEKVEL SAQWEQGVLA DAPYMGIAES IWSERHFGTL VCGMKVTW 598

<212> Type : PRT
<211> Length : 598
SequenceName : SEQ ID 263

SequenceDescription :

Sequence

<213> OrganismName : Treponema pallidum subsp. pallidum str. Nichols
<400> PreSequenceString :
MGRQVMQAGV LAGMVCAASG YAGVLTPQVS GTAQLQWGIA FQKNPRTGPG KHTHGFRTTN 60
SLTISLPLVS KHTHTRRGEA RSGVWAQLQL KDLAVELASS KSSTALSFTK PTASFQATLH 120
CYGAYLTVGT SPSCVVNFAQ LWKPFVTRAY SEKDTRYAPG FSGSGAKLGY QAHNVGNSGV 180
DVDIGFLSFL SNGAWDSTDT THSKYGFGAD ATLSYGVDRQ RLLTLELAGN ATLDQNYVKG 240
TEDSKNENKT ALLWGVGGRL TLEPGAGFRF SFALDAGNQH QSNAHAQTQE RAILKAREVF 300
RRVEGKLVQN LPNIMMPPGI TEQTTLIEMV GLAALIAEGT LGSAIQTVLA AGALAALVSQ 360
LVPNIEQGVR DVFRSSDPRV VTAKLLAFLE RAPMNALNID ALLRMQWKWL SSGIYFATAG 420
TNIFGKRVFA TTRAHYFDFA GFLKLETKSG DPYTHLLTGL NAGVEARVYI PLTYIRYRNN 480
GGYELNGAVP PGTINMPILG KAWCSYRIPL GSHAWLAPHT SVLGTTNRFN IINPAGNLLN 540
ERALQYQVGL TFSPFEKVEL SAQWEQGVLA DAPYMGIAES IWSERHFGTL VCGMKVTW 598

<212> Type : PRT
<211> Length : 598
SequenceName : SEQ ID 264
SequenceDescription :

Sequence

<213> OrganismName : SARS coronavirus Frankfurt 1
<400> PreSequenceString :
MFIFLLFLTL TSGSDLDRCT TFDDVQAPNY TQHTSSMRGV YYPDEIFRSD TLYLTQDLFL 60
PFYSNVTGFH TINHTFGNPV IPFKDGIYFA ATEKSNVVRG WVFGSTMNNK SQSVIIINNS 120
TNVVIRACNF ELCDNPFFAV SKPMGTQTHT MIFDNAFNCT FEYISDAFSL DVSEKSGNFK 180
HLREFVFKNK DGFLYVYKGY QPIDVVRDLP SGFNTLKPIF KLPLGINITN FRAILTAFSP 240
AQDIWGTSAA AYFVGYLKPT TFMLKYDENG TITDAVDCSQ NPLAELKCSV KSFEIDKGIY 300
QTSNFRVVPS GDVVRFPNIT NLCPFGEVFN ATKFPSVYAW ERKKISNCVA DYSVLYNSTF 360
FSTFKCYGVS ATKLNDLCFS NVYADSFVVK GDDVRQIAPG QTGVIADYNY KLPDDFMGCV 420
LAWNTRNIDA TSTGNYNYKY RYLRHGKLRP FERDISNVPF SPDGKPCTPP ALNCYWPLND 480
YGFYTTTGIG YQPYRVVVLS FELLNAPATV CGPKLSTDLI KNQCVNFNFN GLTGTGVLTP 540
SSKRFQPFQQ FGRDVSDFTD SVRDPKTSEI LDISPCSFGG VSVITPGTNA SSEVAVLYQD 600
VNCTDVSTAI HADQLTPAWR IYSTGNNVFQ TQAGCLIGAE HVDTSYECDI PIGAGICASY 660
HTVSLLRSTS QKSIVAYTMS LGADSSIAYS NNTIAIPTNF SISITTEVMP VSMAKTSVDC 720
NMYICGDSTE CANLLLQYGS FCTQLNRALS GIAAEQDRNT REVFAQVKQM YKTPTLKYFG 780
GFNFSQILPD PLKPTKRSFI EDLLFNKVTL ADAGFMKQYG ECLGDINARD LICAQKFNGL 840
TVLPPLLTDD MIAAYTAALV SGTATAGWTF GAGAALQIPF AMQMAYRFNG IGVTQNVLYE 900
NQKQIANQFN KAISQIQESL TTTSTALGKL QDVVNQNAQA LNTLVKQLSS NFGAISSVLN 960
DILSRLDKVE AEVQIDRLIT GRLQSLQTYV TQQLIRAAEI RASANLAATK MSECVLGQSK 1020
RVDFCGKGYH LMSFPQAAPH GVVFLHVTYV PSQERNFTTA PAICHEGKAY FPREGVFVFN 1080
GTSWFITQRN FFSPQIITTD NTFVSGNCDV VIGIINNTVY DPLQPELDSF KEELDKYFKN 1140
HTSPDVDFGD ISGINASVVN IQKEIDRLNE VAKNLNESLI DLQELGKYEQ YIKWPWYVWL 1200
GFIAGLIAIV MVTILLCCMT SCCSCLKGAC SCGSCCKFDE DDSEPVLKGV KLHYT 1255

<212> Type : PRT
<211> Length : 1255
SequenceName : SEQ ID 265
SequenceDescription :

Sequence

<213> OrganismName : SARS coronavirus HSR 1
<400> PreSequenceString :
MFIFLLFLTL TSGSDLDRCT TFDDVQAPNY TQHTSSMRGV YYPDEIFRSD TLYLTQDLFL 60
PFYSNVTGFH TINHTFGNPV IPFKDGIYFA ATEKSNVVRG WVFGSTMNNK SQSVIIINNS 120
TNVVIRACNF ELCDNPFFAV SKPMGTQTHT MIFDNAFNCT FEYISDAFSL DVSEKSGNFK 180
HLREFVFKNK DGFLYVYKGY QPIDVVRDLP SGFNTLKPIF KLPLGINITN FRAILTAFSP 240
AQDIWGTSAA AYFVGYLKPT TFMLKYDENG TITDAVDCSQ NPLAELKCSV KSFEIDKGIY 300
QTSNFRVVPS GDVVRFPNIT NLCPFGEVFN ATKFPSVYAW ERKKISNCVA DYSVLYNSTF 360
FSTFKCYGVS ATKLNDLCFS NVYADSFVVK GDDVRQIAPG QTGVIADYNY KLPDDFMGCV 420
LAWNTRNIDA TSTGNYNYKY RYLRHGKLRP FERDISNVPF SPDGKPCTPP ALNCYWPLND 480
YGFYTTTGIG YQPYRVVVLS FELLNAPATV CGPKLSTDLI KNQCVNFNFN GLTGTGVLTP 540
SSKRFQPFQQ FGRDVSDFTD SVRDPKTSEI LDISPCSFGG VSVITPGTNA SSEVAVLYQD 600

VNCTDVSTAI HADQLTPAWR IYSTGNNVFQ TQAGCLIGAE HVDTSYECDI PIGAGICASY 660
HTVSLLRSTS QKSIVAYTMS LGADSSIAYS NNTIAIPTNF SISITTEVMP VSMAKTSVDC 720
NMYICGDSTE CANLLLQYGS FCTQLNRALS GIAAEQDRNT REVFAQVKQM YKTPTLKYFG 780
GFNFSQILPD PLKPTKRSFI EDLLFNKVTL ADAGFMKQYG ECLGDINARD LICAQKFNGL 840
TVLPPLLTDD MIAAYTAALV SGTATAGWTF GAGAALQIPF AMQMAYRFNG IGVTQNVLYE 900
NQKQIANQFN KAISQIQESL TTTSTALGKL QDVVNQNAQA LNTLVKQLSS NFGAISSVLN 960
DILSRLDKVE AEVQIDRLIT GRLQSLQTYV TQQLIRAAEI RASANLAATK MSECVLGQSK 1020
RVDFCGKGYH LMSFPQAAPH GVVFLHVTYV PSQERNFTTA PAICHEGKAY FPREGVFVFN 1080
GTSWFITQRN FFSPQIITTD NTFVSGNCDV VIGIINNTVY DPLQPELDSF KEELDKYFKN 1140
HTSPDVDLGD ISGINASVVN IQKEIDRLNE VAKNLNESLI DLQELGKYEQ YIKWPWYVWL 1200
GFIAGLIAIV MVTILLCCMT SCCSCLKGAC SCGSCCKFDE DDSEPVLKGV KLHYT 1255

<212> Type : PRT
<211> Length : 1255
SequenceName : SEQ ID 266
SequenceDescription :

Sequence

<213> OrganismName : SARS coronavirus ZJ01
<400> PreSequenceString :
MFIFLLFLTL TSGSDLDRCT TFDDVQAPNY TQHTSSMRGV YYPDEIFRSD TLYLTQDLFL 60
PFYSNVTGFH TINHTFGNPV IPFKDGIYFA ATEKSNVVRG WVFGSTMNNK SQSVIIINNS 120
TNVVIRACNF ELCDNPFFAV SKPMGTQTHT MIFDNAFNCT FEYISDAFSL DVSEKSGNFK 180
HLREFVFKNK DGFLYVYKGY QPIDVVRDLP SGFNTLKPIF KLPLGINITN FRAILTAFSP 240
AQDIWGTSAA AYFVGYLKPT TFMLKYDENG TITDAVDCSQ NPLAELKCSV KSFEIDKGIY 300
QTSNFRVVPS GDVVRFPNIT NLCPFGEVFN ATKFPSVYAW ERKKISNCVA DYSVLYNSTF 360
FSTFKCYGVS ATKLNDLCFS NVYADSFVVK GDDVRQIAPG QTGVIADYNY KLPDDFMGCV 420
LAWNTRNIDA TSTGNYNYKY RYLRHGKLRP FERDISNVPF SPDGKPCTPP ALNCYWPLND 480
YGFYTTTGIG YQPYRVVVLS FELLNAPATV CGPKLSTDLI KNQCVNFNFN GLTGTGVLTP 540
SSKRFQPFQQ FGRDVSDFTD SVRDPKTSEI LDISPCSFGG VSVITPGTNA SSEVAVLYQD 600
VNCTDVSTAI HADQLTPAWR IYSTGNNVFQ TQAGCLIGAE HVDTSYECDI PIGAGICASY 660
HTVSLLRSTS QKSIVAYTMS LGADSSIAYS NNTIAIPTNF SISITTEVMP VSMAKTSVDC 720
NMYICGDSTE CANLLLQYGS FCTQLNRALS GIAAEQDRNT REVFAQVKQM YKTPTLKYFG 780
GFNFSQILPD PLKPTKRSFI EDLLFNKVTL ADAGFMKQYG ECLGDINARD LICAQKFNGL 840
TVLPPLLTDD MIAAYTAALV SGTATAGWTF GAGAALQIPF AMQMAYRFNG IGVTQNVLYE 900
NQKQIANQFN KAISQIQESL TTTSTALGKL QDVVNQNAQA LNTLVKQLSS NFGAISSVLN 960
DILSRLDKVE AEVQIDRLIT GRLQSLQTYV TQQLIRAAEI RASANLAATK MSECVLGQSK 1020
RVDFCGKGYH LMSFPQAAPH GVVFLHVTYV PSQERNFTTA PAICHEGKAY FPREGVFVFN 1080
GTSWFITQRN FFSPQIITTD NTFVSGNCDV VIGIINNTVY DPLQPELDSF KEELDKYFKN 1140
HTSPDVDLGD ISGINASVVN IQKEIDRLNE VAKNLNESLI DLQELGKYEQ YIKWPWYVWL 1200
GFIAGLIAIV MVTILLCCMT SCCSCLKGAC SCGSCCKFDE DDSEPVLKGV KLHYT 1255

<212> Type : PRT
<211> Length : 1255
SequenceName : SEQ ID 267
SequenceDescription :

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<213> OrganismName : SARS coronavirus TW1
<400> PreSequenceString :
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TNVVIRACNF ELCDNPFFAV SKPMGTQTHT MIFDNAFNCT FEYISDAFSL DVSEKSGNFK 180
HLREFVFKNK DGFLYVYKGY QPIDVVRDLP SGFNTLKPIF KLPLGINITN FRAILTAFSP 240
AQDIWGTSAA AYFVGYLKPT TFMLKYDENG TITDAVDCSQ NPLAELKCSV KSFEIDKGIY 300
QTSNFRVVPS GDVVRFPNIT NLCPFGEVFN ATKFPSVYAW ERKKISNCVA DYSVLYNSTF 360
FSTFKCYGVS ATKLNDLCFS NVYADSFVVK GDDVRQIAPG QTGVIADYNY KLPDDFMGCV 420
LAWNTRNIDA TSTGNYNYKY RYLRHGKLRP FERDISNVPF SPDGKPCTPP ALNCYWPLND 480
YGFYTTTGIG YQPYRVVVLS FELLNAPATV CGPKLSTDLI KNQCVNFNFN GLTGTGVLTP 540
SSKRFQPFQQ FGRDVSDFTD SVRDPKTSEI LDISPCSFGG VSVITPGTNA SSEVAVLYQD 600
VNCTDVSTAI HADQLTPAWR IYSTGNNVFQ TQAGCLIGAE HVDTSYECDI PIGAGICASY 660
HTVSLLRSTS QKSIVAYTMS LGADSSIAYS NNTIAIPTNF SISITTEVMP VSMAKTSVDC 720
NMYICGDSTE CANLLLQYGS FCTQLNRALS GIAAEQDRNT REVFAQVKQM YKTPTLKYFG 780
GFNFSQILPD PLKPTKRSFI EDLLFNKVTL ADAGFMKQYG ECLGDINARD LICAQKFNGL 840
TVLPPLLTDD MIAAYTAALV SGTATAGWTF GAGAALQIPF AMQMAYRFNG IGVTQNVLYE 900

NQKQIANQFN KAISQIQESL TTTSTALGKL QDVVNQNAQA LNTLVKQLSS NFGAISSVLN 960
DILSRLDKVE AEVQIDRLIT GRLQSLQTYV TQQLIRAAEI RASANLAATK MSECVLGQSK 1020
RVDFCGKGYH LMSFPQAAPH GVVFLHVTYV PSQERNFTTA PAICHEGKAY FPREGVFVFN 1080
GTSWFITQRN FFSPQIITTD NTFVSGNCDV VIGIINNTVY DPLQPELDSF KEELDKYFKN 1140
HTSPDVDLGD ISGINASVVN IQKEIDRLNE VAKNLNESLI DLQELGKYEQ YIKWPWYVWL 1200
GFIAGLIAIV MVTILLCCMT SCCSCLKGAC SCGSCCKFDE DDSEPVLKGV KLHYT 1255

<212> Type : PRT
<211> Length : 1255
SequenceName : SEQ ID 268
SequenceDescription :

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<213> OrganismName : SARS coronavirus CUHK-Su10
<400> PreSequenceString :
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PFYSNVTGFH TINHTFGNPV IPFKDGIYFA ATEKSNVVRG WVFGSTMNNK SQSVIIINNS 120
TNVVIRACNF ELCDNPFFAV SKPMGTQTHT MIFDNAFNCT FEYISDAFSL DVSEKSGNFK 180
HLREFVFKNK DGFLYVYKGY QPIDVVRDLP SGFNTLKPIF KLPLGINITN FRAILTAFSP 240
AQDIWGTSAA AYFVGYLKPT TFMLKYDENG TITDAVDCSQ NPLAELKCSV KSFEIDKGIY 300
QTSNFRVVPS GDVVRFPNIT NLCPFGEVFN ATKFPSVYAW ERKKISNCVA DYSVLYNSTF 360
FSTFKCYGVS ATKLNDLCFS NVYADSFVVK GDDVRQIAPG QTGVIADYNY KLPDDFMGCV 420
LAWNTRNIDA TSTGNYNYKY RYLRHGKLRP FERDISNVPF SPDGKPCTPP ALNCYWPLND 480
YGFYTTTGIG YQPYRVVVLS FELLNAPATV CGPKLSTDLI KNQCVNFNFN GLTGTGVLTP 540
SSKRFQPFQQ FGRDVSDFTD SVRDPKTSEI LDISPCSFGG VSVITPGTNA SSEVAVLYQD 600
VNCTDVSTAI HADQLTPAWR IYSTGNNVFQ TQAGCLIGAE HVDTSYECDI PIGAGICASY 660
HTVSLLRSTS QKSIVAYTMS LGADSSIAYS NNTIAIPTNF SISITTEVMP VSMAKTSVDC 720
NMYICGDSTE CANLLLQYGS FCTQLNRALS GIAAEQDRNT REVFAQVKQM YKTPTLKYFG 780
GFNFSQILPD PLKPTKRSFI EDLLFNKVTL ADAGFMKQYG ECLGDINARD LICAQKFNGL 840
TVLPPLLTDD MIAAYTAALV SGTATAGWTF GAGAALQIPF AMQMAYRFNG IGVTQNVLYE 900
NQKQIANQFN KAISQIQESL TTTSTALGKL QDVVNQNAQA LNTLVKQLSS NFGAISSVLN 960
DILSRLDKVE AEVQIDRLIT GRLQSLQTYV TQQLIRAAEI RASANLAATK MSECVLGQSK 1020
RVDFCGKGYH LMSFPQAAPH GVVFLHVTYV PSQERNFTTA PAICHEGKAY FPREGVFVFN 1080
GTSWFITQRN FFSPQIITTD NTFVSGNCDV VIGIINNTVY DPLQPELDSF KEELDKYFKN 1140
HTSPDVDLGD ISGINASVVN IQKEIDRLNE VAKNLNESLI DLQELGKYEQ YIKWPWYVWL 1200
GFIAGLIAIV MVTILLCCMT SCCSCLKGAC SCGSCCKFDE DDSEPVLKGV KLHYT 1255

<212> Type : PRT
<211> Length : 1255
SequenceName : SEQ ID 269
SequenceDescription :

Sequence

<213> OrganismName : SARS coronavirus Urbani
<400> PreSequenceString :
MFIFLLFLTL TSGSDLDRCT TFDDVQAPNY TQHTSSMRGV YYPDEIFRSD TLYLTQDLFL 60
PFYSNVTGFH TINHTFGNPV IPFKDGIYFA ATEKSNVVRG WVFGSTMNNK SQSVIIINNS 120
TNVVIRACNF ELCDNPFFAV SKPMGTQTHT MIFDNAFNCT FEYISDAFSL DVSEKSGNFK 180
HLREFVFKNK DGFLYVYKGY QPIDVVRDLP SGFNTLKPIF KLPLGINITN FRAILTAFSP 240
AQDIWGTSAA AYFVGYLKPT TFMLKYDENG TITDAVDCSQ NPLAELKCSV KSFEIDKGIY 300
QTSNFRVVPS GDVVRFPNIT NLCPFGEVFN ATKFPSVYAW ERKKISNCVA DYSVLYNSTF 360
FSTFKCYGVS ATKLNDLCFS NVYADSFVVK GDDVRQIAPG QTGVIADYNY KLPDDFMGCV 420
LAWNTRNIDA TSTGNYNYKY RYLRHGKLRP FERDISNVPF SPDGKPCTPP ALNCYWPLND 480
YGFYTTTGIG YQPYRVVVLS FELLNAPATV CGPKLSTDLI KNQCVNFNFN GLTGTGVLTP 540
SSKRFQPFQQ FGRDVSDFTD SVRDPKTSEI LDISPCSFGG VSVITPGTNA SSEVAVLYQD 600
VNCTDVSTAI HADQLTPAWR IYSTGNNVFQ TQAGCLIGAE HVDTSYECDI PIGAGICASY 660
HTVSLLRSTS QKSIVAYTMS LGADSSIAYS NNTIAIPTNF SISITTEVMP VSMAKTSVDC 720
NMYICGDSTE CANLLLQYGS FCTQLNRALS GIAAEQDRNT REVFAQVKQM YKTPTLKYFG 780
GFNFSQILPD PLKPTKRSFI EDLLFNKVTL ADAGFMKQYG ECLGDINARD LICAQKFNGL 840
TVLPPLLTDD MIAAYTAALV SGTATAGWTF GAGAALQIPF AMQMAYRFNG IGVTQNVLYE 900
NQKQIANQFN KAISQIQESL TTTSTALGKL QDVVNQNAQA LNTLVKQLSS NFGAISSVLN 960
DILSRLDKVE AEVQIDRLIT GRLQSLQTYV TQQLIRAAEI RASANLAATK MSECVLGQSK 1020
RVDFCGKGYH LMSFPQAAPH GVVFLHVTYV PSQERNFTTA PAICHEGKAY FPREGVFVFN 1080
GTSWFITQRN FFSPQIITTD NTFVSGNCDV VIGIINNTVY DPLQPELDSF KEELDKYFKN 1140
HTSPDVDLGD ISGINASVVN IQKEIDRLNE VAKNLNESLI DLQELGKYEQ YIKWPWYVWL 1200

GFIAGLIAIV MVTILLCCMT SCCSCLKGAC SCGSCCKFDE DDSEPVLKGV KLHYT 1255

<212> Type : PRT
<211> Length : 1255
SequenceName : SEQ ID 270
SequenceDescription :

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<213> OrganismName : SARS coronavirus
<400> PreSequenceString :
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PFYSNVTGFH TINHTFGNPV IPFKDGIYFA ATEKSNVVRG WVFGSTMNNK SQSVIIINNS 120
TNVVIRACNF ELCDNPFFAV SKPMGTQTHT MIFDNAFNCT FEYISDAFSL DVSEKSGNFK 180
HLREFVFKNK DGFLYVYKGY QPIDVVRDLP SGFNTLKPIF KLPLGINITN FRAILTAFSP 240
AQDIWGTSAA AYFVGYLKPT TFMLKYDENG TITDAVDCSQ NPLAELKCSV KSFEIDKGIY 300
QTSNFRVVPS GDVVRFPNIT NLCPFGEVFN ATKFPSVYAW ERKKISNCVA DYSVLYNSTF 360
FSTFKCYGVS ATKLNDLCFS NVYADSFVVK GDDVRQIAPG QTGVIADYNY KLPDDFMGCV 420
LAWNTRNIDA TSTGNYNYKY RYLRHGKLRP FERDISNVPF SPDGKPCTPP ALNCYWPLND 480
YGFYTTTGIG YQPYRVVVLS FELLNAPATV CGPKLSTDLI KNQCVNFNFN GLTGTGVLTP 540
SSKRFQPFQQ FGRDVSDFTD SVRDPKTSEI LDISPCAFGG VSVITPGTNA SSEVAVLYQD 600
VNCTDVSTAI HADQLTPAWR IYSTGNNVFQ TQAGCLIGAE HVDTSYECDI PIGAGICASY 660
HTVSLLRSTS QKSIVAYTMS LGADSSIAYS NNTIAIPTNF SISITTEVMP VSMAKTSVDC 720
NMYICGDSTE CANLLLQYGS FCTQLNRALS GIAAEQDRNT REVFAQVKQM YKTPTLKYFG 780
GFNFSQILPD PLKPTKRSFI EDLLFNKVTL ADAGFMKQYG ECLGDINARD LICAQKFNGL 840
TVLPPLLTDD MIAAYTAALV SGTATAGWTF GAGAALQIPF AMQMAYRFNG IGVTQNVLYE 900
NQKQIANQFN KAISQIQESL TTTSTALGKL QDVVNQNAQA LNTLVKQLSS NFGAISSVLN 960
DILSRLDKVE AEVQIDRLIT GRLQSLQTYV TQQLIRAAEI RASANLAATK MSECVLGQSK 1020
RVDFCGKGYH LMSFPQAAPH GVVFLHVTYV PSQERNFTTA PAICHEGKAY FPREGVFVFN 1080
GTSWFITQRN FFSPQIITTD NTFVSGNCDV VIGIINNTVY DPLQPELDSF KEELDKYFKN 1140
HTSPDVDLGD ISGINASVVN IQKEIDRLNE VAKNLNESLI DLQELGKYEQ YIKWPWYVWL 1200
GFIAGLIAIV MVTILLCCMT SCCSCLKGAC SCGSCCKFDE DDSEPVLKGV KLHYT 1255

<212> Type : PRT
<211> Length : 1255
SequenceName : SEQ ID 271
SequenceDescription :

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<213> OrganismName : SARS coronavirus Tor2
<400> PreSequenceString :
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PFYSNVTGFH TINHTFGNPV IPFKDGIYFA ATEKSNVVRG WVFGSTMNNK SQSVIIINNS 120
TNVVIRACNF ELCDNPFFAV SKPMGTQTHT MIFDNAFNCT FEYISDAFSL DVSEKSGNFK 180
HLREFVFKNK DGFLYVYKGY QPIDVVRDLP SGFNTLKPIF KLPLGINITN FRAILTAFSP 240
AQDIWGTSAA AYFVGYLKPT TFMLKYDENG TITDAVDCSQ NPLAELKCSV KSFEIDKGIY 300
QTSNFRVVPS GDVVRFPNIT NLCPFGEVFN ATKFPSVYAW ERKKISNCVA DYSVLYNSTF 360
FSTFKCYGVS ATKLNDLCFS NVYADSFVVK GDDVRQIAPG QTGVIADYNY KLPDDFMGCV 420
LAWNTRNIDA TSTGNYNYKY RYLRHGKLRP FERDISNVPF SPDGKPCTPP ALNCYWPLND 480
YGFYTTTGIG YQPYRVVVLS FELLNAPATV CGPKLSTDLI KNQCVNFNFN GLTGTGVLTP 540
SSKRFQPFQQ FGRDVSDFTD SVRDPKTSEI LDISPCAFGG VSVITPGTNA SSEVAVLYQD 600
VNCTDVSTAI HADQLTPAWR IYSTGNNVFQ TQAGCLIGAE HVDTSYECDI PIGAGICASY 660
HTVSLLRSTS QKSIVAYTMS LGADSSIAYS NNTIAIPTNF SISITTEVMP VSMAKTSVDC 720
NMYICGDSTE CANLLLQYGS FCTQLNRALS GIAAEQDRNT REVFAQVKQM YKTPTLKYFG 780
GFNFSQILPD PLKPTKRSFI EDLLFNKVTL ADAGFMKQYG ECLGDINARD LICAQKFNGL 840
TVLPPLLTDD MIAAYTAALV SGTATAGWTF GAGAALQIPF AMQMAYRFNG IGVTQNVLYE 900
NQKQIANQFN KAISQIQESL TTTSTALGKL QDVVNQNAQA LNTLVKQLSS NFGAISSVLN 960
DILSRLDKVE AEVQIDRLIT GRLQSLQTYV TQQLIRAAEI RASANLAATK MSECVLGQSK 1020
RVDPCGKGYH LMSFPQAAPH GVVFLHVTYV PSQERNFTTA PAICHEGKAY FPREGVFVFN 1080
GTSWFITQRN FFSPQIITTD NTFVSGNCDV VIGIINNTVY DPLQPELDSF KEELDKYFKN 1140
HTSPDVDLGD ISGINASVVN IQKEIDRLNE VAKNLNESLI DLQELGKYEQ YIKWPWYVWL 1200
GFIAGLIAIV MVTILLCCMT SCCSCLKGAC SCGSCCKFDE DDSEPVLKGV KLHYT 1255

<212> Type : PRT
<211> Length : 1255
SequenceName : SEQ ID 272

SequenceDescription :

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<213> OrganismName : SARS coronavirus GD01
<400> PreSequenceString :
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TNVVIRACNF ELCDNPFFAV SKPMGTQTHT MIFDNAFNCT FEYISDAFSL DVSEKSGNFK 180
HLREFVFKNK DGFLYVYKGY QPIDVVRDLP SGFNTLKPIF KLPLGINITN FRAILTAFLP 240
AQDTWGTSAA AYFVGYLKPT TFMLKYDENG TITDAVDCSQ NPLAELKCSV KSFEIDKGIY 300
QTSNFRVVPS RDVVRFPNIT NLCPFGEVFN ATKFPSVYAW ERKRISNCVA DYSVLYNSTF 360
FSTFKCYGVS ATKLNDLCFS NVYADSFVVK GDDVRQIAPG QTGVIADYNY KLPDDFMGCV 420
LAWNTRNIDA TSTGNYNYKY RYLRHGKLRP FERDISNVPF SPDGKPCTPP ALNCYWPLND 480
YGFYTTTGIG YQPYRVVVLS FELLNAPATV CGPKLSTDLI KNQCVNFNFN GLTGTGVLTP 540
SSKRFQPFQQ FGRDVSDFTD SVRDPKTSEI LDISPCSFGG VSVITPGTNA SSEVAVLYQD 600
VNCTDVSTAI HADQLTPAWR IYSTGNNVFQ TQAGCLIGAE HVDTSYECDI PIGAGICASY 660
HTVSLLRSTS QKSIVAYTMS LGADSSIAYS NNTIAIPTNF SISITTEVMP VSMAKTSVDC 720
NMYICGDSTE CANLLLQYGS FCTQLNRALS GIAAEQDRNT REVFAQVKQM YKTPTLKDFG 780
GFNFSQILPD PLKSTKRSFI EDLLFNKVTL ADAGFMKQYG ECLGDINARD LICAQKFNGL 840
TVLPPLLTDD MIAAYTAALV SGTATAGWTF GAGAALQIPF AMQMAYRFNG IGVTQNVLYE 900
NQKQIANQFN KAISQIQESL TTTSTALGKL QDVVNQNAQA LNTLVKQLSS NFGAISSVLN 960
DILSRLDKVE AEVQIDRLIT GRLQSLQTYV TQQLIRAAEI RASANLAATK MSECVLGQSK 1020
RVDFCGKGYH LMSFPQAAPH GVVFLHVTYV PSQERNFTTA PAICHEGKAY FPREGVFVFN 1080
GTSWFITQRN FFSPQIITTD NTFVSGNCDV VIGIINNTVY DPLQPELDSF KEELDKYFKN 1140
HTSPDVDLGD ISGINASVVN IQKEIDRLNE VAKNLNESLI DLQELGKYEQ YIKWPWYVWL 1200
GFIAGLIAIV MVTILLCCMT SCCSCLKGAC SCGSCCKFDE DDSEPVLKGV KLHYT 1255

<212> Type : PRT
<211> Length : 1255
SequenceName : SEQ ID 273
SequenceDescription :

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<213> OrganismName : SARS coronavirus CUHK-W1
<400> PreSequenceString :
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TNVVIRACNF ELCDNPFFAV SKPMGTQTHT MIFDNAFNCT FEYISDAFSL DVSEKSGNFK 180
HLREFVFKNK DGFLYVYKGY QPIDVVRDLP SGFNTLKPIF KLPLGINITN FRAILTAFSP 240
AQDTWGTSAA AYFVGYLKPT TFMLKYDENG TITDAVDCSQ NPLAELKCSV KSFEIDKGIY 300
QTSNFRVVPS GDVVRFPNIT NLCPFGEVFN ATKFPSVYAW ERKKISNCVA DYSVLYNSTF 360
FSTFKCYGVS ATKLNDLCFS NVYADSFVVK GDDVRQIAPG QTGVIADYNY KLPDDFMGCV 420
LAWNTRNIDA TSTGNYNYKY RYLRHGKLRP FERDISNVPF SPDGKPCTPP ALNCYWPLND 480
YGFYTTTGIG YQPYRVVVLS FELLNAPATV CGPKLSTDLI KNQCVNFNFN GLTGTGVLTP 540
SSKRFQPFQQ FGRDVSDFTD SVRDPKTSEI LDISPCSFGG VSVITPGTNA SSEVAVLYQD 600
VNCTDVSTAI HADQLTPAWR IYSTGNNVFQ TQAGCLIGAE HVDTSYECDI PIGAGICASY 660
HTVSLLRSTS QKSIVAYTMS LGADSSIAYS NNTIAIPTNF SISITTEVMP VSMAKTSVDC 720
NMYICGDSTE CANLLLQYGS FCTQLNRALS GIAAEQDRNT REVFAQVKQM YKTPTLKYFG 780
GFNFSQILPD PLKPTKRSFI EDLLFNKVTL ADAGFMKQYG ECLGDINARD LICAQKFNGL 840
TVLPPLLTDD MIAAYTAALV SGTATAGWTF GAGAALQIPF AMQMAYRFNG IGVTQNVLYE 900
NQKQIANQFN KAISQIQESL TTTSTALGKL QDVVNQNAQA LNTLVKQLSS NFGAISSVLN 960
DILSRLDKVE AEVQIDRLIT GRLQSLQTYV TQQLIRAAEI RASANLAATK MSECVLGQSK 1020
RVDFCGKGYH LMSFPQAAPH GVVFLHVTYV PSQERNFTTA PAICHEGKAY FPREGVFVFN 1080
GTSWFITQRN FFSPQIITTD NTFVSGNCDV VIGIINNTVY DPLQPELDSF KEELDKYFKN 1140
HTSPDVDLGD ISGINASVVN IQKEIDRLNE VAKNLNESLI DLQELGKYEQ YIKWPWYVWL 1200
GFIAGLIAIV MVTILLCCMT SCCSCLKGAC SCGSCCKFDE DDSEPVLKGV KLHYT 1255

<212> Type : PRT
<211> Length : 1255
SequenceName : SEQ ID 274
SequenceDescription :

Sequence

<213> OrganismName : SARS coronavirus BJ01

<400> PreSequenceString :
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TNVVIRACNF ELCDNPFFAV SKPMGTQTHT MIFDNAFNCT FEYISDAFSL DVSEKSGNFK 180
HLREFVFKNK DGFLYVYKGY QPIDVVRDLP SGFNTLKPIF KLPLGINITN FRAILTAFSP 240
AQDTWGTSAA AYFVGYLKPT TFMLKYDENG TITDAVDCSQ NPLAELKCSV KSFEIDKGIY 300
QTSNFRVVPS GDVVRFPNIT NLCPFGEVFN ATKFPSVYAW ERKKISNCVA DYSVLYNSTF 360
FSTFKCYGVS ATKLNDLCFS NVYADSFVVK GDDVRQIAPG QTGVIADYNY KLPDDFMGCV 420
LAWNTRNIDA TSTGNYNYKY RYLRHGKLRP FERDISNVPF SPDGKPCTPP ALNCYWPLND 480
YGFYTTTGIG YQPYRVVVLS FELLNAPATV CGPKLSTDLI KNQCVNFNFN GLTGTGVLTP 540
SSKRFQPFQQ FGRDVSDFTD SVRDPKTSEI LDISPCSFGG VSVITPGTNA SSEVAVLYQD 600
VNCTDVSTAI HADQLTPAWR IYSTGNNVFQ TQAGCLIGAE HVDTSYECDI PIGAGICASY 660
HTVSLLRSTS QKSIVAYTMS LGADSSIAYS NNTIAIPTNF SISITTEVMP VSMAKTSVDC 720
NMYICGDSTE CANLLLQYGS FCTQLNRALS GIAAEQDRNT REVFAQVKQM YKTPTLKYFG 780
GFNFSQILPD PLKPTKRSFI EDLLFNKVTL ADAGFMKQYG ECLGDINARD LICAQKFNGL 840
TVLPPLLTDD MIAAYTAALV SGTATAGWTF GAGAALQIPF AMQMAYRFNG IGVTQNVLYE 900
NQKQIANQFN KAISQIQESL TTTSTALGKL QDVVNQNAQA LNTLVKQLSS NFGAISSVLN 960
DILSRLDKVE AEVQIDRLIT GRLQSLQTYV TQQLIRAAEI RASANLAATK MSECVLGQSK 1020
RVDFCGKGYH LMSFPQAAPH GVVFLHVTYV PSQERNFTTA PAICHEGKAY FPREGVFVFN 1080
GTSWFITQRN FFSPQIITTD NTFVSGNCDV VIGIINNTVY DPLQPELDSF KEELDKYFKN 1140
HTSPDVDLGD ISGINASVVN IQKEIDRLNE VAKNLNESLI DLQELGKYEQ YIKWPWYVWL 1200
GFIAGLIAIV MVTILLCCMT SCCSCLKGAC SCGSCCKFDE DDSEPVLKGV KLHYT 1255

<212> Type : PRT
<211> Length : 1255
SequenceName : SEQ ID 275
SequenceDescription :

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<213> OrganismName : SARS coronavirus
<400> PreSequenceString :
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KSNHSFLVQA GNVQLRVIGH SMQNCLLRLK VDTSNPKTPK YKFVRIQPGQ TFSVLACYNG 120
SPSGVYQCAM RPNHTIKGSF LNGSCGSVGF NIDYDCVSFC YMHHMELPTG VHAGTDLEGK 180
FYGPFVDRQT AQAAGTDTTI TLNVLAWLYA AVINGDRWFL NRFTTTLNDF NLVAMKYNYE 240
PLTQDHVDIL GPLSAQTGIA VLDMCAALKE LLQNGMNGRT ILGSTILEDE FTPFDVVRQC 300
SGVTFQ 306
<212> Type : PRT
<211> Length : 306
SequenceName : SEQ ID 276
SequenceDescription :

Sequence

<213> OrganismName : SARS coronavirus
<400> PreSequenceString :
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PLTTAAKLMV VVPDYGTYKN TCDGNTFTYA SALWEIQQVV DADSKIVQLS EINMDNSPNL 180
AWPLIVTALR ANSAVKLQ 198
<212> Type : PRT
<211> Length : 198
SequenceName : SEQ ID 277
SequenceDescription :

Sequence

<213> OrganismName : SARS coronavirus
<400> PreSequenceString :
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ANMDQESFGG ASCCLYCRCH IDHPNPKGFC DLKGKYVQIP TTCANDPVGF TLRNTVCTVC 120
GMWKGYGCSC DQLREPLMQ 139
<212> Type : PRT
<211> Length : 139
SequenceName : SEQ ID 278
SequenceDescription :

Sequence

<213> OrganismName : SARS coronavirus
<400> PreSequenceString :
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<212> Type : PRT
<211> Length : 113
SequenceName : SEQ ID 279
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
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SMAFGVSAIS EGDRSIALGA SSYSLGQYSM ALGRYSKALG KLSIAMGDSS KAEGANAIAL 180
GNATKATEIM SIALGDTANA SKAYSMALGA SSVASEENAI AIGAETEAAE NATAIGNNAK 240
AKGTNSMAMG FGSLADKVNT IALGNGSQAL ADNAIAIGQG NKADGVDAIA LGNGSQSRGL 300
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AVLDENTLQW DQTKGKYSAA HGTSSPTASV ITDVADGTIS ASSKDAVNGS QLKATNDDVE 480
ANTANIATNT SNIATNTANI ATNTTNITNL TDSVGDLQAD ALLWNETKKA FSAAHGQDTT 540
SKITNVKDAD LTADSTDAVN GSQLKTTNDA VATNTTNIAN NTSNIATNTT NISNLTETVT 600
NLGEDALKWD KDNGVFTAAH GTETTSKITN VKDGDLTTGS TDAVNGSQLK TTNDAVATNT 660
TNIATNTTNI SNLTETVTNL GEDALKWDKD NGVFTAAHGN NTASKITNIL DGTVTATSSD 720
AINGSQLYDL SSNIATYFGG NASVNTDGVF TGPTYKIGET NYYNVGDALA AINSSFSTSL 780
GDALLWDATA GKFSAKHGTN GDASVITDVA DGRISDSSSD AVNGSQLHGV SSYVVDALGG 840
GAEVNADGTI TAPTYTIANA DYDNVGDALN AIDTTLDDAL LWDADAGENG AFSAAHGKDK 900
TASVITNVAN GAISAASSDA INGSQLYTTN KYIADALGGD AEVNADGTIT APTYTIANAE 960
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LNATNMMIEQ NTQIINQLAG NTDATYIQEN GAGINYVRTN DDGLAFNDAS AQGVGATAIG 1080
YNSVAKGDSS VAIGQGSYSD VDTGIALGSS SVSSRVIAKG SRDTSITENG VVIGYDTTDG 1140
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RGAQTNYTAY NMDAPQNSVG EFSVGSADGQ RQITNVAAGS ADTDAVNVGQ LKVTDAQVSQ 1320
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SIAAADNSVA LGTGSVATEE NTISVGSSTN QRRITNVAAG KNATDAVNVA QLKSSEAGGV 1440
RYDTKADGSI DYSNITLGGG NGGTTRISNV SAGVNNNDVV NYAQLKQSVQ ETKQYTDQRM 1500
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<212> Type : PRT
<211> Length : 1588
SequenceName : SEQ ID 280
SequenceDescription :

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<213> OrganismName : Escherichia coli O157:H7
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VINTVTYAAT VLADGTWSVG VPAADVSNWP AGTVNITVSG TNTAGTTSTI THPVTVDLAA 240
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VPAADLSVLR DGDATVQASV STINGNTASA THAYSVDATA PTLAINTIAT DDILNAAEAG 360
NPLTISGSST AEAGQTVTVT LNGVTYSGSV QADGSWSVSL PTADLSNLTA SQYTVSASVS 420
DKAGNPASAN HGLAVDLTVP VLTINTVSGD DIINAAEHGQ ALVISGSSTG GEAGDVITVT 480
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TIGINTIATD DVIKATEKGA DLQITGTSNQ PAGTTITVTL NGQNYTATTD SNGNWSATVP 600
ASAVSALGEA NYTVTANVTD TAGNSNSASH NVLVNSALPA VTINAVATDD IINAABSGNA 660
QTISGQVTGA AQGDTVTVTL GGNTYTATVQ SNLSWSVDVP AADIQALGNG DLTVNASVIN 720
GVGNTGSGSR DITIDANLPG LRVDTVAGDD VINSIEHNQA LVITGSSSGL TAGTALTVEI 780

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GKNYTTTLDA SGNWSVGIPA ADVTALATGS QTITASLSDR AGNSDSTTHD VTVDLSGPTL 1140
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TAGTTTSISH PVTVDLAAVA ITTNTLSTDD VINAAEKGSD LQLSGTTSGV EAGQTITVIF 1380
GGKSYTTTVA ADNTWGLTIP AVDVATLPDG AANVQASVSN VAGNSTQATH AYSVDATAPS 1440
VTINTIATDD ILNAAEAGSA LTISGTSTAE AGQTVTVTLN GVNYSGNVQA DGSWSVSVPT 1500
GDLASLTASS YTVNASVSDK ARNSASATHN LTVDLAAPVV TINTVAGDDI INATEHGQAQ 1560
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AGNSGTASHT VTVALGAPVL AINTIAVDDI INAAEKGADL AITGTSNQPA GTQITVTLNG 1680
QNYTTTADAS GNWSVTVPAS RVSALGEATY TVTAAATDAD GNSGSASHNV QVNTALPGVT 1740
INVVATDDII NAAEAGVEQT ISGQVTGAAA GDTVTVTLGG ATYTATVQAN LSWSVDVPAS 1800
ALQELGNGEL TISASVTNSV GNTGNGTREI TIDANLPGLR VDTVAGDDVV NIIEHGQALV 1860
ITGSSSGLAA GSNVTLTING QTYVAAVLAD GTWSVGVPAV DVSAWPAGSV TIAASGSTSA 1920
GNPVSVTHPV TVDLSAVAVS INAITADDVI NAAEKGAALT LSGSTSGVEA GQTVTVTFGG 1980
KTYSATVAAN GSWSTSVPAA DMAALRDGDA SAQASVSNVN GNSATTTHAY SVDASAPTVT 2040
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LSTLTASNYT VNAAVSDKAG NPASVNHNLT VDTSVPVVTI NTVAGDDVIN ATEHAQAQII 2160
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NYSATTDASG NWTLTVPVSD LAALGQANYT VSASATSAAG NTASSQANLL VDSGLPDVTI 2340
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ALGNGELTVN ASVTNAVGNT GSGTRDITID ASLPGLRVDT VAGDDVVNII EHAQAQVITG 3060
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TSITHPLTVD LTAVAISMNS ITSDDAINAA EKGAALTLSG STSGVEAGQT VTVTFGGKTY 3180
TTTVAANGSW STTVPAADLA ALRDGDASAQ VRVTNVNGNS ATATHEYSVD SAAPTVTINT 3240
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IGNGGHDTLL YKLLNASDAT GGNGSDVVNG FTVGTWEGTA DTDRIDIREL LQGSGYTGNG 5220
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<212> Type : PRT
<211> Length : 5291
SequenceName : SEQ ID 281
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
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TLTPGESNTN ESGIAQATLA GVAFGEQTVT ASLANNGASD NKTVHFIGDT AAAKIIELTP 240
VPDSIIAGTP QNSSGSVITA TVVDNNGFPV KGVTVNFTSN AATAEMTNGG QAVTNEQGKA 300
TVTYTNTRSS IESGARPDTV EASLENGSST LSTSINVNAD ASTAHLTLLQ ALFDTVSAGD 360
TTNLYIEVKD NYGNGVPQQE VTLSVSPSEG VTPSNNAIYT TNHDGNFYAS FTATKAGVYQ 420
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EVTFTLPEDV RANFTLGDGG KVVTDTEGKA KVTLKGTKAG AHTVTASMAG GKSEQLVVNF 540
IADTLTAQVN LNVTEDNFIA NNVGMTRLQA TVTDGNGNPL ANEAVTFTLP ADVSASFTLG 600
QGGSAITDIN GKAEVTLSGT KSGTYPVTVS VNNYGVSDTK QVTLIADAGT AKLASLTSVY 660
SFVVSTTEGA TMTASVTDAN GNPVEGIKVN FRGTSVTLSS TSVETDDRGF AEILVTSTEV 720
GLKTVSASLA DKPTEVISRL LNAKADINSA TITSLEIPEG QVMVAQDVAV KAHVNDQFGN 780
PILNESVTFS AEPPEHMTIS QNIVSTDTHG IAEVTMTPER NGSYMVKASL ANGSSYEKDL 840
VVIDQKLTLS ASSPLIGVNS PTGATLTATL TSANGTPVEG QVINFSVTPE GATLSGGKVR 900
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TNSDLSTLKA TVEDGSGNLI EGLTVYFALK SGSATLTSLT AVTDQNGIAT TSVRGAITGS 1020
VTVSAVTTAG GMQTVDITLV AGPADASQSV LKNNRSSLKG DFTDSAELHL VLHDISGNPI 1080
KVSEGLEFVQ SGTNAPYVQV SAIDYSKNFS GEYKATVTGG GEGIATLIPV LNGVHQAGLS 1140
TTIQFTRAED KIMSGTVLVN GANLPTTTFP SQGFTGAYYQ LNNDNFAPGK TAADYEFSSS 1200
ASWVDVDATG KVTFKNVGSK WERITATPKT GGPSYIYEIR VKSWWVNAGD AFMIYSLAEN 1260
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<212> Type : PRT
<211> Length : 1345
SequenceName : SEQ ID 282
SequenceDescription :

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<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
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LDTVAQTSAF PWGWLAGAAV GGGALGALLA SGGDGDSKTE VINNPTPPAE PGNATPSFLV 180
TDNQGDQRGI LATNDITDDT TPTFSGSGQA GATIQIKDSN GNTIASTQVD NNGHWSVSLP 240
TQSAGEHTWS VVQIVGSTIT DAGSITLTID NSQASVQVAT TAGDNIINAS EQAAGFTLSG 300
TSSHLAQGTE LTVTLNGKTY TTSVGANGAW SVQVPTADAQ ALGEGNQAVL VSGKDATGNT 360
VTGAQLLTVD TQPPTLAINT IAQDNIISAA EHNVALVLSG TSNAEAGQTV TLTVNGKSHT 420
ATVGSDGTWQ VTLPATEVQA LAEGNYAVNA SVSDRAGNTT SHSANFTVDT SAPVVSVNTV 480
AGDDILNNAE QAVAQIISGQ VSGASPGDTV TVKLGTHVLT GIVLADGSWN VALDPAVTRT 540
LDRGANTIFV TVTDAAGNTG AASRAITLVG VSPLITINTV SGDDIISGAE KGAPLTLTGS 600
TQQAETGQTV TVTLAGQSFT TTVQADGSWS LTVPAAAMGN LPDGAVAITA SVTDLSGNTG 660
NTSRTITVDS QAPALSIDPL TADNIINAAE SGQDLPITGT TDAQPGQTVT VTLNGQTYQG 720
VVQPDGTWSV TVPAANVGAL ADGNATVTAS VNDVAGNPSS VSRVALVDAT PPVVTINPVA 780
TDNVINTPEH AQAQIISGTV TGAQAGDIVT VTLNNVDYTT VVDGSGNWSL GVPASVVSGL 840
ADGSYPVSVS VTDKAGNTGS QSLTVTVNTA APLIGINSIA GDDVINASEK GADLQITGTS 900
DQPVNTAITV TLNGQNYTTT TDASGNWSVT VPASAVTALG QANYTVTAAV TSDIGNSATA 960
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VHNYSVDSSA PTIIINTVAS DNIVNASEAD AGVTVSGSTT AEAGQIVTIT LNSPTVQTYQ 1320
ATVQADGSWS INIPAADLEA LTDGSHTLTA TVNDKAGNPA STTHNLAVDL TVPVLTINTI 1380
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<212> Type : PRT
<211> Length : 1461
SequenceName : SEQ ID 283
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
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VNVLGGTWRL YDSGNNARPL NVGQSGTGTL NIKQKGHVDG GYLRLGTQAA GVGTVNVEGE 180
DSVLTTELFE IGSYGTGSLN ITDKGYVTSS IVAILGYQAN SNGKVVVEKG GEWLIKNNDS 240
SIEFQIGNQG TGEATIREGG LITAENTIIG GNATGVGTLN VQDQDSVITV RRLYNGYFGN 300
GAVNISNNGL INNKEYSLVG VQDGSHGVVN VTDKGHWNFL GTGEAFRYIY IGDAGDGELN 360
VSREGKVDSG IITAGMKETG TGNLTVKDKN SVITNLGTNL GYDGHGEMNI SNEGLVVSNG 420
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SGIGTLNLMD ATSSFDTVGI NVGNFGSGIV NVSNGATLNS TGYGFIGGNA SGKGIVNIST 540
DSLWNLKTSS TNAQLLQVGV LGTGELNITT GGIVKARDTQ IALNDKSKGD VRVDGQNSLL 600
ETFNMYVGTS GTGTLTLTNS GTLNVEGGEV YLGVFEPAVG TLNIGAAHGE AAADAGFITN 660
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VNDGLLTIAS HTADGVTGMG SSEVTIASPG TLDILASTNS AGDYTLTNAL KGDGLMRVQL 780
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GGLAMNGGTL IFDTDIPAAT LAEGYISVDT LVVGASDYTW KGRNYQVNGT GDVLIGVPKP 900
WNDPMANNPL TTLNLLEHDD NHVGVQLVKA QTVIGSGGSL TLRDLQGDEV EADKTLHIAQ 960
NGTVVAEGDY GFRLTTAPGD GLYVNYGLKA LNIHGGQKLT LAEHGGAYGA TADMSAKIGG 1020
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QTVETFTGQM GSTVLFKEGS LTVNKGGISQ GELTGGGNLN VTGGTLAVEG LNARYNALTS 1140
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<212> Type : PRT
<211> Length : 1343
SequenceName : SEQ ID 284
SequenceDescription :

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<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
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GIGLTINDYG TSVDLGSGSK IKTDGSTGVY IGGLNGNNAN GAARFTATDL TIDVQGYSAM 240
GINVQKNSVV DLGTNSSIKT SGDNAHGLWS FGQVSANALT VDVTGAAANG VEVRGGTTTI 300
GADSHISSAQ GGGLVTSGSD ATINFSGTAA QRNSIFSGGS YGASAQTATA VINMQNTDIT 360
VDRNGSLALG LWALSGGRIT GDSLAITGAA GARGIYAMTN SQIDLTSDLV IDMSTPDQMA 420
IATQHDDGYA ASRINASGRM LINGSVLSKG GLINLDMHPG SVWTGSSLSD NVNGGKLDVA 480
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NGVKPWA 547
<212> Type : PRT
<211> Length : 547
SequenceName : SEQ ID 285
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7

<400> PreSequenceString :
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YHLSNGMESK SVDTRSIYRE LGATLSYNMR LGNGMEVEPW LKAAVRKEFV DDNRVKVNSD 180
GNFVNDLSGR RGIYQAGIKA SFSSTLSGHL GVGYSNGAGM ESPWNAVAGV NWSF 234

<212> Type : PRT
<211> Length : 234
SequenceName : SEQ ID 286
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
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IKGFNSQKGL FDVAIEGDST ATAFKLTSRL ITNTLTQLDT SGSTLNVGVD YNGAAVEKTG 120
DTVMIDTANG VLGGMLSPLA NGYNASNRTT AQDGFTFSII SGTTNGTTAV TDYSTLPEGI 180
WSGDVSVQFD ATWTS 195
<212> Type : PRT
<211> Length : 195
SequenceName : SEQ ID 287
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MTAESYDDNY LDDEDADWTA TGQGQKSAGD TSFTLAWKPG EEGQKGLIGW FESGDVRAYK 60
IRFPNGTVDV FRGWVSSIGK AVTAKEVITR TVKVTNVGKP SVAEERSKIT PVSAIKVTPT 120
SGTVAKGKTT TLTVSFEPES ATDKTFRAVS ADPSKATISV KDMTITVNGV ATGKVQIPVV 180
SGNGQFAAVA EVTVTEAGAA G 201
<212> Type : PRT
<211> Length : 201
SequenceName : SEQ ID 288
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MTAESYDDNY LDDEDADWTA TGQGQKSAGD TSFTLAWKPG EEGQKGLIGW FESGDVRAYK 60
IRFPNGTVDV FRGWVSSIGK AVTAKEVITR TVKVTNVGKP SVAEERSKIT PVSAIKVTPT 120
SGTVAKGKTT TLTVSFEPES ATDKTFRAVS ADPSKATISV KDMTITVNGV ATGKVQIPVV 180
SGNGQFAAVA EVTVTEAGAA G 201
<212> Type : PRT
<211> Length : 201
SequenceName : SEQ ID 289
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MLYNIPCRIY ILSTLSLCIS GIVSTATATS SETKISNEET LVVTTNRSAS NLWESPATIQ 60
VIDQQTLQNS TNASIADNLQ DIPGVEITDN SLAGRKQIRI RGEASSRVLI LIDGQEVTYQ 120
RAGDNYGVGL LIDESALERV EVVKGPYSVL YGSQAIGGIV NFITKKGGDK LASGVVKAVY 180
NSATAGWEES IAVQGSIGGF DYRINGSYSD QGNRDTPDGR LPNTNYRNNS QGVWLGYNSG 240
NHRFGLSLDR YRLATQTYYE DPDGSYEAFS VKIPKLEREK VGVFYDTDVD GDYLKKIHFD 300
AYEQTIQRQF ANEVKTTQPV PSPMIQALTV HNKTDTHDKQ YTQAVTLQSH FSLPANNELV 360
TGAQYKQDRV SQRSGGMTSS KSLTGFINKE TRTRSYYESE QSTVSLFAQN DWQFADHWTW 420
TMGVRQYWLS SKLTRGDGVS YTAGIISDTS LARESASDHE MVTSTSLRYS GFDNLELRAA 480
FAQGYVFPTL SQLFMQTSAG GSVTYGNPDL KAEHSNNFEL GARYNGNQWL IDSAVYYSEA 540
KDYIASLICD GSIVCNGNTN SSRSSYYYYD NIDRAKTWGL EISAEYNGWV FSPYISGNLI 600
RRQYETSTLK TTNTGEPAIN GRIGLKHTLV MGQANIISDV FIRAASSAKD DSNGTETNVP 660
GWATLNFAVN TEFGNEDQYR INLALNNLTD KRYRTAHETI PAAGFNAAIG FVWNF 715

<212> Type : PRT
<211> Length : 715
SequenceName : SEQ ID 290
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MTKMSRYALI TALAMFLAGC VGQREPAPVE EVKPAPEQPA EPQQPVPTVP SVPTIPQQPG 60
PIEHEDQTAP PAPHIRHYDW NGAMQPMVSK MLGADGVTAG SVLLVDSVNN RTNGSLNAAE 120
ATETLRNALA NNGKPTLVSA QQLSMAKQQL GLSPQDSLGT RSKAIGIARN VGAHYVLYSS 180
ASGNVNAPTL QMQLMLVQTG EIIWSGKGAV SQQ 213
<212> Type : PRT
<211> Length : 213
SequenceName : SEQ ID 291
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MKSKVLALLI PALLGAGAAH AAEVYNKDGN KLDLYGKVDG LHYFSDNSAK DGDQSYARLG 60
FKGETQINDQ LTGYGQWEYN IQANNTESSK NQSWTRLAFA GLKFSDYGSF DYGRNYGLDR 120
YAA 123
<212> Type : PRT
<211> Length : 123
SequenceName : SEQ ID 292
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MATPNPLEPV KGAGTTLWVY NGKGDAYANP LSDDDWQRLA KVKDLTPGEM TAEPYDDNYL 60
DDEDADWTAT GQGQKSAGDT SFTLAWKPGE EGQKGLIGWF ESGDVRAYKI RFPNGTVDVF 120
RGWVSSIGKA VTAKEVITRT VKVTNVGKPS VAEERSEITP ATAIKVTPTS GTVAKGKTTT 180
LTVSFEPESA TDKTFRAVSA DPSKATISVK DMTITVNGVA TGKVQIPVVS GNGQFAAVAE 240
VTVTEAGAAG 250
<212> Type : PRT
<211> Length : 250
SequenceName : SEQ ID 293
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MATPNPLEPV KGAGTTLWVY NGKGDAYANP LSDDDWQRLA KVKDLTPGEM TAEPYDDNYL 60
DDEDADWTAT GQGQKSAGDT SFTLAWKPGE EGQKGLIGWF ESGDVRAYKI RFPNGTVDVF 120
RGWVSSIGKA VTAKEVITRT VKVTNVGKPS VAEERSEITP ATAIKVTPTS GTVAKGKTTT 180
LTVSFEPESA TDKTFRAVSA DPSKATISVK DMTITVNGVA TGKVQIPVVS GNGQFAAVAE 240
VTVTEAGAAG 250
<212> Type : PRT
<211> Length : 250
SequenceName : SEQ ID 294
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MGWTDMLPEF GGDSYTNADN FMTGRANGVA TYRNTDFFGL VNGLNFAVQY QGNNEGASNG 60
QEGTNNGRDV RHENGDGWGL STTYDLGMGF SAGAAYTSSD RTNDQVNHTA AGGDKADAWT 120
AGLKYDANNI YLATMYSETR NMTPFGDSDY AVANKTQNFE VTAQYQFDFG LRPAVSFLMS 180
KGRDLHAAGG ADNPAGVDDK DLVKYADVGA TYYFNKNMST YVDYKINLLD EDDSFYAANG 240
ISTDDIVALG LVYQF 255

<212> Type : PRT
<211> Length : 255
SequenceName : SEQ ID 295
SequenceDescription :

Sequence

<213> OrganismName : Haemophilus influenzae Rd
<400> PreSequenceString :
MGFIMKLTKT ALCTALFATF TFSANAQTYP DLPVGIKGGT GALIGDTVYV GLGSGGDKFY 60
TLDLKDPSAQ WKEIATFPGG ERNQPVAAAV DGKLYVFGGL QKNEKGELQL VNDAYRYNPS 120
DNTWMKLPTR SPRGLVGSSG ASHGDKVYIL GGSNLSIFNG FFQDTVAAGE DKAKKDEIAA 180
AYFDQRPEDY FFTTELLSYE PSTNKWRNEG RIPFSGRAGA AFTIQGNELV VVNGEIKPGL 240
RTAETHQGKF TAKGVQWKNL PDLPAPKGKS QDGLAGALSG YSNGHYLVTG GANFPGSIKQ 300
FKEGKLHAHK GLSKAWHNEV YTLNNGKWRI VGELPMNIGY GFSVSYNNKV LLIGGETDGG 360
KALTSVKAIS YDGKKLTIE 379
<212> Type : PRT
<211> Length : 379
SequenceName : SEQ ID 296
SequenceDescription :

Sequence

<213> OrganismName : Haemophilus influenzae Rd
<400> PreSequenceString :
MGEQYMLTTI LSFLIVTTVV AYVSWLKTKG DDLKSSKGYF LAGRGLSGLV IGCSMVLTSL 60
STEQLIGVNA VSYKGNFSVI AWTVPTVIPL CFLALYIIGW L 101
<212> Type : PRT
<211> Length : 101
SequenceName : SEQ ID 297
SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :
MKNQHKNPLT KALMKTYPYN HFLFFCFILG AFLLGLLSPA YALSIITTKE IDANLLNGAI 60
ESRVVLGKRV PKVEAHGFYF RNNATNSIDI EITSLLRDNQ SFPLTSSAKT SLKIPPNAKI 120
KKSTILVLKG ENAEEVAKIL GVSKEEYQKL ENIAQTKAAN DPMYANTPFS NGSDSSFYDN 180
NPNSPSNNAI NGKDGANGSN GYGANGNDGV NGISGSNGAN GSHSNNNAIG SGIDTDGVLG 240
VDGVNGSSSS SGGSVGGYEN NFTNHGSTNN NTGGYDNFNN GSSSGGSLGN GGLFPIPFGN 300
GDTNNSNNST NTTSPTNGSS SNNATNPSSQ ENNYSSQYCK VPELSPNNTM KLDVIAKDGS 360
CISMNALRDD TKCAYRYDFE AGKAIKQTQY YYVDRENKTQ NIGGCVDLQG AQYAMQLYKD 420
DSKCALQTTS DKGYGMGKTQ TFQTEIVFRG MDNLIHVAVP CSDYARVQDR IVRYEKNDKT 480
QTLTPIVDQY YNDPNNPNKQ EILNRGIATQ LSSQYQEFAC GQWEYNDAKL EAKRPTMLKS 540
YNKLNGEWVE VTPCNPEAGI KSGAVVSPYV MGVPSSKVLS DITTSHYFRI ERKNYGEREQ 600
CQKLYGVNRC QPQYSILILV SPIGAPLTKP LPPKPLNLIY AQPKIMKNTP QPIILSPLKP 660
PSTGLKAF 668
<212> Type : PRT
<211> Length : 668
SequenceName : SEQ ID 298
SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :
MPVIRVLVML ATMMMKLVKT AKEKKVFKNV GISIMGIAFW EAIKDSIKKQ IKKSDWICGN 60
VKTADDYLKT HPNSWFNSAI GVTAITAMLM NVCFADDQSK KEVAQAQKEA ENARDRANKS 120
GIELEQEEQK TEQEKQKTEQ EKQKTEQEKQ KTEQEKQKTE QEKQKTSNIE TNNQIKVEQE 180
QQKTEQEKQK TNNTQKDLVN KAEQNCQENH NQFFIKKLGI KAGIAIEIEA ECKTPKPTKT 240
NQTPIQPKHL PNSKQPHSQR GSKAQELIAY LQKELESLPY SQKAIAKQVD FYRPSSIAYL 300
ELDPRDFNAT EEWQKENLKI RSKAQAKMLE MRSLKPDPQA HLSTSQSLLL VQKIFADVSK 360
EIKVVANTEK KVEKAGYGYS KRM 383
<212> Type : PRT
<211> Length : 383
SequenceName : SEQ ID 299

SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :
MNYPNLPNSA LEISEQPEVK EITNELLKQL QNALRSNAHF SEQVELSLKC IVRILEVLLS 60
LDFFKNANEI DSSLRNSIEW LTNAGESLKL KMKEYERFFS EFNTSMHANE QEVTNTLNAN 120
AENIKSEIKK LENQLIETTT RLLTSYQIFL NQARDNANNQ ITKNKTQSLE AITQAKNNAN 180
NEISNNQTQA ITNITEAKTN ANNEISNNQT QAITNINEAK ESATTQINAN KQEAINNITQ 240
EKTQATSEIT EAKKTDHYQN IDFFEFE 267
<212> Type : PRT
<211> Length : 267
SequenceName : SEQ ID 300
SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :
MKFFSKDLFK KVTPLFLSVY FLSPTLTQAK SRFYVASQYQ VGKMIMKKYN DLKRTIEGAS 60
FSLGWEINPT NYWFYSRYYF FMDYGNVILN KRTGAQANMF TYGFGGDLIM EYNKNPLYVF 120
SLFYGMQVAE NTWTISKHSA NFIIDDWRSI QGFSLKTSNF RMLGLVGFKF QTVLFHHDAS 180
IEVGIKWPFA FEYDSPFVRL FSVFISHTFY L 211
<212> Type : PRT
<211> Length : 211
SequenceName : SEQ ID 301
SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :
MKKFTLSLFL CCTLLNAEED IFRNNTNETD LTNSFEHGKE NNNLIPAKSD SLESFKEQEN 60
KEKAKQLMDL KALQSVYFSK NRKLQDNNFN VLYVAGNTNK IRLRYAMTTT FIFDNDPIIY 120
VSLGDPSDFE LTYPTNDHYD LSNMLVIKPL LIGVDTNLTV VGASGTIYTL LFV 173

<212> Type : PRT
<211> Length : 173
SequenceName : SEQ ID 302
SequenceDescription :

Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
MLDYVPWIGN GYRYGNNHRG SNSSTSGVTT QGQSQNASSN EPAPTFSNVG VGLKANVNGT 60
LSGSRTTPNQ QGTPWLTLDQ ANLQLWTGAG WRNDKNGQSD ENYTNFASAK GSTNQQGSTT 120
GGSAGNPDSL KQDKADKSGD SVTVAEATSG DNLTNYTNLP PTSPPHPTDR TRCHSPTRTT 180
PSGCSCSCAA CWAASRCWSI RVGKMITVSL IPPTKNGLTP N 221
<212> Type : PRT
<211> Length : 221
SequenceName : SEQ ID 303
SequenceDescription :

Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
MDDITAPQTS AGSSSGTSTN TSGSRSFLPT FSNVGVGLKA NVQGTLGGRQ TTTTGNNIPK 60
WATLDQANLQ LWTGAGWRND KTTSGSTGNA NDTKFTSATG SGSGQGSSSG TNTSAGNPDG 120
LQADKVDQNG QVKTSVQEAT SGDNLTNYTN LPPANLTPTA DWPNALSPTN KNNAQRAQLP 180
LRGLLGSIPV LVNKSGQDDN SKFKAEDQKW SYTDLQSDQT KLNLPAYGEV NGLLNPALVE 240
TYFGNTRASG SGSNTTSSPG IGFKIPEQSG TNTTSKAVLI TPGLAWTPQD VGNIVVSGTS 300
FSFQLGGWLV TFTDFIKPRA GYLGLQLTGL DVSEATQREL IWAKRPWAAF RGSWVNRLGR 360
VESVWDFKGV WADQAQLAAQ AATSSTTTTA TGATLPEHPN ALAYQISYTD KDSYKASTQG 420
SGQTNSQNNS PYLHFIKPKK VESTTQLDQG LKNLLDPNQV RTKLRQSFGT DHSTQPQPQS 480

LKTTTPVFGR SSGNLSSVFS GGGAGGGSSG SGQSGVDLSP VERVSGH 527

<212> Type : PRT
<211> Length : 527
SequenceName : SEQ ID 304
SequenceDescription :

Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
MLKLAVGIFI SPTLTRFSTG FNLAGSVLDQ VLDYVPWIGN GHRYGNNHRG VDDITAPKTG 60
AGSSSGTSTN TSGSRSFLPT FSNVGVGLKA NVQGTLGGSQ TTTTGKDIPK WPTLDPANLQ 120
LWTGAGWRND KASNKQSDEN HTTFKSATGS GQQGGSTTGG SAGNPDSLKQ DKISKSGQNL 180
TTQDGAPQSN STTESASNYD HLPPNLTPTS DWPNALSFTN KNNAQRAQLF LRGLLGSIPV 240
LVNRSGSDDS NKFQATDQKW SYTDLKSDQT KLNLPAYGEV NGLLNPALVE TYFGTTRAGG 300
SGSNTTSSPG IGFKIPEQNN DSKAVLITPG LAWTPQDVGN LVVSGTSLSF QLGGWLVTFT 360
DFVKPRAGYL GLQLTGLDAS DATQRALIWA KRPWAAFRGS WVNRLGRVES VWDLKGVWQD 420
QAQAAAQAAT TAAATGDALP EHPNALAYQI SSTDKDSYKA STQSSGQTNS QNTSPYLHLI 480
KPKKVENTTQ LDQGLKTCWT PTRFAPSCAK ALVQTIPPKP NPNPSKQPHR CLGRIVVTLA 540
VCLVVGVLEE QTAPIRWTSP PLNGWVGGLW GNYPVGVGGI VVRILKVCKT LLFISIFISI 600
FFLNCSLTLF IWTTASLATG LTVVGHFTST TTTLKRQQFS YTRPDEVALR HTNAINPRLT 660
PWTYRNTSFS SLPLTGENPG AWALVRDNTA KGITAGSGSQ QTTYDPTRTE AALTTATTFV 720
LRRYDLAGRC TTSTFRS 737

<212> Type : PRT
<211> Length : 737
SequenceName : SEQ ID 305
SequenceDescription :

Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
MLDYIPWIGN GHRYGNDHRG SNSSTSGVTT QGQQSQNASG TEPASTFSNV GVGLKANVQG 60
TLGGSQTTTT GKDIPKWPTL DQANLQLWTG AGWRNDKASS GQSDENHTKF TSATGSGQQG 120
SSSGTTNSAG NPDSLKQDKV DKSGDSVTVA ETTSGDNLTN YTNLPPNLTP TADWPNALSF 180
TNKNNAQRAQ LFLRALLGSI PVLVNKSGQD DSNKFQATDQ KWSYTELKSD QTKLNLPAYG 240
EVNGLLNPAL VEVYGLSSTQ GSSTGAGGAG GNTGGDTNTQ TYARPGIGFK LPSTDSESSK 300
ATLITPGLAW TAQDVGNLVV SGTSLSFQLG GWLVTFTDFI KPRSGYLGLQ LTGLDANDSD 360
QRELIWAPPA LNRLSWQLGQ PLGPRGECVG FQGGVGGSSS VRLASSYKYH HRNEGYLIGA 420
HQCFGLSGEL YRPGFVQGFH SKLRPKPKHL PLPALGAGEK SRFLW 465

<212> Type : PRT
<211> Length : 465
SequenceName : SEQ ID 306
SequenceDescription :

Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
MLGSIPVLVN RSGSDSNKFQ ATDQKWSYTD LQSDQTKLNL SAYGEVNGLL NPALVETYFG 60
TTRTSSTANQ NSTTVPGIGF KIPEQNNDSK ATLITPGLAW TPQDVGNLVV SGTTVSFQLG 120
GWLVTFTDFV KPRAGYLGLQ LSGLNASDSD QRELIWAPRP WAAFRGSWVN RLGRVESVWD 180
LKGVWADQAQ LAAQAATSST TTTATGATLP EHPNALAYQI SYTDKDSYKA STQGSGQTNS 240
QNNSLYLHLI KPKKVESTTQ LDQGLKNLLD PNQVRTKLRQ SFGTDHSTQP QPQSLKTTTP 300
VFGAMSGNLG SVLSGGGAGG AGSTNSVDLS PVERVSGSLT INRNFSY 347

<212> Type : PRT
<211> Length : 347
SequenceName : SEQ ID 307
SequenceDescription :

Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
MGQQGQSGTS AGNPDSLKQD KISKSGDSLT TQDGNATGQQ EATNYTNLPP NLTPTADWPN 60
ALSFTNKNNA HRAQLFLRGL LGSIPVLVNR SGSDSNKFQA TDQKWSYTDL QSDQTKLNLP 120
AYGEVNGLLN PALVETYFGN TRAGGSGSNT TSSPGIGFKI PEQNNDSKAT LITPGLAWTP 180

QDVGNLVVSG TSLSFQLGGW LVSFTDFIKP RAGYLGLQLS GLDASDSDQR ELIWAKRPWA 240
AFRGSWVNRL GRVESVWDLK GVWADQAQLA AQAATSEASG SALAPHPNAL AFQVSVVEAS 300
AYSSSTSSSG SGSSSNTSPY LHLIKPKKVE STTQLDQGLK NLLDPNQVRT KLRQSFGTDH 360
STQPQSLKIT TPVFGTSSGN IGSVLSGGGA GGGSSGSGQS GVDLSPVERV SGH 413

<212> Type : PRT
<211> Length : 413
SequenceName : SEQ ID 308
SequenceDescription :

Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
MGLQLSGLDA SDSDQRELIW AKRPWAAFRG SWVNRLGRVE SVWDLKGVWA DQAHSAVSES 60
QAATSSTTTT ATGDTLPEHP NALAYQISST DKDSYKASTQ GSGQTNSQNT SPYLHLIKPK 120
KVTASDKLDD DLKNLLDPNE VRVKLRQSFG TDHSTQPQPQ PLKTTTPVFG TNSGNLGSVL 180
SGGGTTQDSS TTNQLSPVQR VSGWLVGQLP STSDGNTSST NNLAPNTNTG NEVVGVGDLS 240
KRASIESSRL WIALKP 256
<212> Type : PRT
<211> Length : 256
SequenceName : SEQ ID 309
SequenceDescription :

Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
MRDNTAKGIT AGSGSQQTTY DPARTEATLT TTTFALRRYD LAGRALYDLD FSKLNPQTPT 60
RDANCQITFN PFGGFGLSGS APQQWNEVKN KVPVEVAQDP TDPYRFAVLL VPRSVVYYEQ 120
LQRGLALPNQ GSSSGSGQQN TTIGAYGLKV KNAEADTAKS NEKLQGDESK SSNGSSSTST 180
TTQRGSTNSD TKVKALKIEV KKKSDSEDNG QLQLEKNDLA NAPIKRGEES GQSVQLKADD 240
FGTAPSSSGS GGNSNPGSPT PWRPWLATEQ IHKDLPKWSA SILILYDAPY ARNRTAIDRV 300
DHLDPKVMTA NYPPSWRMPK WNHHGLWDWK ARDVLFQTTG FDESNTSNTK QGFQKEADSD 360
KSAPIALPFE AYFANIGNLT WFGQALLVFG GNGHVTKSAH TAPLSIWLYI YLVKAVTFRL 420
LLANSLLSKS NIYKKTAN 438
<212> Type : PRT
<211> Length : 438
SequenceName : SEQ ID 310
SequenceDescription :

Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
MRDNIAKGIT AGSNTQQTTY DPTRTEATLT TATTFALRRY DLAGRALYDL DFSKLNPQTP 60
TRDQTGQITF NPFGGFGLSG AAPQQWNEVK DKVPVEVAQD PSNPYRFAVL LVPRSVVYYE 120
QLQRGLALPN QGSSSGSGQQ NTTIGAYGLK VKNAEADTAK SNEKLQGYES KSSNGSSSTS 180
TTQRGGSSNE NKVKALQVAV KKKSGSQGNS GDQGTEQVEL ESNDLANAPI KRGSNNNQQV 240
QLKADDFGTA PSSSGSGTQD GTPTPWTPWL TTEQIHNDPA KFAASILILY DAPYARNRTA 300
IDRVDHLDPK VMTANYPPSW RTPKWNHHGL WDWKARDVLL QTTGFFNPRR HPEWFDGGQT 360
VADNEKTGFD VDNSENTKQG FQKEADSDKS APIALPFEAY FANIGNLTWF EQALLVFGIC 420
LS 422
<212> Type : PRT
<211> Length : 422
SequenceName : SEQ ID 311
SequenceDescription :

Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
MLWPFRWVWW KRVLTSQTRA PAKPNPLTVP PTCTWWSLRK LPNPTKLDDD LKNLLDPNEV 60
RARMLKSFGT ENFTQPQPQP QALKTTTPVF GTSSGNLGSV LSGGGYHAGL KHHQSTVTRS 120
TGEWVDR 127
<212> Type : PRT
<211> Length : 127

SequenceName : SEQ ID 312
SequenceDescription :

Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
MRDNSAKGIT AGSESQQTTY DPTRTRAALT ASTTFALRRY DLAGRALYDL DFSRLNPQTP 60
TRDQTGQITF NPFGGFGLSG AAPQQWNEVK NKVPVEVAQD PSNPYRFAVL LVPRSVVYYE 120
QLQRGLALPN QGSSSGSGQQ NTTIGAYGLK VKNAEADTAK SNEKLQGDES KSSNGSSSTS 180
TTTQRGGSSG DTKVKALQVA VKKKSGSQGN SGEQGTEQVE LESNDLANAP IKRGEESGQS 240
VQLKAADFGT TPSSSGSGGN SNPGSPTPWR PWLATEQIHK DLPKWSASIL ILYDAPYARN 300
RTAIDRVDHL DPKVMTANYP PSWRTPKWNH HGLWDWKARD VLLQTTGFFN SRRHPEWFDQ 360
GQAVADNTQT GFDTDDTDNK KTRLSKGSWL RQAGPDEPPV WSVLRQHWQP HLVRASAFGV 420
WDLFVLIN 428
<212> Type : PRT
<211> Length : 428
SequenceName : SEQ ID 313
SequenceDescription :

Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
MFGLKVKNAE ADTAKSNEKL QGAEATGSST TSGSGQSTQR GGSSGDTKVK ALQVAVKKKS 60
GSQGNSGDQG TEQVELESND LANAPIKRGS NPASPTQGSR LRHHPIQFGI WSIRHPHPLK 120
AVACDRANSQ GPPQMIRLDP HSVRCALCL 149
<212> Type : PRT
<211> Length : 149
SequenceName : SEQ ID 314
SequenceDescription :

Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
MFGLKVKDAT VDSSKQSTES LKGEESSSSS TTSSTSTTQR GGSSGDTKVK ALQVAVKKKS 60
DSEDNGQIEL ETNNLANAPI KRGSNNNQQV QLKADDFGTS PSSSESGQSG TPTPWTPWLA 120
TEQIHKDLPK WSASILILYD APYARNRTAI DRVDHLDPKV MTANYPPSWR TPKWNHHGLW 180
DWKARDVLVQ TTGFFNPRRH PDWFDQGQAV AENTQTGFDT DDTDNKKQGF RKQGEQSPAP 240
IALPFEAYFA NIGNLTWFGQ ALLVFGICLS 270
<212> Type : PRT
<211> Length : 270
SequenceName : SEQ ID 315
SequenceDescription :

Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
MGSQNQGSTT TTSAGNPDSL VTDKVDQKGQ VQTSGQNLSD TNYTNLSPNF TPTSDWPNAL 60
SFTNKNNAQR AQLFLHGLLG SIPVLVNKSG ENNEKFQATD QKWSYTELKS DQTKLNLPAY 120
GEVNGLLNPA LVETYFGTTR TSSTANQNST TVPGIGFKIP EQNNDSKAVL ITPGLAWTPQ 180
DVGNLVVSGT SFSFQLGGWL VSFTDFVKPR AGYLGLQLTG LDASDATQRA LIWAPPALSG 240
LSWQLGQPVG PRGECVGFEG GVGGSSSVRL ARIYHHRNRG YLTGAPECFG LSGECGGSEC 300
LQAKHELRPN PIH 313
<212> Type : PRT
<211> Length : 313
SequenceName : SEQ ID 316
SequenceDescription :

Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
MSFGLVGTVN NNGWKSPFRH ETKYRAGYDK FKYYKTHYRG AKKAGTNDDR WRWTAWFDLD 60
FAHQKIVLIE RGELHRQADL KKSDPATNET SKTVWGSIKE KLLQNVNNLH SEKGVFLWFR 120

QSGFTTTRN
<212> Type : PRT
<211> Length : 129
SequenceName : SEQ ID 317
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MAEPLAVDPT GLSAAAAKLA GLVFPQPPAP IAVSGTDSVV AAINETMPSI ESLVSDGLPG 60
VKAALTRTAS NMNAAADVYA KTDQSLGTSL SQYAFGSSGE GLAGVASVGG QPSQATQLLS 120
TPVSQVTTQL GETAAELAPR VVATVPQLVQ LAPHAVQMSQ NASPIAQTIS QTAQQAAQSA 180
QGGSGPMPAQ LASAEKPATE QAEPVHEVTN DDQGDQGDVQ PAEVVAAARD EGAGSSGQQ 240
PGGGVPAQAM DTGAGARPAA SPLAAPVDPS TPAPSTTTTL 280
<212> Type : PRT
<211> Length : 280
SequenceName : SEQ ID 318
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MRYLIATAVL VAVVLVGWPA AGAPPSCAGL GGTVQAGQIC HVHASGPKYM LDMTFPVDYP 60
DQQALTDYIT QNRDGFVNVA QGSPLRDQPY QMDATSEQHS SGQPPQATRS VVLKFFQDLG 120
GAHPSTWYKA FNYNLATSQP ITFDTLFVPG TTPLDSIYPI VQRELARQTG FGAAILPSTG 180
LDPAHYQNFA ITDDSLIFYF AQGELLPSFV GACQAQVPRS AIPPLAI 227
<212> Type : PRT
<211> Length : 227
SequenceName : SEQ ID 319
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MKMVKSIAAG LTAAAAIGAA AAGVTSIMAG GPVVYQMQPV VFGAPLPLDP ASAPDVPTAA 60
QLTSLLNSLA DPNVSFANKG SLVEGGIGGT EARIADHKLK KAAEHGDLPL SFSVTNIQPA 120
AAGSATADVS VSGPKLSSPV TQNVTFVNQG GWMLSRASAM ELLQAAGN 168
<212> Type : PRT
<211> Length : 168
SequenceName : SEQ ID 320
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MTYSPGNPGY PQAQPAGSYG GVTPSFAHAD EGASKLPMYL NIAVAVLGLA AYFASFGPMF 60
TLSTELGGGD GAVSGDTGLP VGVALLAALL AGVALVPKAK SHVTVVAVLG VLGVFLMVSA 120
TFNKPSAYST GWALWVVLAF IVFQAVAAVL ALLVETGAIT APAPRPKFDP YGQYGRYGQY 180
GQYGVQPGGY YGQQGAQQAA GLQSPGPQQS PQPPGYGSQY GGYSSSPSQS GSGYTAQPPA 240
QPPAQSGSQQ SHQGPSTPPT GFPSFSPPPP VSAGTGSQAG SAPVNYSNPS GGEQSSSPGG 300
APV 303
<212> Type : PRT
<211> Length : 303
SequenceName : SEQ ID 321
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MKCPGVSDCV ATVRHDNVFA IAAGLRWSAA VPPLHKGDAV TKLLVGAIAG GMLACAAILG 60
DGIASADTAL IVPGTAPSPY GPLRSLYHFN PAMQPQIGAN YYNPTATRHV VSYPGSFWPV 120
TGLNSPTVGS SVSAGTNNLD AAIRSTDGPI FVAGLSQGTL VLDREQARLA NDPTAPPPGQ 180

LTFIKAGDPN NLLWRAFRPG THVPIIDYTV PAPAESQYDT INIVGQYDIF SDPPNRPGNL 240
LADLNAIAAG GYYGHSATAF SDPARVAPRD [illegible]TNSLGA TTTTYFIRTD QLPLVRALVD 300
MAGLPPQAAG TVDAALRPII DRAYQPGPAP AVNPRDLVQG IRGIPAIAPA IAIPIGSTTG 360
ASAATSTAAA TAAATNALRG ANVGPGANKA LSMVRGLLPK GKKH 404

<212> Type : PRT
<211> Length : 404
SequenceName : SEQ ID 322
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
[illegible] 60
KAPHCPAESD QTPAGAAGDG DLPEVGGRVT SPVQPPVAAL TGYSANIGGL SVPHSWNLPP 120
AVRQVAAMFP GATPMYMTGS SDGSYAGLAA AGLAGTGLAG LAARGGSAPT PAAAAPAGAG 180
GAGPAATRPA AQQTPAVPAA AAGSAIPGLP PGLPPGVVAN LAATLAAIPG ATIIVVPPSP 240
NANQ 244

<212> Type : PRT
<211> Length : 244
SequenceName : SEQ ID 323
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MDVALGVAVT DRVARLALVD SAAPGTVIDQ FVLDVAEHPV EVLTETVVGT DRSLAGENHR 60
LVATRLCWPD QAKADELQHA LQDSGVHDVA VISEAQAATA LVGAAHAGSA VLLVGDETAT 120
LSVVGDPDAP PTMVAVAPVA GADATSTVDT LMARLGDQAL APGDVFLVGR SAEHTTVLAD 180
QLRAASTMRV QTPDDPTFAL ARGAAMAAGA ATMAHPALVA DATTSLPRAE AGQSGSEGEQ 240
LAYSQASDYE LLPVDEYEEH DEYGAAADRS APLSRRSLLI GNAVVAFAVI GFASLAVAVA 300
VTIRPTAASK PVEGHQNAQP GKFMPLLPTQ QQAPVAPPPP DDPTAGFQGG TIPAVQNVVP 360
RPGTSPGVGG TPASPAPEAP AVPGVVPAPV PIPVPITIPP FPGWQPGMPT IPTAPPTTPV 420
TTSATTPPTT PPTTPVTTPP TTPPTTPVTT PPTTPPTTPV TTPPTTVAPT TVAPTTVAPT 480
TVAPTTVAPA TATPTTVAPQ PTQQPTQQPT QQMPIQQQTV APQTVAPAPQ PPSGGRNGSG 540
GGDLFGGF 548

<212> Type : PRT
<211> Length : 548
SequenceName : SEQ ID 324
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MKNARTTLIA AAIAGTLVTT SPAGIANADD AGLDPNAAAG PDAVGFDPNL PPAPDAAPVD 60
TPPAPEDAGF DPNLPPPLAP DPLSPPAEEA PPVPVAYSVN WDAIAQCESG GNWSINTGNG 120
YYGGLRFTAG TWRANGGSGS AANASREEQI RVAENVLRSQ GIRAWPVCGR RG 172

<212> Type : PRT
<211> Length : 172
SequenceName : SEQ ID 325
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MTRLIPGCTL VGLMLTLLPA PTSAAGSNTA TTLFPVDEVT QLETHTFLDC HPNGSCDFVA 60
GANLRTPDGP TGFPPGLWAR QTTEIRSTNR LAYLDAHATS QFERVMKAGG SDVITTVYFG 120
EGPPDKYQTT GVIDSTNWST GQPMTDVNVI VCTHMQVVYP GVNLTSPSTC AQANFS 176

<212> Type : PRT
<211> Length : 176
SequenceName : SEQ ID 326
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MTPGLLTTAG AGRPRDRCAR IVCTVFIETA VVATMFVALL GLSTISSKAD DIDWDAIAQC 60
ESGGNWAANT GNGLYGGLQI SQATWDSNGG VGSPAAASPQ QQIEVADNIM KTQGPGAWPK 120
CSSCSQGDAP LGSLTHILTF LAAETGGCSG SRDD 154
<212> Type : PRT
<211> Length : 154
SequenceName : SEQ ID 327
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MMQQAVSGIT GALGGAVGGV MGPLTQLPQQ AMQAGQGAMQ PLMSALQQTY GAEGLDVADG 60
ARLVDSIEGE PGLGGEPGAG DVGAGGGGGG TTPTGYLGPP PVPTSSPPTT PAGAPAKSVT 120
PDPVSGTPRA SGPAGMTGMP MVPPGALGAG AEGANKDKPV EKRVTGCAEW STGQGPLNST 180
AECSGEICRR QAGGHQVDAT DPCCAERRQG 210
<212> Type : PRT
<211> Length : 210
SequenceName : SEQ ID 328
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MIRELVTTAA ITGAAIGGAP VAGADPQRYD GDVPGMNYDA SLGAPCSSWE RFIFGRGPSG 60
QAEACHFPPP NQFPPAETGY WVISYPLYGV QQVGAPCPKP QAAAQSPDGL PMLCLGARGW 120
QPGWFTGAGF FPPEP 135
<212> Type : PRT
<211> Length : 135
SequenceName : SEQ ID 329
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MKTTGTTIKL GIVWLVLSVF TVMIIVVFGQ VRFHHTTGYS AVFTHVSGLR AGQFVRAAGV 60
EVGKVAKVTL IDGDKQVLVD FTVDRSLSLD QATTASIRYL NLIGDRYLEL GRGHSGQRLA 120
PGATIPLEHT HPALDLDALL GGFRPLFQTL DPDKVNSIAS SIITVFQGQG ATINDILDQT 180
ASLTATLADR DHAIGEVVNN LNTVLATTVK HQTEFDRTVD KLEVLITGLK NRADPLAAAA 240
AHISSAAGTL ADLLGRIVHC CTAASGTSRA SSSRS 275
<212> Type : PRT
<211> Length : 275
SequenceName : SEQ ID 330
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MTPRSLVRIV GVVVATTLAL VSAPAGGRAA HADPCSDIAV VFARGTHQAS GLGDVGEAFV 60
DSLTSQVGGR SIGVYAVNYP ASDDYRASAS NGSDDASAHI QRTVASCPNT RIVLGGYSQG 120
ATVIDLSTSA MPPAVADHVA AVALFGEPSS GFSSMLWGGG SLPTIGPLYS SKTINLCAPD 180
DPICTGGGNI MAHVSYVQSG MTSQAATFAA NRLDHAG 217
<212> Type : PRT
<211> Length : 217
SequenceName : SEQ ID 331
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MISTTRIDFL WILSVAFASM IALATLLTLI NQVVGTPYIP GGDSPAGTDC SELASWVSNA 60
ATARPVFGDR FNTGNEEAAL AARGFQQGTA PNALVIGWNG HHTAVTLPDG TPVSSGEGGG 120
VRVGGGGAYQ PKFTHHMYLP MDVDAGEDQP PAPDEPVTAV DDVEPEMPAP CPTQRPPVTP 180
RHNLCNKLRT MPGALSAALA AAAPVWPAPI SGCRGFSTSL LAKRNHPVIV GK 232

<212> Type : PRT
<211> Length : 232
SequenceName : SEQ ID 332
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MTTMITLRRR FAVAVAGVAT AAATTVTLAP APANAADVYG AIAYSGNGSW GRSWDYPTRA 60
AAEATAVKSC GYSDCKVLTS PTACGAVAAN DRAYQGGVGP TLAAAMKDAL TKLGGGYIDT 120
WACN 124
<212> Type : PRT
<211> Length : 124
SequenceName : SEQ ID 333
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MAGLNIYVRR WRTALHATVS ALIVAILGLA ITPVASAATA RATLSVTSTW QTGFIARFTI 60
TNSSTAPLTD WKLEFDLPAG ESVLHTWNST VARSGTHYVL SPANWNRIIA PGGSATGGLR 120
GGLTGSYSPP SSCLLNGQYP CT 142
<212> Type : PRT
<211> Length : 142
SequenceName : SEQ ID 334
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MLTRAIKTQL VLLTVLAVIA VVVLGWYFLR IPSLVGIGRY TLYAELPRSG GLYRTANVTY 60
RGITIGKVTG VEPTERGARA TMSIDNGYQI PTDASANVHS VSAVGEQFVD LVSTRTSGPY 120
LRHGQTITTT TVPSQIGPAL DAANRGLAVL PKDRVASVLH EASEAVGGLG SSLNRLIEAT 180
QAIAHDVRGS LEDIDDIIER SAPIIDSQVN SGNEIARWAA NLNTLAAQTA QTDPAVRSIL 240
ANAAPTADQV NATFSDVRES LPQTLANLEV VIDMLKRYHN GVEQALVFLP QSGAIAQSVT 300
TEFPGQAGLG VGGLALNQPP PCLTGFLPAS EWRSPADTST APLPKGTYCR IPMDASNVVR 360
GARNNPCVDV PGKRAATPRE CRSNEAYVPG GTNPWYGDPN QMLSCPAPAA RCDQPVKPGQ 420
VIPAPSVNNG INPLPADQLP GTPPPVNDPL QRPGSGTVQC NGQQPNPCVY TPSTFPTTIY 480
DVQSGKVVAP DGVVYSVEAS THAGADGWKV MLAPTG 516
<212> Type : PRT
<211> Length : 516
SequenceName : SEQ ID 335
SequenceDescription :

Sequence

<213> OrganismName : Rickettsia prowazekii
<400> PreSequenceString :
MLNNTQFLNL MKSYMKPEFY MSSIKNTTNL DLSSITNTIQ KAMNIFFTTN KISTESMQSL 60
FKKNSEIIQN NINTILNSTK EVINSKDFKQ ATEYHQKCVK SIYETSMDNA KELANIAYEA 120
SNKIFEAANK HITKNIHNAS NNIHNTAEQV QKNFNNKSA 159
<212> Type : PRT
<211> Length : 159
SequenceName : SEQ ID 336
SequenceDescription :

Sequence

<213> OrganismName : Rickettsia prowazekii
<400> PreSequenceString :
MNIKLVTYFL ILVSSLKVNA DLNHIQDSFK YQEAEQLTIE LPWNDCTAIH KFLEEKLFFS 60
EQQIKKENKI HEKYKQFYLQ HNNKLSDFSM QFLEKKSEIN SVETLISGFL KFCEDNFQTS 120
KSKSHSLNFF QKQQDQWLHN IRNENYKTYY KKKYEDNTFR NIN 163
<212> Type : PRT
<211> Length : 163
SequenceName : SEQ ID 337
SequenceDescription :

Sequence

<213> OrganismName : Rickettsia prowazekii
<400> PreSequenceString :
MKKLLLIATA SATILSSSVS FAECIDNEWY LRADAGVAMF NKEQDKATGV KLKSNKAIPI 60
DLGIGYYISE NVRADLTLGT TIGGKLKKYG AATNTHFTGT NVSVSHKPTV TRLLINGYVD 120
LTSFDMFDVF VGGGVGPALV KEKISGVSGL ASNTKNKTNV SYKLIFGTSA QIADGVKVEL 180
AYSWINDGKT KTHNVMYKGA SVQTGGMRYQ SHNLTVGVRF GI 222
<212> Type : PRT
<211> Length : 222
SequenceName : SEQ ID 338
SequenceDescription :

Sequence

<213> OrganismName : Rickettsia prowazekii
<400> PreSequenceString :
MKKNMRKQML KIISIIIISL LLSSCSESTR DENGLLTDSQ STIIRDYIIS QNSKNLKVNL 60
KEKFGSNLKG VKLIGIKLTN EDLSGIDFTS CEILRTDFMG SNLEKAILTN SVIQESNFAD 120
SVIKNISGYN ADFQGSIFNN ITLQNTNFVQ SNFSDTAFNK STIINVNFEN SKFSNVLWCH 180
SNIDSSNFQK THLKNNSFKN TNVMNSIFYG ADLGKSVINN TNFTNNYFES SDLSNTKFTS 240
VIIKDSNFTQ SIFNSVNFNN IQSNNSFFSY TSFEDSTLHN IHLTKCDLQN STINSSVFNN 300
FKIDNAILTN MSLNDNTFNN LSIKNSNTNF VRINKSKGFN ITLLNTNYSN AIFSNNDLKE 360
FKVINTDLNN SEIINSNFTN GQFNNVNFSQ SLIQNVNFTD VKITLGNLNQ VALINSNLIN 420
TNIINSVLSN SQINNINYQA YYSFINTNVS NNIVINDNSN QIPPNNIVIN SEKDLQNISN 480
LANMNLTNFN LSNLVFNGVD FSKSIFKKAN LTNTVIKNSI LKDANFSAAI LTKTDFSKSI 540
LTGSIFKFAQ IDQTCFSNSD LTNTDFTEAT IKNTAFDNAN THGIKGLE 588
<212> Type : PRT
<211> Length : 588
SequenceName : SEQ ID 339
SequenceDescription :

Sequence

<213> OrganismName : Porphyromonas gingivalis W83
<400> PreSequenceString :
MIQKFTNVKL NDMRKILSFL MMCSLHLGLQ SQTWHGDPDS VAALPSIGIQ ESSCTRITFE 60
VVFPGFYSVE KREGNQVFQR ISMPGCGSFG NLGEAELPVL KKMIAVPEFS TANVAVKIKE 120
TETFDNYNIY PNPTYVVEEL PEGGTYLVEA FAINNDYYSQ NVSLPSTHYV YSQDGYFRSQ 180
RFIEVTLYPF RYNPVRQEIL FAKKIEVTIT FDNPQPPLQK NTGIFNKVAS SAFINYEADG 240
KSAIENDMVF SRGTTTYISG NVASNLPQNC DYLVIYDDMF NVNQQPHDEI KRLCEHRAFY 300
NGFDVAAVSI KDVLNSFPSN ATSYINETKL KNFIRSVYNQ SNAKRTLDGK LGYVLLIGKP 360
LSKYLADTDN TKVPTSFIHN VSLIPSHPTF GSICASDYFF SCVSPLDTVG DLFIGRFSVT 420
NAHELHNLIE KTINKEISYN PIAHKNILYA EGKGCDAPIL RLFLKEIASG YTVNSILKSN 480
QVSAIDSIFD CLNNGSHHFY FNTHGMPTVW GIGQGLDVNT LTARLNNTSS QGLCTSLSCS 540
SAVADSTIRS LGEVLTTYAP NKGFSAFLGG SRATQYAVYL EGPCPPSEFY EYLPYSLYHN 600
LSTVVGEMLL SSIINTNSVD TYSKFNFNLL GDPALNIMAH GMEVSNCITL PNNTIISSPI 660
TIKNGGCLKI PEKGVLHFTN NGSIQVMSGG TLEIGNQAKI SGETGANPTF ITVYGDGLAI 720
NKQVEIDNID RLNLFSTHSV MPKFHFDSVK FNSAPLYTTN CIVEISNCEF TNRSDIISKN 780
CDLSVENSMF SSSGITVFKP MATSSITGLS TKAKITDNTF FATGNFAYHI TNTPGLTATS 840
NAAIKLDNIP EYYISGNKIV NCDEALVLNN SGNRTNRLHN ITRNVIKNCR IGSTLYNSYG 900
IYNRNKISNN HIGVRLLNNS CFYFDNAPVI NEEDKQTFIS NRTWQLYSSN GTFPLNFHYN 960
SLQGGDTDTW IYNDTYTNRY IDVSNNHWGN NDLFDPNQVF NTPDLFIWIP FWDGLPNGRS 1020
GNSSAEAVEF QTALDCIGNS DYLSAKVALK MMVETYPESD FAIAALKELF RIEKMSGNDY 1080
EGLKDYFRSN PTIISSQNLF PTADFLSARC DIVCENYQSA IDWYENRLNS EISYQDSVFA 1140
VIDLGDIYWN MQLDSLRGTG IDLNILSCEQ RKSLESHQNV KNYLLSTLPE STGTLLPPLE 1200

CNKSSLDKSK IISISPNPAK AVVTIIYYTD NPSCSVIKIY GINGASADIT GLPKHLSEGY 1260
YSIQFNTSNF DPGFYLVTLN VDQKIIDTEK LRIK 1294

<212> Type : PRT
<211> Length : 1294
SequenceName : SEQ ID 340
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MQGKNTIVTT GDYSIGLLSQ TSGNLNTDTI IRVNSDGSVT PSFSDGDDTF IVTAGNHAVG 60
VLACASPGSA CACVSSLDEE STADTGSNEN NAIAKLDMAK GEITTHGTES YAAYANGTVV 120
KAGDTLDYIN ASVTLTDVDI TTHGDNAHAI AARQGTVSFN QGEIYTTGPD AAIAKIYNGG 180
TVTLKNTSAV AHQGSGIVLE SSINGQEATV DILSGSSLRS ANEILYHKDE TSNVTITDSE 240
VSSAADVFIN NIKGHLTVDA TNSKITGSAN ISTDDNTHTY LSLSDNSTWD IKADSTVSNL 300
TVDNSTVYIS RADGRDVEPT RLTITENYVG NNGVLHLRTE LDDDNSATDK VVINGNTSGT 360
TRVKVTNAGG SGAYTLNGIE IISVEGESNG EFIKDSRIFA GAYEYSLTRG NTEATNKNWY 420
LTNFQATSGG ETNSGGSSAP TVAPTPVLRP EAGSYVANLA AANTLFVMRL NDRAGETRYI 480
DPVTEQERSS RLWLRQIGGH NAWRDSNGQL RTTSHRYVSQ LGGDLLTGGF TDSDSWRLGV 540
MAGYARDYNL THSSVSDYRS KGSVRGYSAG LYATWFADDI SKKGAYIDSW AQYSWFKNSV 600
KGDELAYESY SAKGATVSLE AGYGFALNKS FGLEAAKYTW IFQPQAQAIW MGVDHNAHTE 660
ANGSRIENDA NNNIQTRLGF RTFIRTQEKN SGPHGDDFEP FVEMNWIHNS KDFAVSMNGV 720
KVEQDGVSNL GEIKLGVNGN LNPAASVWGN VGVQLGDNGY NDTAVMVGLK YKF 773

<212> Type : PRT
<211> Length : 773
SequenceName : SEQ ID 341
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MTKLKLLALG VLIATSAGVA HAEGKFSLGA GVGVVEHPYK DYDTDVYPVP VINYEGDNFW 60
FRGLGGGYYL WNDATDKLSI TAYWSPLYFK AKDSGDHQMR HLDDRKSTMM AGLSYAHFTQ 120
YGYLRTTLAG DTLDNSNGIV WDMAWLYRYT NGGLTVTPGI GVQWNSENQN EYYYGVSRKE 180
SARSGLRGYN PNDSWSPYLE LSASYNFLGD WSVYGTARYT RLSDEVTDSP MVDKSWTGLI 240
STGITYKF 248

<212> Type : PRT
<211> Length : 248
SequenceName : SEQ ID 342
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MKKIALAGLA GMLLVSASVN AMSISGQAGK EYTNIGVGFG TESTGLALSG NWTHNDDDGD 60
VAGVGLGLNL PLGPLMATVG GKGVYTNPNY GDEGYAAAVG GGLQWKIGNS FRLFGEYYYS 120
PDSLSSGIQS YEEANAGARY TIMRPVSIEA GYRYLNLSGK DGNRDNAVAD GLYVGVNASF 180

<212> Type : PRT
<211> Length : 180
SequenceName : SEQ ID 343
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MTTLTARVFT TAEIIYRKTV IALVCHLNCS RQETVTMNKT IMALAIMMAS FAANASVLPE 60
TPVPFKSGTG AIDNDTVYIG LGSAGTAWYK LDTQAKDKKW TALAAFPGGP REQATSAFID 120
GNLYVFGGIG KNSEGLTQVF NDVHKYNPKT NSWVKLMSHA PMGMAGHVTF VHNGKAYVTG 180
GVNQNIFNGY FEDLNEAGKD STAIDKINAH YFDKKAEDYF FNKFLLSFDP STQQWSYAGE 240
SPWYGTAGAA VVNKGDKTWL INGEAKPGLR TDAVFELDFT GNNLKWNKLD PVSSPDGVAG 300
GFAGISNDSL IFAGGAGFKG SRENYQNGKN YAHEGLKKSY STDIHLWHNG KWDKSGELSQ 360

GRAYGVSLPW NNSLLIIGGE TAGGKAVTDS VLISVKDNKV TVQN 404

<212> Type : PRT
<211> Length : 404
SequenceName : SEQ ID 344
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MATGGAALAG KAVMGAAAGA AGGASALQAA FQKASASMET GGDMSSMGSV VSSGGNGGGE 60
AGTAGSSPFA QAAGFGDSGS SSSGGGFAKA AKLATGTASE LAKGVGSQVK QGPQERVSET 120
TGGKLAASIR ESMEPKEASQ SGQFEGNSLG ADSGPDSNEV RS 162

<212> Type : PRT
<211> Length : 162
SequenceName : SEQ ID 345
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MKRVLIPGVI LCGADVAQAV DDKNMYMYFF EEMTVYAPVP VPVNGNTHYT SESIERLPTG 60
NGNISDLLRT NPAVRMDSTQ STSLNQGDIR PEKISIHGAS PYQNAYLIDG ISATNNLNPA 120
NESDASSATN ISGMSQGYYL DVSLLDNVTL YDSFVPVEFG RFNGGVIDAK IKRFNADDSK 180
VKLGYRTTRL DWLTSHIDEN NKSAFNQGSS GSTYFSPDFK KNFYTLSFNQ ELADNFGVTA 240
GLSRRQSDIT RADYVSNDGI VAGRAQYKNV IDTALSKFTW FASDRFTHDL TLKYTGSSRD 300
YNTSTFPQSD REMGNKSYGL AWDMDTQLAW AKLRTTVGWD HISDYTRHDH DIWYTELSCT 360
YGDITGRCTR GGLGHISQAV DNYTFKTRLD WQKFAVGDVS HQPYFGAEYI YSDAWTERHN 420
QSESYVINAA GKKTNHTIYH KGKGSLGIDN YTLYMADHIS WRNVSLMPGV RYDYDNYLSN 480
HNISPRFMTE WDIFADQTSM ITAGYNRYYG GNILDMGLRD IRNSWTESVS GNKTLTRYQN 540
LKTPYNDELA MGLQQKIDKN VIARASEAHD QISKSSRTDS ATKTTITEYN NDGKTKTHSF 600
NLSFELAEPL HIRQVDINPQ IVFSYIKSKG NLSLNNGYEE SNTGDNQVVY NGNLVSYDSV 660
PVADFNNPLK ISLNMDFTHQ PSGLVWANTL AWQEARKARI ILGKTNAQYI SEYSDYKQYV 720
DEKLDSSLTW DTRLSWTPQF LKQQNLTISA DILNVLDSKT AVDTTNTGVA TYASGRTFWL 780
DVSMKF 786

<212> Type : PRT
<211> Length : 786
SequenceName : SEQ ID 346
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MKKTLLAIML AGTAFASQAG TLVSQGTEAS ANLTLTKPIV VNNTIQPVKG VYSGTLTAWT 60
PLATGIVGAS DGQSHDYAVT FPDDIYAESS TSADAVISGD NNPDHKLKVS LTTLEQDPPS 120
AASEEIGGKR YMMLKNTGTG GAYRVVSHMK EQVVEPDSYT IRTQAYIYAE 170

<212> Type : PRT
<211> Length : 170
SequenceName : SEQ ID 347
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MGIYHWSRKT KMKRTKSIRH ASFRKNWSAR HLTPVALAVA TVFMLAGCEK SDETVSLYQN 60
ADDCSAANPG KSAECTTAYN NALKEAERTA PKYATREDCV AEFGEGQCQQ APAQAGMAPE 120
NQAQAQQSSG SFWMPLMAGY MMGRLMGGGA GFAQQPLFSS KNPASPAYGK YTDATGKNYG 180
AAQPGRTMTV PKTAMAPKPA TTTTVTRGGF GESVAKQSTM QRSATGTSSR SMGG 234

<212> Type : PRT
<211> Length : 234
SequenceName : SEQ ID 348
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MTKMSRYALI TALAMFLAGC VGQREPAPVE EVKPAPEQPA EPQQPVPTVP SVPTIPQQPG 60
PIEHEDRTAP PAPHIRHYDW NGAMQPMVSK MLGADGVTAG SVLLVDSVNN RTNGSLNAAE 120
ATETLRNALA NNGKFTLVSA QQLSMAKQQL GLSPQDSLGT RSKAIGIARN VGAHYVLYSC 180
ASGNVNAPTL QMQLMLVQTG EIIWSGKGAV SQQ 213
<212> Type : PRT
<211> Length : 213
SequenceName : SEQ ID 349
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MTKLMQFVQR CYYMTNKKMY FILILVFTLL QVCFFALWKA RDGSTTSLEC TSTLTRNAKT 60
DHSLYYSANL SVILKKDGSG SFTIVGLTDE DTPRKFSHSY FFTYKIDSNG RISGNAKAKV 120
SGLENQIKDE NFRLNFLDAS LTGKGNARLS KFNNVYIFSI PGLIINTCAP I 171

<212> Type : PRT
<211> Length : 171
SequenceName : SEQ ID 350
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MGRISSGGMM FKAITTVAAL VIATSAMAQD DLTISSLAKG ETTKAAFNQM VQGHKLPAWV 60
MKGGTYTPAQ TVTLGDETYQ VMSACKPHDC GSQRIAVMWS EKSNQMTGLF SAIDEKTSQE 120
KLTWLNVNDA LSIDGKTVLF AALTGSLENH PDGFNFK 157
<212> Type : PRT
<211> Length : 157
SequenceName : SEQ ID 351
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
MKKQFLEKAV FTVAATAATV VLGNKMADAD TYTLQEGDSF FSVAQRYHMD AYELASMNGK 60
DITSLILPGQ TLTVNGSAAP DNQAAAPTDT TQATTETNDA NANTYPVGQC TWGVKAVATW 120
AGDWWGNGGD WASSASAQGY TVGNTPAVGS IMCWTDGGYG HVAYVTAVGE DGKVQVLESN 180
YKDQQWVDNY RGWFDPNNSG TPGSVSYIYP N 211
<212> Type : PRT
<211> Length : 211
SequenceName : SEQ ID 352
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
MSIKNILENK TTTIKVSFAG IATAASLILP MAVQAETTYT VKSGDTLSEI ASTHGTTVDK 60
LAKLNKINNI HLIHAGQILE LDAATEDTDA TPVQESQINE AETSASAKTS QTSEVTTTAP 120
VQESQTSEVI TSAPAETSQT SEVPTEANQT NEVSSAVSVE TSQTSEATTS APVETSQTSE 180
ATTAEPTETK TSQTNEVAAS AEENQTTSNT SGLSTSDAAA KEFIAQKESG GNYNAKNGQY 240
YGRYQLSDSY LNGDLSEENQ ERVADAYVSS RYGSWTAAQA FWNANGWY 288
<212> Type : PRT
<211> Length : 288
SequenceName : SEQ ID 353
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
MKCQAFEDFK ATSLNKLSYT TGGATDGEII ANRMLQGKAT KGEITMYTWN IIQNGWVNSL 60
VSWGIGGYNS SIGYSAQGNR GFSNYPYDVS MDSDNSSSSS NTTGGYVNYN QSFNSGW 117

<212> Type : PRT
<211> Length : 117
SequenceName : SEQ ID 354
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
MRYSQICRKS LALLATGMIL TTSTLPSISI LAEDSTGAPA RPDGQAPAGG GANTTTYDYS 60
GINSGVLVAN GSKVTSSSKT KSTTSAQNTA LVQNGGSLTL HKANLIKSGD DNNGDNDNFY 120
GINSILLAVN ERSKAYVSNS KLKASSSGSN GIFATDKATI YANKTSIATT ADNSRGLDAT 180
YNGNIIANKM AISTKGAHSA AIATDRGGGN ISTTNSSLNT SGSGSPLLYS TGNIQVNHVT 240
GTSSNSQIAG MEGLNTILIH NSNLISTMTN KTASDPIANG VIIYQSQSGD AEATTGQSAH 300
FELSKSKLTS SITSGSMFYL TNTSANIILN QSTLNFDANK AKLLTVAGNS ANNWGTPGSN 360
GATVNFTGHK QTLKGDVDVD SISTLNMYLL DKTNYTGKTA VSTNSTNISP STSPITMNIS 420
KNSKWVLTGH STVTNLNAEK GAKIVDKDGK TVSVISSSGQ KLVKGKSKYS LTVTGTYSQK 480
VTTSSSNKPS SSYINRSDFD NYFKTTTAFV NNTKNTSN 518

<212> Type : PRT
<211> Length : 518
SequenceName : SEQ ID 355
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
MNKIGDTLRD ARIEKKLSFD DVVDKTGIAP HYILAMELDQ LKLLPEGKTN EYLEKYAHAV 60
GLDPVSIIHG YRNQEMSDEL ILPSSAELAA SSDSNIEKKN EGKSIEEPQE LAIDSLDVTQ 120
NITEETPQIE DFKVESEEAS KKIEKIPSRL SKYDYDEEPK KKFPWALILL ILLALTIISY 180
VGYVVYNQLQ TDSNKTELST STKKSKDTKN DANSTTQSQT SITTDFADGG NNITLSNTNG 240
KVEVTFTLTG DEESWVSATN TTDGESGTTL TATDKTYTVT LAEGSTTSML TVGSPSGVEI 300
TINGQKVDTT NLVNAGLTNI NLTVQ 325

<212> Type : PRT
<211> Length : 325
SequenceName : SEQ ID 356
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
MKSRKRQRKG LVRKNEIIIL TLFVASAVSL LAFTNSFGVL AKSLHLEKIN KSITISLPFG 60
KKKMEQTARY YSGEQVQISS SAKKDSLGKG LSHYQNWIGT VKKIKSQKDS RQKHHYSYEV 120
TFDNGKALKY VQEKDLVKTK RSKYSKGQIV KLKSSATADL DGSSLTDYRA SAGKIDHISY 180
NHSNTTGGYK YDITFDEGGK VTNIQEKDLD KVYEVQLKSE NTAAQNNEIL KQAFAYAKQH 240
SGTILSLPNG EFKIGSQTPD KDYITLTSDT EIRGDNTTLL VEGSAYWFAF ATGTSASDGV 300
KNFTMRNINI KASDLEKGNQ FMIMADHGDN WKICNNSFTM VHKKGSHIFD LGSLQNSAFE 360
GNQFTGYAPE LTNVSKIDDN ADLHDFYSEV IQLDAAESSG VWDGGLIKAI DPNYENYNKE 420
KQLCNNITIA NNSFVPYIDS HGKIIAYSGT IGQHSSDVGL VKIYDNVFSN SLVSRFNQNG 480
KSEAWIFKAI HLKSNYNNAV YANSIS 506

<212> Type : PRT
<211> Length : 506
SequenceName : SEQ ID 357
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
MRKLKVALFA SSILGMLAVS SYTAADTEDN QVTISHYNEQ AGTFDVNAVQ AANGKTIQSI 60
DVAIWSEENG QDDLKWYHAS NDGSNQLTVH FNAENHGSKV GSYIAHAYIT YTDGNRVGVN 120

LGKRKLSLSA PQLSLKQGGL QLFSKLKPSA ADQLFSAVWS DENGQDDLHW YTADADGNTL 180
AGYANHKGYG TYHVHTYLKQ NGKMIPISAQ DIDIPKPKVK IQIDKINDTS YDVVVNNVPP 240
YISSVAIPVW SEQNGQDDLK WYQATKVADG IFKTTVYLKT HRFELGNYQA HIYGDSQLSK 300
KLDGLGETHF NVPSIINYED PQVTIDHYNI NKGTFDVTVA ETDNSKAIQS ISAAVWSDAN 360
QANLYWYEAK QLANGKAAIT VDVQKHGNQT GSYNVHVYVH YNDGTTSGHV LANQQLNQIV 420
HYQPSAVRIT AYMNEKNTYP VGQCTWGVKE LAPWIPNWLG NGGQWASTVA VKGFKIGTVP 480
KVGAIACWSD GGYGHVAYVT HVESNNRIQV KEANYKNQQY ISNFRGWFDP TTSYLGRLTY 540
IYPD 544

<212> Type : PRT
<211> Length : 544
SequenceName : SEQ ID 358
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
MANNYSRRQQ PTKKTKGTSR KRPTEHIKTG FSALQKSVAI IAGILGIITA LITINNYRNS 60
SHNDKKDSTS KTTIIKEKEV DDSNSNNNAA NSQAENDSNN NNNSAESNQN QTATTANDSN 120
SNSANQNQAN SQSQANNQQN QNNANAGQ 148

<212> Type : PRT
<211> Length : 148
SequenceName : SEQ ID 359
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
MKIFSFGTIR NNTALKPNYD DTTAFSGFGT IRNNTALKQS TNCASWFNRF GTIRNNTALK 60
LTILINGVSF CFGTIRNNTA LKPRGPIFVS TFRNRAIHLS QISASK 106

<212> Type : PRT
<211> Length : 106
SequenceName : SEQ ID 360
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
MKRKRNLYFL IGLFLTVFLL IGCSMQKKTK SESSSTSQKT TLQTKQSSEK STDAKQTTEA 60
HSESSQSSSH SNNEETLAPI DTGAVLKADY SSMAGTWKNE EGQTLTFDQR GLTTPGMTVS 120
LLNIDQDGNL LLNVETGTKK NLTLYIVPAN KTLSNQYFSN GQSDESDKTK DRIVSSESLN 180
SGKFTNRVYY HVSTH 195

<212> Type : PRT
<211> Length : 195
SequenceName : SEQ ID 361
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
MTPKKIKIAL TALISLMLAL FLFLFNHHSV RENSQQEKLK ISKASSKKSQ TSTSSVMTSS 60
RKATEQTSQA QTQSQSQAEQ SNPNVILPIP QELVGTYKGS SPQASEITFT ISSNGQLRAQ 120
ANFDPASDIN DVTATVSGVR KVGADTYIWE FVSGSSAALL PGVTGIGGLG KMQPGFILKG 180
GQLTPIMFTG SVDGEIDYSH PNPYPVSLNK Q 211

<212> Type : PRT
<211> Length : 211
SequenceName : SEQ ID 362
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
MKKIINVIVL SLSVFFLIAC SNSSTGEKTS QSSEETKVRL IVKTDSNKTD EKVAFKKGAT 60

VMDVLKDNYK VKESGGFITT IDGVTQDKKA GRYWMFDVND KLASKAADKI KVKNGDKIEF 120
YLKVYKGKN 129
<212> Type : PRT
<211> Length : 129
SequenceName : SEQ ID 363
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
MSNKPWEEKV TDATTDNEEM TRNSKDASII STPILTILLS LFFLIIIGIL FFVLYTSNGG 60
SNEKAATSGF YSSSKTVKKA KNEANSQTDE QTTEAETSSS ETTSSSSDSD GETITVQGGE 120
GAAAIAARAG ISVDKLYELN PEHMTHGYWY ANPGDNIKIK 160
<212> Type : PRT
<211> Length : 160
SequenceName : SEQ ID 364
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
MPDNRMNYSI DSNMQFPLVE ITLETGEFAY IQRGSMVYHT PSVTLNTKVN GRGSGLGKLV 60
GAIGRSVTSG ESFFITQAVS NASDGKLALA PSMPGQVIAL ELGEKQYRLN DGAFLALDGS 120
AQYQMKAQSV GRALFGGQGG LFVMTTEGQG TLLANSFGSI KKIELQNQEI TIDNAHVVAW 180
SRDLNYDIHL ENGFMQSIGT GEGVVNTFRG TGEIYVQSLN LQQFAGVLQG FITNTNR 237

<212> Type : PRT
<211> Length : 237
SequenceName : SEQ ID 365
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
MKKNYFWYGL LGLLALYLIT IAFIPGFHIF FSNMLMLALF FMLIALSNRS IFFFFLALGF 60
LSIYLKDIFH FDYSTGPLFT GIIIIGVILN SFLKPHYSYS YKGNHYFNMK QHANYIDNET 120
DVFLKTLFSE NTSYVTSQEL NKIIIDTKFG EQSVDLSQAQ FMTDSPEIHI DVSFGETNLR 180
IPNNWKIINK THSPFASISF SGFPSTNGDF INVTLTGTVA MGSLNIQY 228
<212> Type : PRT
<211> Length : 228
SequenceName : SEQ ID 366
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pneumoniae R6
<400> PreSequenceString :
MKSITKKIKA TLAGVAALFA VFAPSFVSAQ ESSTYTVKEG DTLSEIAETH NTTVEKLAEN 60
NHIDNIHLIY VDQELVIDGP VAPVATPAPA TYAAPAAQDE TVSAPVAETP VVSETVVSTV 120
SGSEAEAKEW IAQKESGGSY TATNGRYIGR YGSWTAAKNF WLNNGWY 167
<212> Type : PRT
<211> Length : 167
SequenceName : SEQ ID 367
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pneumoniae R6
<400> PreSequenceString :
MKHSHKKSFD WYSMQQRYSI RKYYFGAASV LLGTALVLGA AASVQTVQAE ENKQETTNSI 60
SVGRGEAATK PAEVSASNKE KTYAAPTVAN PVETTPVKTE EVTKPAEKVE EAKDKKEEVT 120
HQDAVDKSKL LTALSRAKKL ESKLYTEASA ANLQTSIQAG QSLLGKADAT EAELSAAESS 180
IQSFIIGLEL RSNSNKETVS ETPVAKKADA VESKEGAKPA ATTERSAVDS AILPTSTADK 240
VETTSAPASI NEILKLGLSL SDARQNPAIR KEDVNRGYSG FRAASNPANP IVSGSGNTVA 300

FADISQGGRS YSFRGYGNSR GGNSIHYDVT TVRSGNSVNF TISYSAPGDS REFVNNNFIL 360
DKGDGFGNPS NATITSSNPR VREQSKSISQ GANYVSHSGY SMTSAISTNT EQTIRFSLPI 420
INLNGDLSVR LKPVTFNVDQ GGGGAATSND PYSNSNYYYR ANPLYLDANP YGGTNNKTVS 480
EDIDFQTVYL PTSKLPEGQT RLVREGEKGQ RQITYKVHRF GNETLLGLPI SNSVTKEAKP 540
RIMQIGVAKD LIDTVKPRVD QNKVGDTNNL TFYLDNDGNG VYTEGVDELV QKIAIKDGAK 600
GEKGDQGERG LTGAKGEKGD RGERGLTGAQ GAKGEKGDRG ERGLTGAQGA KGEKGDRGER 660
GLTGAQGAKG EKGDRGERGL TGAQGAKGEK GAQGERGLTG AQGAKGEKGD QGERGLTGAQ 720
GAKGEKGDQG ERGLTGAQGA KGEKGAQGER GLTGTQGAKG EKGDRGERGL TGAQGAKGEK 780
GDRGERGLTG AQGAKGEKGA QGERGLTGAQ GAKGEKGDQG ERGLTGAQGE KGDRGERGLT 840
GAKGEKGDQG ERGITGAKGE KGAQGERGLT GAQGAKGEKG DQGERGLTGA QGEKGAQGQA 900
GRDGVTPTVT VKDNKNDGTH TITINDGRGN VTSTVVRDGF DGASPLVATQ RNDADKTTTV 960
IFYYDKNGNN ELDASDKKLK EVVIADGAKG EKGDKGEQGL QGRDGEQGPK GEDGKTPTVK 1020
VTDGQDGTHT ITINDGKGGI TTTVVRDGFD GASPLVSTHR NEADKTTTVI FYYDLNDNNQ 1080
FDEGDTKLKE VVIADGKQGP KGDKGDNGKD GFTPEVTVTD NNNGTHTITI TQPDNRPSLT 1140
TIVKNGEDGK TPKVKAERDD AKKQTTLTFY IDKDGDGSYT AGKDELVQTT VVKDGQDGAA 1200
GASGRDGKEV LNGKVDPTTE GKDGDTFVNT QTGDVFVKKG NTWEPAGNIK GPKGDKGADG 1260
AKGEKGAQGE RGLTGAQGVK GEKGDQGERG LTGSKGEKGD QGERGLTGAQ GAKGDKGEQG 1320
LQGRDGAQGP KGADGQRGPA GPQGPKGEQG NPGTPGKDGK SLIAVKNGVL VTITPVEGRP 1380
QTTFVEDGQK GADGKTPTVT ITEGQNGTHT LTVHNPGSPD VTTTIRDGAT GQAGRDGKDV 1440
LNGKVNPQPN QGKNGDKYIN IETGDVYVKN NGNWDKEGNI KGPKGDKGAD GAKGEKGDQG 1500
ERGLTGAQGA KGADGAVGRD GRDGKDVLNG KANPEAHQGK DGDKYVNTET GDVFVKNNGN 1560
WDKEGNIKGP KGDKGADGAK GEKGDRGERG LTGAQGAKGA DGAAGRDGRD GRDGKDVLNG 1620
KVNPEANQGK DGDKYVNTET GDVFVKNNGN WDKEGNIKGS KGDKGERGED GKTPEVTVTP 1680
GKDGHSTDIT FTVPGKDPVT VNVKDGENGL NGKTPKVDLL RVQGKNGNPS HTIVTFYTDE 1740
NNDGKYTPGT DELLGSEMIK DGAKGADGRD GKSLLTVKDG KETKVYQEDP ANPGQPLNPE 1800
KPLAVIRDGV DGKSPTVTAV RKDEAGHKGV EITVDNHDGS QPTTVFVQDG AKGKTGATGQ 1860
DGQTPTITTQ RGQDGQSTVV TITTSGKDPV TFTVKDGKNG KDGRAPKIKV EDITSPSRIR 1920
RDTDAAATPT RNGIRVTVYD DVNDNGVYDE GVDKVLNSKD IYNGIDGRDG SAPTITTKDN 1980
GDGTHTITVQ NPDGSESTTV VKDGKDGKTA NITTTENPDG SHTITVTNPD GSTKETVVKN 2040
GKDGKTPKVE VTDNNDGTHT VKVTDGDGNV TNAIIKDGKD GKAATATTTE NPDGSHTVTI 2100
TNPDGTKNEF VVKNGRDGVD GRTPTASVRD NGDGSHTIVI TNPEGVTTET TVRDGKSPKV 2160
TITDEQNGTH KISVLNGDGT TTETIIKDGK SPVATVRDNQ DGTYTIRVEN GNGTVSETTV 2220
RDGKSPTAKV VDNGDGTHTI TVVNSDGITT TTTVRDGREP KLEVIDNNDG SHTIKVTGAD 2280
GKGTTTTIFD GKSPKANIVD NGDGTHTLTI VDSDGREYKS IIKDGKDGKD SVSPTVTVKN 2340
NNDGTHVVTI TNPDGSKTEM VIKDGKDGKS PKVSVEDNGD GSHTITIINS DGTVTKTVIK 2400
DGKDGRDGRD GRDGKDGKDG KCGCQDKPVT PSNDKPVPPT PNVPTPEVPV KPVPAQPTPN 2460
VPTPEVPVQP TPAVSTPEVP VKPVPAVPEQ PVVPTPAQPA TPVNANPVAP TTGKENRGDK 2520
LPETGSQSDY ISVLLGSGLL LSLYVGRRKE D 2551

<212> Type : PRT
<211> Length : 2551
SequenceName : SEQ ID 368
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pneumoniae R6
<400> PreSequenceString :
MKKRMLLAST VALSFAPVLA TQAEEVLWTA RSVEQIQNDL TKTDNKTSYT VQYGDTLSTI 60
AEALGVDVTV LANLNKITNM DLIFPETVLT TTVNEAEEVT EVEIQTPQAD SSEEVTTATA 120
DLTTNQVTVD DQTVQVADLS QPIAEAPKEV ASSSEVTKTV IASEEVAPST GTSVPEEQTA 180
ETSSAVAEEA PQETTPAEKQ ETQTSPQAAS AVEATTTSSE AKEVASSNGA TAAVSTYQPE 240
ETKIISTTYE APAAPDYAGL AVAKSENAGL QPQTAAFKEE IANLFGITSF SGYRPGDSGD 300
HGKGLAIDFM VPERSELGDK IAEYAIQNMA SRGISYIIWK QRFYAPFDSK YGPANTWNPM 360
PDRGSVTENH YDHVHVSMNG 380

<212> Type : PRT
<211> Length : 380
SequenceName : SEQ ID 369
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pneumoniae R6
<400> PreSequenceString :
MTILGKDTVQ QSAKGESVTQ EATPEYKLEN TPGGDKGGNT GSSDANANEG GGSQAGGSAH 60
TGSQNSAQSQ ASKQLATEKE SAKNAIEKAA KNKQDEIKGA PLSDKEKAEL LARVEAEKQA 120
ALKEIENAKT MEDVKEAETI GVQAIAMVTV PKRPVAPNAA PKTTSAPQAT AGTMQDVTYQ 180
SPAGKQLPNT GSASSAALAS LGLVVATSGF ALLGRKTRRR K 221

<212> Type : PRT
<211> Length : 221
SequenceName : SEQ ID 370
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pneumoniae R6
<400> PreSequenceString :
MMTTGCSMGA YHALNFFLQH PDVFTKVIAL SGVYDARFFV GDYYNDDAIY QNSPVDYIWN 60
QNDGWFIDRY RQAEIVLCTG LGAWEQDGLP SFYKLKEAFD KKQIPAWFAE WGHDVAHDWE 120
WWRKQMPYFL GNLYL 135
<212> Type : PRT
<211> Length : 135
SequenceName : SEQ ID 371
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pneumoniae R6
<400> PreSequenceString :
MNKGLFEKRC KYSIRKFSLG VASVMIGATF FGTSPVLADS VQSGSTANLP ADLATALATA 60
KENDGHDFEA PKVGEDQGSP EVTDGPKTEE ELLALEKEKP AEEKPKEDKP AAAKPETPKT 120
VTPEWQTVEK KEQQGTVTIR EEKGVRYNQL SSTAQNDNAG KPALFEKKGL TVDANGNATV 180
DLTFKDDSEK GKSRFGVFLK FKDTKNNVFV GYDKDGWFWE YKSPTTSTWY RGSRVAAPET 240
GSTNRLSITL KSDGQLNASN NDVNLFDTVT LPAAVNDHLK NEKKILLKAG SYDDERTVVS 300
VKTDNQEGVK TEDTPAEKET GPEVDDSKVT YDTIQSKVLK AVIDQAFPRV KEYSLNGHTL 360
PGQVQQFNQV FINNHRITPE VTYKKINETT AEYLMKLRDD AHLINAEMTV RLQVVDNQLH 420
FDVTKIVNHN QVTPGQKIDD SRKLLSSISF LGNALVSVSS DQTGAKFDGA TMSNNTHVSG 480
DDHIDVTNPM KDLAKGYMYG FVSTDKLAAG VWSNSQNSYG GGSNDWTRLT AYKETVGNAN 540
YVGIHSSEWQ WEKAYKGIVF PEYTKELPSA KVVITEDANA DKKVDWQDGA IAYRSIMNNP 600
QGWKKVKDIT AYRIAMNFGS QAQNPFLMTL DGIKKINLHT DGLGQGVLLK GYGSEGHDSG 660
HLNYADIGKR IGGVEDFKTL IEKAKKYGAH LGIHVNASET YPESKYFNEK ILRKNPDGSY 720
SYGWNWLDQG INIDAAYDLA HGRLARWEDL KKKLGDGLDF IYVDVWGNGQ SGDNGAWATH 780
VLAKEINKQG WRFAIEWGHG GEYDSTFHHW AADLTYGGYT NKGINSAITR FIRNHQKDAW 840
VGDYRSYGGA ANYPLLGGYS MKDFEGWQGR SDYNGYVTNL FAHDVMTKYF QHFTVSKWEN 900
GTPVTMTDNG STYKWTPEMR VELVDADNNK VVVTRKSNDV NSPQYRERTV TLNGRVIQDG 960
SAYLTPWNWD ANGKKLSTDK EKMYYFNTQA GATTWTLPSD WAKSKVYLYK LTDQGKTEEQ 1020
ELTVKDGKIT LDLLANQPYV LYRSKQTNPE MSWSEGMHIY DQGFNSGTLK HWTISGDASK 1080
AEIVKSQGAN DMLRIQGNKE KVSLTQKLTG LKPNTKYAVY VGVDNRSNAK ASITVNTGEK 1140
EVTTYTNKSL ALNYVKAYAH NTRRNNATVD DTSYFQNMYA FFTTGSDVSN VTLTLSREAG 1200
DEATYFDEIR TFENNSSMYG DKHDTGKGTF KQDFENVAQG IFPFVVGGVE GVEDNRTHLS 1260
EKHDPYTQRG WNGKKVDDVI EGNWSLKTNG LVSRRNLVYQ TIPQNFRFEA GKTYRVTFEY 1320
EAGSDNTYAF VVGKGEFQSG RRGTQASNLE MHELPNTWTD SKKAKKATFL VTGAETGDTW 1380
VGIYSTGNAS NTRGDSGGNA NFRGYNDFMM DNLQIEEITL TGKMLTENAL KNYLPTVAMT 1440
NYTKESMDAL KEAVFNLSQA DDDISVEEAR AEIAKIEALK NALVQKKTAL VADDFASLTA 1500
PAQAQEGLAN AFDGNLSSLW HTSWGGGDVG KPATMVLKEA TEITGLRYVP RGSGSNGNLR 1560
DVKLVVTDES GKEHTFTATD WPDNNKPKDI DFGKTIKAKK IVLTGTKTYG DGGDKYQSAA 1620
ELIFTRPQVA ETPLDLSGYE AALAKAQKLT DKDNQEEVAS VQASMKYATD NHLLTERMVE 1680
YFADYLNQLK DSATKPDAPT VEKPEFKLSS VASDQGKTPD YKQEIARPET PEQILPATGE 1740
SQFDTALFLA SVSLALSALF VVKTKKD 1767
<212> Type : PRT
<211> Length : 1767
SequenceName : SEQ ID 372
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pneumoniae R6
<400> PreSequenceString :
MKLYNKSELR YSRIFFDKRP PAFAFILIIS TAIILSGALV GAAYIPKNYI VKANGNSVIT 60
GTEFLSAISS GKVVTLHKSE GDMVNAGDVI ISLSSGQEGL QASSLNKQLV KLRAKEAIFQ 120
KFEQSLNEKY NRMSNSGEEQ EYYGKVEYYL SQLNSENYNN GTQYSKIQDE YTKLNKITAE 180
RNQLDADLQT LQNELIQLQQ QGDSPSLSDT TSADDKAKLE TKILEITTKI EALKTNITSK 240
NSEIDSQQSN IKDMNRTYND PTSQAYNIYA QLVSELGTAR SNNNKSITEL EANLGVATGQ 300
DKAHSILAPN EGTLHYLVPL KQGMSIQQGQ TIAEVSGKEK GYYVEAFVLA SDISRVSKGA 360
KVDVAITGVN SQKYGTLKGQ VRQIDSGTIS QETKEGNISL YKVMIELETL TLKHGSETVV 420

LQKDMPVEVR IVYDKETYLD WILEMLSFKQ 450

<212> Type : PRT
<211> Length : 450
SequenceName : SEQ ID 373
SequenceDescription :

Sequence

<213> OrganismName : Neisseria meningitidis Z2491
<400> PreSequenceString :

MNKGLHRIIF SKKHSTMVAV AETANSQGKG KQAGSSVSVS LKTSGDLCGK LKTTLKTLVC 60
SLVSLSMVLP AHAQITTDKS APKNQQVVIL KTNTGAPLVN IQTPNGRGLS HNRYTQFDVD 120
NKGAVLNNDR NNNPFLVKGS AQLILNEVRG TASKLNGIVT VGGQKADVII ANPNGITVNG 180
GGFKNVGRGI LTIGAPQIGK DGALTGFDVR QGTLTVGAAG WNDKGGADYT GVLARAVALQ 240
GKLQGKNLAV STGPQKVDYA SGEISAGTAA GTKPTIALDT AALGGMYADS ITLIANEKGV 300
GVKNAGTLEA AKQLIVTSSG RIENSGRIAT TADGTEASPT YLSIETTEKG AAGTFISNGG 360
RIESKGLLVI ETGEDISLRN GAVVQNNGSR PATTVLNAGH NLVIESKTNV NNAKGSANLS 420
AGGRTFINDA TIQAGSSVYS STKGDTELGE NTRIIAENVT VLSNGSIGSA AVIEAKDTAH 480
IESGKPLSLE TSTVASNIRL NNGNIKGGKQ LALLADDNIT AKTTNLNTPG NLYVHTGKDL 540
NLNVDKDLSA ASIHLKSDNA AHITGTSKTL TASKDMGVEA GLLNVTNTNL RTNSGNLHIQ 600
AAKGNIQLRN TKLNAAKALE TTALQGNIVS DGLHAVSADG HVSLLANGNA DFTGHNTLTA 660
KADVNAGSVG KGRLKADNTN ITSSSGDITL VAGNGIQLGD GKQRNSINGK HISIKNNGGN 720
ADLKNLNVHA KSGALNIHSD RALSIENTKL ESTHNTHLNA QHERVTLNQV DAYAHRHLSI 780
TGSQIWQNDK LPSANKLVAN GVLALNARYS QIADNTTLRA GAINLTAGTA LVKRGNINWS 840
TVSTKTLEDN AELKPLAGRL NIEAGSGTLT IEPANRISAH TDLSIKTGGK LLLSAKGGNA 900
GAPSAQVSSL EAKGNIRLVT GETDLRGSKI TAGKNLVVAT TKGKLNIEAV NNSFSNYFPT 960
QKAAELNQKS KELEQQIAQL KKSSPKSKLI PTLQEERDRL AFYIQAINKE VKGKKPKGKE 1020
YLQAKLSAQN IDLISAQGIE ISGSDITASK KLNLHAAGVL PKAADSEAAA ILIDGITDQY 1080
EIGKPTYKSH YDKAALNKPS RLTGRTGVSI HAAAALDDAR IIIGASEIKA PSGSIDIKAH 1140
SDIVLEAGQN DAYTFLKTKG KSGKIIRKTK FTSTRDHLIM PAPVELTANG ITLQAGGNIE 1200
ANTTRFNAPA GKVTLVAGEE LQLLAEEGIH KHELDVQKSR RFIGIKVGKS NYSKNELNET 1260
KLPVRVVAQT AATRSGWDTV LEGTEFKTTL AGADIQAGVG EKARVDAKII LKGIVNRIQS 1320
EEKLETNSTV WQKQAGRGST IETLKLPSFE SPTPPKLSAP GGYIVDIPKG NLKTEIEKLS 1380
KQPEYAYLKQ LQVAKNINWN QVQLAYDRWD YKQEGLTEAG AAIIALAVTV VTSGAGTGAV 1440
LGLNGAAAAA TDAAFASLAS QASVSFINNK GDVGKTLKEL GRSSTVKNLV VAAATAGVAD 1500
KIGASALNNV SDKQWINNLT VNLANAGSAA LINTAINGGS LKDNLGDAAL GAIVSTVHGE 1560
VASKIKFNLS EDYITHKIAH AIAGCAAAAA NKGKCQDGAI GAAVGEIVGE ALTNGKNPAT 1620
LTAKEREQIL AYSKLVAGTV SGVVGGDVNT AANAAKVAIE NNLLSQEEYA LREKLIKKAK 1680
GKGLLSLDWG SLTEQEARQF IYLIEKDRYS NQLLDRYQKN PSSLNNQEKN ILAYFINQTS 1740
GGNTAWAASI LKTPQSMGNL TIPSKDINNT LSKAYQTLSR YDSFDYKSAV AAQPALYLLN 1800
GPLGFSVKAA TVAAGGYNIG QGAKAISNGE YLHGTVQVVN GTLMVAGSVS AQAAISAKPA 1860
PVTRYLSNDS APALRQALTA ESQRIRMKLP EEYRQIGNLA IAKIDVKGLP QRMEAFSSFQ 1920
KGEHGPISLP ETKIFKPISV DKYHNIASPP RGTLRNIDGE YKLLETIAQQ LGNNRNVSGR 1980
IDLFTELKAC QSCSNVILEF RNRYPNIQLN IFTGK 2015

<212> Type : PRT
<211> Length : 2015
SequenceName : SEQ ID 374
SequenceDescription :

Sequence

<213> OrganismName : Neisseria meningitidis Z2491
<400> PreSequenceString :

MDLIQTPNKQ FVDGDRRTPG TPVPAWWLNQ LQGELYSILN AVGIEPNKAD HAQVLSAIKT 60
LAADASQVAS IDALRKYSGT GYVNVNAYHA NTTVGGGVFV ADKADKSTAD NGCTVIVSTD 120
GTRWKRVFSG MLNLHDFGYV ASKNNALSTL NAAESAALDV VVDCLGLSID TGNIYPQKNK 180
YTNGKFVING KTVDVQYQPI RSGIGRFISG TGAAANLKSN EWTGAGLIVI GEGAMEQMEK 240
CVSSIAIGDR AQGFSKVSRD NIAIGADSLI NVQAATEWYD QSRMEGTRNI GIGGNAGRGI 300
TSGYSNVSIG RNAGQGLGEG SSNIALGAGA MAGTAPVGFS GDIEVFWPSS TSRTIAIGEA 360
VLQTYQGRAA QTAIGANAAR NTKKAEKVTA IGSAAMENLE RNRAPNGGDV VWTGTEAGTY 420
AQSGKNITLT FPNIRGAQAT YWVGIRLTSG TAQTLQNDVV PAQVVSVNGN TLIIQSSKEL 480
TATGAAELKY VYSVNSTATK NEELTIIGAN AMNKALTAGY STIIGVDAAL LGDNYQKTTA 540
IGASSLRTGS HISTTAIGYW VIPLASSEKC VAIGDSAGYR NVQGDFLTGK ITNSIAIGYG 600
ARINGDNEIQ IGTTGQTLYA PTAVNIRSDG RDKADVKPLT NGLDFVMKLK PMTGYYDRRD 660
SYVDELFKDL PADERADKVR EWWANPIKDG SHKEDRLRHW FIAQDIAALE DEYGRLPMVN 720
KTNDTYTVEY ETFIPVLTKA IQEMAARIET LETEMKESKK 760

<212> Type : PRT

<211> Length : 760
SequenceName : SEQ ID 375
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pyogenes MGAS8232
<400> PreSequenceString :
MKNISRKCFM TSVVCIILGG ILLGAGYATG GLQDIKHQTA PKKVIKTFDQ ITALDIDSSA 60
STITVETGPV QRPTVTYYTH PKFIDPIVTT LTGKTLSLSQ KPKDIVITGG IEILGFTLNN 120
SRQEKNYRSI TITVPEKTSL NEVKGSNVPH TTLSNLTVQD MQFDGNLTLL HTKVKKATIT 180
GMLEATKSQL TNLELKADYS FSNLTDSSVE NGTISLGNGQ LTTKDTTLKA INIQSLHPGG 240
IEAERTTLEN VTFTVSKSKE EEEENDYYDN DAIFTAHALT LKGTNTISGG DIDVDITLTK 300
AKAIAYRART ENGKVSLGSQ LTPAKIGKES TSDVISYVAE NKAATGNLTV NLNKGDITIK 360

<212> Type : PRT
<211> Length : 360
SequenceName : SEQ ID 376
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pyogenes MGAS8232
<400> PreSequenceString :
MFKKENLKQR YFNFGLVALA LTILAIIFAF SSKNADTKSY AKKSESKMVT IDKAPKNNHA 60
ITKEESKEKA KSIASEPIPT VENSVAPTVT EEAPVVQQEV TQTVQQVSSV AYNPNNVVLS 120
NGNTAGIVGS QAAAQMAAAT GVPQSTWEHI IARESNGNPN AANASGASGL FQTMPGWGST 180
ATVEDQVNAA LKAYSAQGLS AWGY 204

<212> Type : PRT
<211> Length : 204
SequenceName : SEQ ID 377
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pyogenes MGAS8232
<400> PreSequenceString :
MLEELKTLIK NPKLMITMIG VALVPALYNL SFLGSMWDPY GRVNDLPIAV VNHDKPAKRA 60
DKSLTIGNDM VDKMSKSKDL DYHFVSSKSA QKGLKKGDYY MVITLPEDLS QRATTLLNPE 120
PQKLTIRYQT SKGHGMVAAK MGETAMAKLK ESVSQNITKT YTSAVFSSMT DLQSGLKEAS 180
TGSQALDSGA KTAQMGSQML SDNLAGLSSA SWQFQQGTNR LTSGLTAYTA GVSQVKDGLG 240
QLSTDMPVYL NGVSRLSQGA SQLNQGLSQL TQSTTLSDDK AKRIQSLEVG LPVLNQGIQQ 300
LNENLSTMQV PKLNTDELGN NLAAIAQAAQ QLLVKEAAAH KEQLAVLQAT SAYQSLTAEQ 360
QGELTAALTQ TDKGEAVAPA QTILRSVQTL STSLQSLSQE DQSKQLEQLK EAVAQIANQS 420
NQALPGASSA LTELSTGLAK VNGSLNQQVL PGSNQLTTGL AQLNRYNTAI GSGVIKLSEG 480
ANALSSKSGE LLDGSHQLSE GATKLADGSS QLSQGGHQLT SGLTELSTGL SILNGSLAKA 540
SQQLSLVSVT DKNAKAVAKP LVLNEKDKDG VKINGIGMAP YMIAVSLMVV ALSTNVIFAN 600
SLSGRPVKDK WDWAKQKFVI NGFISTMGSI VLYLAIQLLG FEARYGMETL GFIMLSGWTF 660
MALVTALVGW DDRYGSFASL VMLLLQVGSS GGSYPIELSG AFFQKLHPFL PMTYVVSGLR 720
QTISLSGHIG VEVKVLTGFL LAFMVLSLLI YRPKKTV 757

<212> Type : PRT
<211> Length : 757
SequenceName : SEQ ID 378
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pyogenes MGAS8232
<400> PreSequenceString :
MSRDPTYTIN EHDLSFADGR FYVTFKADKS SETVRLNSSC LGNTIIKKLQ VEDDNTMHDF 60
VKPKVTTQQA FGLAQQVKEL DLQLKDPKSD LWGKIKFNNK AMLVEYANKE MSSAIAQSAE 120
QILLQVKSID DERYSKFEQT LNGIKQTVKS ESVESARTQL ASMFDSRISG LDGKYSRLSQ 180
TIDSLSSRLD DGVGNYSTLS QKVSGIDLRV SNAANDVSRL SQTAQGLQSQ ITNANQNYSS 240
LSQTVQGLQT TVRDNQSNAT SRINQLSDLI STKVSKGDVE TTIAQSYDKI AFAIRDKLPA 300
SKMSGSEIIS AINLDRSGVK ITGKNITLDG NSYISNAVIK DAHIANMDAG KINTGYLNAN 360
RIATEAITGE KIKMDYAFFN KLTANEGYFR TLFAKDIFAT SVQSVTLSAS KITGGVLAAT 420
NGASQWDLNN ANMTFNRDAT INFNSKNNAL VRKDGTHTAF VHFSNATPKG YRGSALYASI 480

GITSSGDGID SASSGRFAGL RSFRYATGYN HTAAVDQTEL YGDNVLIADD FSINRGFKFR 540
PDKMEKVLDM NDLYAAVVAL GRCWGHLANV GWNTAHSNFT SAVSRELNNY ITKI 594

<212> Type : PRT
<211> Length : 594
SequenceName : SEQ ID 379
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pyogenes MGAS8232
<400> PreSequenceString :
MAADGKVTIL VDVDGKQVKV LNSELDDKVAK HGDKGSSSLK KFAVGAGVFK LASAAVDLVS 60
QSLGKAITRF DTLEKYPRVM KAMGHSAEDV ARSTDKIANG IDGLPTTLDE VVGTAQRLTS 120
ITKDINKSTN LTLALNNAFL ASGASSEAAS RGLEQYAQML SAGKVDMQAW KTLQETMPYA 180
LQQTAEAFGF AGASAQKDFY EALKNGQITF DQFSNKLIEL NDGVGGFAEL AKENSKGIET 240
SFNNIKNAIA KGVANSIKAL DDLSKAATGK GIADHFDSLK VVINASFSAI NASIKASTPL 300
FKLLFSVIGA GISVVKALSP ALVGVASGLA AMRAVNETIT MIKALNRAWV MASASMSIGA 360
TTIKTVTAVQ AVSTTMTKAD MVARLSQLGV LKASTVIYGV MTGAISLSTA ATIASTAAVT 420
ALKAALVALT GPVGWVVGAI GALVAVGVSL WSWLTKESDE TKKLKKEQEG LVESNKQLRD 480
SVREGVQERK KGLESVKEST AAHQKLADEI IKLAAKENKT AGEKQNLKNK IDQLNGSIDG 540
LNLAYDKNSN SLSHNADQIK SRISAMEAES TWQTAQQNLL NIEQKRSEVS KKLAENADLR 600
KKWNEEANVS DSVRKEKIAE LTEEEAKLKN MQTQLQEEYN KTSATQQAAA DAMAAAEESG 660
SARQVIAYEN MSEAQRTAID NMRTKYSELL ETTTSIFDAI EQKTALSVDQ MNTNLEKNRA 720
ATEQWATNLE ILAQRGVDQG ILEQLRRMGP EGATQTQVFV DATDAELAPL QENFRAATET 780
AKNAMGSVLD SAGVEMPEKV KGMVTNVSTG LQAELQAANF AQLGQEIPNG VSQGISQGAG 840
KASDASVKMG QEVKRSFQGE LGIHSPSRVF TEYGGHITDG LSNGVTNGTS KVMQTMQSLA 900
QQMSQKGQQI VNDMRSKSNQ ITDAFSTMSG PMHSHGVNAM QGLANGIYAG SGAALAAAQS 960
IAARITATIQ SALDIHSPSR VMRDEVGRFI PQGIAVGIDA DRKVIDSSMQ KLKESMTINA 1020
TPEIASGFGG GVAGIANQTT NNSNNSFTLN VKVDESDGNS HEKYQRLFRE FSWYIQQQQG 1080
RLGDVK 1086
<212> Type : PRT
<211> Length : 1086
SequenceName : SEQ ID 380
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pyogenes MGAS8232
<400> PreSequenceString :
MAKEPWEEKI VDDTIGTRTR KSRNAFISTP WLTALLSVFF VIIVAILFIF FYTSNSGSNR 60
QAETNGFYGA STHKKTRKAS NAKKTSSSST TTDTTPSSEE TLASSEGTGE TLTVLAGEGA 120
ASIAARAGIS VEQLQALNPE HMTQGYWYAN PGDQVTIK 158
<212> Type : PRT
<211> Length : 158
SequenceName : SEQ ID 381
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pyogenes MGAS8232
<400> PreSequenceString :
MSKRGKIKIT TKTKLITASV ITLVLIITGV VLWKQQQNTL TADIAKEPYS TVSVTEGSIA 60
SSTLLSGTVK ALSEEYIYFD ANKGNDATVT VKIGDQVTQG QQLVQYNTTT AQSAYDTAVR 120
SLNKIGRQIN HLKTYGVPAV STETNKDEAT GEETTTTVQP SAQQNANYKQ QLQDLNDAYA 180
DAQAEVNKAQ IALNDTVVIS SVSGTVVEVN NDIDPSSKNS QTLVHVATEG QLQVKGTLTE 240
YDLANVKVGQ SVKIKSKVYS NQEWTGKISY VSNYPTESNA GSTTPAGSTG AGSSTGAAYD 300
YKIDIISPLN QLKQGFTVSV EVVNEAKQAL VPLTAVIKKD KKHYVWTYDD ATGKAKKVEV 360
TLGNADAQQQ EIHKGVAVGD IVIANPDKNI KPDKKLEGVI SIGTNTKPEK DSQSKNKKSG 420
VDK 423
<212> Type : PRT
<211> Length : 423
SequenceName : SEQ ID 382
SequenceDescription :

Sequence

<213> OrganismName : Treponema pallidum
<400> PreSequenceString :
MLRLPTARAC ITMGTMIRHT FTHRCGALLC ALALGSSTMA ATAAAKPKKG QMQKLRQRPV 60
WAPTGGRYAS LDGAFTALAN DASFFEANPA GSANMTHGEL AFFHTTGFGS FHAETLSYVG 120
QSGNWGYGAS MRMFFPESGF DFSTTTEPVC TPASNPIKQR GAIGIINFAR RIGGLSLGAN 180
LKAGFRDAQG LQHTSVSSDI GLQWVGNVAK SFTSEEPNLY IGLAATNLGL TVKVSDKIEN 240
CTSTCEKCGC CKERCCCNGK KACCKDCDCN CPCQDCNDKG TVHATDTMLR AGFAYRPFSW 300
FLFSLGATTS MNVQTLASSD AKSLYQNLAY SIGAMFDPFS FLSLSSSFRI NHKANMRVGV 360
GAEARIARIK LNAGYRCDVS DISSGSGCTG AKASHYLSLG GAILLGRN 408
<212> Type : PRT
<211> Length : 408
SequenceName : SEQ ID 383
SequenceDescription :

Sequence

<213> OrganismName : Treponema pallidum
<400> PreSequenceString :
MSRTFRAWQC VGALCALSPL LPAYSSEGVR EVPPSQSPQV VVAYEPIRPG DQLLKIGIVA 60
GCQLYIAGGN GTNGSSSSGT NGNGNGKLLG GGGFHLGYEY FFTKNFSLGG QVSFECYRTT 120
GSNYYFSVPI TVNPTYTFAV GRWRIPLSLG VGLNIQSYLS KKAPGLIAEA SAGLYYQYTP 180
DWSIGGIVAY TQLGDIASSP DKCRAVGLAT IDFGVRYHF 219
<212> Type : PRT
<211> Length : 219
SequenceName : SEQ ID 384
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
atgataaatt taagtaagga agcaacggtg gggaaagcat taacccctat tgctatactt 60
atgatgttgt cttttcctgt agcttctcaa gcggcgggat tagtcataaa aaatggaacg 120
gtatataacg ccaatggtgt gccagtcgtt gacatcaaca aacctaacgg tagcggttta 180
tctcataata tctgggataa cctaaacgtt gataaaaatg gtgtcgtttt caataatagc 240
gctaatgaat ccagtacttc acttgccgga aatattcagg gaaacagtaa tctgacctcc 300
gggtcggcga aggtgatcct gaatgaggtt acttccaaaa atccttcaac cattaatggg 360
atgatggaag ttgcagggga taaagcggat ctgattattg ccaacccgaa tggtattact 420
gtaaacggtg gcggttcaat caatacaggt aaacttacct taaccaccgg gacgccggat 480
atccaggatg acaagctggc cggttactcc gtgaacggcg gtaccattac gctcggtaaa 540
ctggataacg ccagcccgac agaaattctg tcccgtaacg tggtagttaa cggcaaagtg 600
tctgccgatg agctgaacgt tgttgctggc aataactatg ttaatgccgc aggccaggtg 660
accggtagcg tatccgccac ggggtcccgt aacggttaca gcgtagatgt tgccaaactg 720
ggcggaatgt atgcgaacaa aatcagtctg gtcagcaccg agaaaggtgt gggggttcgc 780
aacctcggcg ttattgctgg gggtgttaat ggtgtcagca tcgattccaa aggtaacctg 840
ttaaacagta acgcccagat tcagtctgca agcacgatca acctgacaac aaatggtact 900
ctggataaca ccaccggtac ggtgacatct gtaggcacta tctcgcttaa taccaacaag 960
aatactatcg tgaatacccg tgcgggtaac atctctacga tgggcgatat ctacgttaac 1020
agcggtacga ttgacaatac taacggcaag cttgcggctg caggaatgct ggcggttgat 1080
accaataacg ccacgctgat taactctggt aaagggagtt ctgtcgggat tgaagcgggg 1140
ctcgtggcgc tgaaaaccgg aacgctcaac aacagcaatg gtcagattcg cggtggctat 1200
gtgggtcttg aatccgctgc gctgaataac aacaacggtg atatccagac caccggcgat 1260
atcgccatta tcagtaacgg taatgtggat aacaacaaag gtctgatccg ttcgtccacc 1320
gggcatatcg ttattggcgc ggcaggtagc gtaaataatg gttcaaccaa aaccgccgat 1380
accggcagtt ctgactctct gggcattatt gcagataccg gcgtagaaat tggtgcgaac 1440
aacatcaata acaacggcgg acagattgcg tctaatggca acgtctccct gtcaagttac 1500
agcacgatcg acgactatgc gggcaaaatt ctgtccaaca gcaaagtgat tatcaaggga 1560
agctctctgc gtaacgatac cgggggggatc agcggtaagc agggtattga agtcgccgtt 1620
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ttagccaact ccgtggataa ccacggcggc ttcatgatgg ggcagaacat cacgatggag 1740
tcgatgtctg gcgtcaataa caacacagcg ctgatcgtgg ccagcaaaaa actgaagata 1800
aatgcgcgcg gcagtatcga aaaccgcgat ggcaataact tcggtaatgc ttatggtctg 1860
tacttcggca tgcctcagca aacgggtgga atggtcggca aggaaggcat cgagctttcc 1920
gggcagaaca tctataacaa caacagccgt cttatcgctg aggatggtcc tctgactctg 1980
caggcgcaga acacgttcga caacacgcgt gctctggtca ccagcggggc ggatgcatct 2040
attcaggttg gcggaacgta ttacaacaac tacgctacca cctggagtgc gggcaacctg 2100

gatatcgacg cgaccacgct gcaaaacagc agcagcggta cgatgatcga taacaatgcg 2160
accgggttca tagcatctga taaaaacctg tcactggaag tggtgaatag ccttaccaac 2220
tacggctgga tcagcggtaa aggcgatgtt gatgtcacgg tgaataacgg caacctgtat 2280
aaccgcaata ccattgcggc tgaaaagggg ctggatattg ccgcgttgaa cggtattgaa 2340
aactggaagg atatttctgc tggcggcgac ctgacgatga acaccaatcg ccatgtgacc 2400
aacaactcca acagcaatat ggtggggcag aatattgtta ttaacgcggt taacgatatc 2460
aacaaccgtg gcaacattgt cagtgacgct gacctgaacg tgacgaccaa aggcaacctg 2520
tataactatc tctatatggt agggtatggg gatatcgcat tgtcggcaaa tagcgtggcg 2580
aacaataacg cgaccatcga agcgacaggc gatctgatta tcgattcgaa gggtaacgtg 2640
ggtaacaacc gcggtaatct gcatgcgttg aacggcgtgt tgtctgttaa aggcaacaat 2700
ctgaacaacg ataacggtga aattcgtggt tatggcgatg tcacgctggc actgacgggc 2760
aactacgaca gctataaggg ttcgctgacc tctgaaacgg gcgacgtgac tctgacggcg 2820
aacattgtag acaacgccta tggtttgatt gccggtgaga atgtttctgt cgatgctaaa 2880
tcgacgattt acaacaacac tgcgctgatc gcggcgaata aaaagctggt tattaacgct 2940
ggcggcaacc tcgaaaaccg cgacgggaat aacttcctgc gtaataacgg cgcgctgttt 3000
ggaattaccg acaacgttgg cggcatcgta ggtaaagaag gtgtcacgct ttctgctcag 3060
aacgtctaca acaataacag cagcatcatc gctgaaaatg gtccgcttaa tctgctgtcc 3120
aggggaacgc tggataatac ccgcgcgctt cttagcagtg gggctgatgc catcatccgt 3180
gcggcaggga cgttctacaa caactatgcc accacgtaca gcgccggtaa tctcgacgtt 3240
tatgcggcgt cgttgaacaa cgccagcgat ggtcgcctgg aagacaatac cgccacgggc 3300
gtgattgcgt ctgacaaaaa cctggatctg agcgttgata acagtgtcac taactatggt 3360
tggatcagcg gtaaaggaga tgtgcatttc aatgttctga aaggcacgct gtataaccgt 3420
aatgccatcg cggcggacaa cgcgctgacc attaatgccc tgaacggtgt tgagaacttt 3480
aaagacattg tggcgggtac tgcgctgact attgatacgc agaagtatgt taccaacaac 3540
agcaacagta atatgttggg acaaaccatc gcgatcaatg ccgtgaatga cattaataac 3600
cgtggaaata ttgtgggtga ttattctctg ggtgttaaaa ccaccggtaa tatttataac 3660
tacctcaata tgctgagtta tggtgtcgct ggcgtatcgg caaataaggt tacgaatagc 3720
ggtaaagacg ctgttctcgg tggcttctac ggtttagcgt tagaagcaaa cgaaactgat 3780
aacaccggta ctattgtcgg catgtaa 3807

<212> Type : DNA
<211> Length : 3807
SequenceName : SEQ ID 385
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
gtgaacacaa tacacttgcg ctgtctcttc aggatgaatc ccctggtctg gtgcctgtgg 60
gctgatgttg cagcaaagct aaggtcgctt aaacgctact cagtattcac ttttcagagg 120
atgaaattta tgaacaggac cagtccctat tattgtcgtc gctcagtact ttccttattg 180
atatctgcct tgatatatgc cccgcccggg atggctgcct tcactcctga tgttattggt 240
gtggtaaacg atgagactgt agatggcagc caacgagtag atgaacgagg tacaacaaat 300
aacactcata ttatcaacca tggccagcag aatgtttatg gcggggtatc taatggaagt 360
cttattgaat ctggtggata tcaagatgta ggaaggcata acaattatgt ggggcagtct 420
aataatacca ccattaacgg gggcagacag tcaattcatg acgggggtat ttccacaggt 480
acgataatcg agagtggcaa tcaggacgtt tataaagggg gtatcagcaa tggaacgaca 540
attaagggcg gtgcttcacg cgtagaggga gggagtgcga atggaacact cattgatggt 600
ggtagccaga tagtaaaagt tcaagggcat gctgatggta caacgataaa taagtctggc 660
tctcaggacg tagtacaagg aagtctggca acgaacacaa ccataaatgg tggtcgacag 720
tatgttgaac agagcacagt agaaacaacc accatcaaaa atggcggtga gcaaagagta 780
tatgagagcc gtgcgctgga cacgacgatt gaaggcggaa ctcagtctct gaatagtaag 840
tcaacggcaa aaaatactca gatctattct ggtggtacgc aaattattga taacaccagc 900
tcctcggatg ttattgaagt ttattccggt ggcgtgcttg atgttagtgg tggtacggca 960
acaaatgtta cccagcacga tggtgcaatt ttaaaaacta acactaacgg tacgacggtg 1020
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<212> Type : DNA
<211> Length : 4716
SequenceName : SEQ ID 386
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :

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<212> Type : DNA
<211> Length : 2916
SequenceName : SEQ ID 387
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
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gtttatgtaa accttgcgcc tgccgtgaat gtggggcaaa acctggtcgt agatctttcg 180
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taa 903

<212> Type : DNA

<211> Length : 903
SequenceName : SEQ ID 388
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
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ttgcttggta aatcctgtac tcctgtaatc aatggcaact tacttgcaga aattcatttc 180
cccacaattg ctgccagcga tttaatgcaa cgtggtcagt cagatcgcgt accgttagtt 240
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tatttttaa 549
<212> Type : DNA
<211> Length : 549
SequenceName : SEQ ID 389
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
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<212> Type : DNA
<211> Length : 2850
SequenceName : SEQ ID 390
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
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tttcctctga caacggtcag tgcagcaaac aatgtgcctg gaaatacatt aatagatatt 180
gctaatgcaa catcttctga aaattatagc gttctgtgta actgtgattc aaaacatagc 240
aatggcgctt atcacgaaat atattatacc gcagaccctg ctcccggtat ggtttatagc 300
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taa 1083

<212> Type : DNA
<211> Length : 1083
SequenceName : SEQ ID 391
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
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<212> Type : DNA
<211> Length : 4254
SequenceName : SEQ ID 392
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
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<212> Type : DNA
<211> Length : 4740
SequenceName : SEQ ID 393
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
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<212> Type : DNA
<211> Length : 2805
SequenceName : SEQ ID 394
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
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<212> Type : DNA
<211> Length : 681
SequenceName : SEQ ID 395
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
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<212> Type : DNA
<211> Length : 1071
SequenceName : SEQ ID 396
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
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<212> Type : DNA
<211> Length : 3984
SequenceName : SEQ ID 397
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
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<212> Type : DNA
<211> Length : 549
SequenceName : SEQ ID 398
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
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<212> Type : DNA
<211> Length : 564
SequenceName : SEQ ID 399
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
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<212> Type : DNA
<211> Length : 3753
SequenceName : SEQ ID 400
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
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<212> Type : DNA
<211> Length : 2943
SequenceName : SEQ ID 401
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
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<212> Type : DNA
<211> Length : 564
SequenceName : SEQ ID 402
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
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gttggctttg gtaacaacgc gaccgctcat cagtactaa 459

<212> Type : DNA
<211> Length : 459
SequenceName : SEQ ID 403
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
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cgtctggcgc taagtggtgg attacgccat gacatgggag gattaacggg ggggagtaat 1620
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<212> Type : DNA
<211> Length : 1677
SequenceName : SEQ ID 404
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
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atggctgcgc ctacagtcac ttttcagggt gaagtaaccg atcagacctg ttccgtaaat 120
atcaacggtc aaaccaattc agtagtattg atgccgaccg tagccatggc tgacttcggt 180
gcaacttttag ctgatggtca gagcgcaggc cagacgccgt ttacggtttc tgtgtctaac 240
tgccaggctc caactggtgc agatcaggca atcaacacca ccttcctggg ctacgacgtt 300
gacgctagca cgggtgttat gggaaaccgt gataccagca gcgatgcggc gaaaggcttt 360
ggcattcagt taatggattc cagcacttct ggtaacccag taactctggc tggcgcgact 420
aacgtaccgg gtctgaccct gaaagttggc gataccgaag ccagctacga cttcggtgcg 480
cgttacttcg ttatcgatag cgctgctgcc actgccggta aaattaccgc tgtcgcagaa 540
tacaccctga gctacctcta a 561

<212> Type : DNA
<211> Length : 561
SequenceName : SEQ ID 405
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
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aacaatggcc tgatgacgtt caacgcgacg ctgggcggcg ataattcacc caccgataag 120
atgaacgtga aaggcgatac ccaagggaac actcgcgttc gggttgataa cattggcggc 180
gtcggtgcgc aaacggtcaa cggtattgaa ctcattgagg ttggcggtaa ttctgcaggt 240
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gggaagggga atgacgagaa aaactggtat ctgaccagta aatgggacgg cgtaacgcca 360
gcggatacac ccgatcccat caataatccc cctgttgtgg atccggaagg cccatcagtt 420
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ggccagctaa atactcaggc taaccgctat gtattgcagc taggcggcga tttggcgcag 660
tggagtagca acgcgcagga tcgctggcat cttggcgtga tggcaggcta cgccaatcag 720

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cgaaatctcg gtgaagtacg taccggggtt gaggcgaaag taaataacaa ccttagcctg 1320
tgggggaatg tcggtgtgca actaggtgat aaaggctata gcgatactca gggcatgctg 1380
ggagtgaaat atagctggta a 1401

<212> Type : DNA
<211> Length : 1401
SequenceName : SEQ ID 406
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
atgtcatatc tgaatttaag actttaccag cgaaacacac aatgcttgca tattcgtaag 60
catcgtttgg ctggtttttt tgtccggctc tttgtcgcct gtgcttttgc cgtacaggca 120
cctttgtcat ctgccgaact ctattttaat ccgcgctttt tagcggatga tccccaggct 180
gtggccgatt tatcgcgttt tgaaaatggg caagaattac cgccagggac gtatcgcgtc 240
gatatctatt tgaataatgg ttatatggca acgcgtgatg tcacatttaa tacgggcgac 300
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acggcttctg tcgccggtat gaatctgctg gcggatgatg cctgtgtgcc attaaccaca 420
atggtccagg acgctactgc gcatttagat gttggtcagc agcgactgaa cctgacgatc 480
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ggaaaagttc aggtgaaatg gggagaagag gaaaatgctc attgtgtcgc caattatcaa 2580
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<212> Type : DNA

<211> Length : 2637
SequenceName : SEQ ID 407
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
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ttaatgctat ggtgcgctca aaccgctgct tatagcgggc agtgtcatac cactcagggg 120
aatccgtata ttggcgtcaa ttttggcgtt aaaaccctgg aggaagaaga aaatacgact 180
ggggtagtaa aagacaaatt ttatcagtgg aacgaatcga atgattatta tgtttcctgt 240
gattgcgata aagacaatgt cagaagtggc cgatgggcat tcgccgcgga ttcaccgtta 300
gtctatttag gcgacaactg gtacaaaatt aatgactatc ttgccgccaa agttttattg 360
caggttaaag gcagttctcc tacagcggtt cctttcgaaa acgtggggac tggggcagat 420
acccggtggc atatttgtga ccccggcggt caacgtttag gcggccaggg agctagcggt 480
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cctatggcgc tggcgcgatt atttgaatgc tacaacatac ccgcaggtga ttcctgcacg 600
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tgttccgtca atgccggaga aacaatcgag gtcgatctgg gcgacgtatt tgcggctaac 720
tttcgtgttg tagggcataa gcctcttggg gccagaacgg cagaacttgc aattccagtc 780
aggtgtaaca cgggaaacgc ggggttagtt aacgtcaacc tgagtctgac ggcaaccaca 840
gaccccagct atccccaggc gattaagacg tcacgtcctg gcgtgggcgt ggtggtgacc 900
gatagccaga acaacattat ttcccctgct ggtggaacat taccgctctc tattcctgat 960
gatgcagaca gtatcgcgtg a 981
<212> Type : DNA
<211> Length : 981
SequenceName : SEQ ID 408
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
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gctctggccg ctgccacgac ggttaatggt gggaccgttc actttaaagg ggaagttgtt 120
aacgccgctt gcgcagttga tgcaggctct gttgatcaaa ccgttcagtt aggacaggtt 180
cgtaccgcat cgctggcaca ggacggagca accagttctg ctgtcggttt taacattcag 240
ctgaatgatt gcgataccaa tgttgcatct aaagccgctg ttgcctttt aggtacggtg 300
attgatgcgg gtcataccaa cgttctggct ctgcagagtt cagctgcggg tagcgcaaca 360
aacgttggtg tgcagatcct ggacagaacg ggtgctgcgc tgacgctgga tggtgcgaca 420
ttcagtgagc aaacaaccct gaataacggt actaacacca ttccgttcca ggcgcgttat 480
tatgcaatcg gcgaggcaac cccgggtgct gctaatgcgg atgcgacctt caaggttcag 540
tatcaataa 549
<212> Type : DNA
<211> Length : 549
SequenceName : SEQ ID 409
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
atgaaattaa aagtcatcgc tacactgatt gctactgttg ccgtgggtgt aagctttaac 60
agcaattttg cttctgcgag tacaacgtcc gcttctttaa ccgtaaacag taacctgact 120
atgggtacct gcagtgctca gataatggat aatagtaata aagtgatcaa tgaagtggtc 180
tttggcaatg tttatatttc tgaactcggt gcaaaaagca aagtgcaaca gtttaaaatt 240
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gctagcgcag caaccagaac ggctgtggaa gtatggacta cagatacacc ggaaagcaat 420
ggcagtacgc aattccattg tgctcaaaag ataccagtgc ctgtgacgct tcccgccgac 480
accacaactc agccttacga ttaccgttta agtgcacgga tgaccgttgc ggaaggtaga 540
ttggtaaccg atgtaagacc gggtaatttc cgctctccca cgactttcac gatcacttat 600
cagtaa 606
<212> Type : DNA
<211> Length : 606
SequenceName : SEQ ID 410

SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
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cagctggttt atgggaccgc caataatacg aaaatcaatc ctggcggaga acagcatatt 120
aaagaatttg gtataagtag taatactgaa attaacggcg ggtatcagta cattgaaatg 180
aatggcaccg cagaatactc agtattaaat gatggttatc aaattgttca aatgggtggc 240
gcggcaaacc agactacgct caataatggt gtgctacagg tttatggcgc agcgaatgat 300
cccacgatta aaggcgggcg cttaatcgtt gaaaaagatg ggattaccgt ccttgccgct 360
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gtggtgaaag ttgaccgttt tgccaacacc atccatggca agatgagtaa tggggcaaca 2040
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<212> Type : DNA
<211> Length : 2511
SequenceName : SEQ ID 411
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
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tatcacatga agataagctc tactcagctt agtctggcgt cacaaatggt cgaggttccg 180
acagaaatag ccgaagctac atgggatgta aatattcaac taagaggcga tgccataggg 240
tgtaaatctc ttggggatag taaggcagtt cactttctta atacagctga cccaagttta 300
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ctacctgcac aaagtggcgc agataacttc ataccaagca cccagacgaa atgggcctat 480
gagtacagtg atcaaagttg gtatttacgt tttcgcttat tcataactcc tgaatttaaa 540

cccaagaatg gtgtttccag cggaacaacg atagcaggaa agattgcgtc atggtatata 600
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aacgcgacct tctcctttac ctacgaataa 1110

<212> Type : DNA
<211> Length : 1110
SequenceName : SEQ ID 412
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli 0157:H7
<400> PreSequenceString :
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tgtgccctgt tttatagcag caacggtgct gcggcggaca ccgtggaata tgacagttcc 120
tttttaatgg gaactggcgc atcaacgatt gatgttaaac gttatgctca aggcaacccg 180
acaccgccgg gtctctataa tgtccgcgta tttgtaaacg gtcaggcgac ttccagctta 240
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gaagaagagg attgtctgga tctggcaaag tcatacgaaa aggcggatgt gtgctttgac 420
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gcggtagacg ttacccattc ccgtgctgaa attccggatg ataaaaccta ccaggggcaa 1320
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tgtcaggtag caaatcacta a 2601

<212> Type : DNA
<211> Length : 2601
SequenceName : SEQ ID 413
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
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gtgaatgcgg cgacggatct tggcccggca ggggatattc atttctccat cactatcacc 120
actaaagctt gcgagatgga aaaaagcgat ctcgaagtcg atatgggaac aatgacgctg 180
caaaaacctg cggcagtcgg tacggtgttg agcaagaaag atttcaccat tgaactcaaa 240
gagtgcgatg ggatatccaa agcgaccgtt gagatggaca gtcagtcgga cagcgatgat 300
gattccatgt ttgcccttga ggctggtggc gcaacgggtg ttgcgttgaa gatagaggac 360
gataaaggaa cgcagcaagt tcccaaaggc tccagcggaa cgccgattga atgggcgatt 420
gatggcgaaa ccacgtcgct tcactaccag gcgagttatg tggtcgtcaa cactcaggcc 480
actggtggca cagcgaatgc ccttgtaaat ttttccatca cctatgagta a 531

<212> Type : DNA
<211> Length : 531
SequenceName : SEQ ID 414
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
atgaaataca ataacattat tttcctcggt ttatgtctgg ggttaaccac ctattctgct 60
ttatccgcag atagcgttat taaaattagc gggcgcgtcc tcgattatgg ctgcacagtc 120
tcatcggatt cgcttaattt taccgtagat ctccaaaaaa acagtgccag acaatttcca 180
acgaccggta gcacaagtcc agccgtccct tttcagatta cgttaagtga atgcagcaaa 240
gggacaacgg gggttcgggt tgcatttaac ggtattgagg acgcagaaaa taatactctg 300
ttgaaactgg atgagggaag caatacggcc tccggtttag gtatagaaat actggacgga 360
aatatgcgtc cggtgaaact gaatgacctt catgccggga tgcagtggat cccactggta 420
ccagaacaga acaatatttt gccttactcc gctcgtctga agtcaactca gaagtccgtc 480
aatccgggac tggtgagggc ttcggcaacc tttacccttg aatttcaata a 531

<212> Type : DNA
<211> Length : 531
SequenceName : SEQ ID 415
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
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atacaggcag ccgatgtcac catcacggtg aacggtaagg tcgtcgccaa accgtgcaca 120
gtttccacca ccaatgccac ggttgatctc ggcgatcttt attctttcag tctgatgtct 180
gccggggcgg catcggcctg gcatgatgtt gcgcttgagt tgactaattg tccggtggga 240
acgtcaaggg tcactgccag cttcagcggg gcagccgaca gtaccggata ttataaaaac 300
caggggaccg cgcaaaacat ccagttagag ctacaggatg acagtggcaa cacattgaat 360
actggcgcaa ccaaaacagt tcaggtggat gattcctcac aatcagcgca cttcccgtta 420
caggtcagag cattgacggt aaatggcgga gccactcagg gaaccattca ggcagtgatt 480
agcatcacct atacctacag ctga 504

<212> Type : DNA
<211> Length : 504
SequenceName : SEQ ID 416
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
atgaaaagag cgcctcttat aacaggactt ttgttgatat ccacatcctg cgcttatgcc 60
tcctcagaag ggtgtggagc tgacagcact agcggtgcga caaattacag cagtgtggtt 120
gatgatgtta cggtgaacca gacagataac gtgacaggac gggagtttac ctctgcaacg 180
ctaagtagca ctaactggca atacgcctgt tcctgctctg cgggtaaggc agttaaactt 240
gtctatatgg tcagccccgt acttaccacc actggacatc agacaggata ttacaaactc 300
aatgacagcc tggatattaa aaccatgaac cgccccggaa atcctggaga ctaa 354

<212> Type : DNA
<211> Length : 354
SequenceName : SEQ ID 417
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli 0157:H7
<400> PreSequenceString :
atgaaaaaag cacttctcgc agccgctctg gttatggctt ctggttccgc cctggctgta 60
gatggtggtc atatcgactt taacggtatg gtacagtccg gtacctgtaa agtgggtgtg 120
gtagatactg gtatgcatag cgttaccact gatggcgtgg ttaccctgga tactgcgaat 180
gttactgata cttttgctga agttagcgca actgctgtcg gtttactgcc gaaagagttc 240
atgatttctg ttgagtgtga tccaggtgct ccgaagaatg ctgagttaac tatgggttct 300
gcaagttacg cgaacaccag cggtaccctg aataacaata tgaacatcac tgttaacggt 360
attgcaccgg ctcagaacgt aaacattgca gttcataaca tgaaaaacaa agctggcgct 420
gctgaaatta agcaggtcca tatgaacaac tcttctgaag ttcaggaact gacattagac 480
gcagaaggta aaggccagta cgtatttaac gcatcttacg ttaaagcacc gaacagcccg 540
gctgtaactg ctggtcatgt aaccactaac gcgctgtaca ccgttgctta taagtaa 597

<212> Type : DNA
<211> Length : 597
SequenceName : SEQ ID 418
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli 0157:H7
<400> PreSequenceString :
atgaaaccaa atatgattgt aggagcatta gcgttaactt ctgtgtttat ggcaggtcac 60
ctacaggcgg ctgatggaac agtccatttc cgtggtgaaa ttattgacag tacttgcgaa 120
gtcactcctg aaactaaaga tcaggtcgtt gatttaggca aagtaaaccg tacagccttt 180
agtggcgtcg atgatgtggc tgccccgacg gcttttttcta tcgatctgac tcaatgcccg 240
gaaaccttta agtccgccgc aattcgtttc gatggtaatg aagatgctca tggtaatggc 300
aacctggcaa ttggtacccc gctggataac tctaacgatg ctgccgctgg tattagcccg 360
agtgataaca gtggggatta tactggtgcg ggtgccgtta gtgcagcgaa aggcgtagct 420
attcgtttat ataaccgtgc agataacact caggtcaagt tatatgaaaa ttctgcatca 480
actccgattt ctaatggtaa tgcatccatg aagttcatgg ctcgttatat tgctacggaa 540
acgactattg accctggtac agctaacgcc gactcgcagt ttacagttga atatataaaa 600
taa 603

<212> Type : DNA
<211> Length : 603
SequenceName : SEQ ID 419
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli 0157:H7
<400> PreSequenceString :
gtgccaattt tccagcgtga aggccatctc aaatatagct ttgccgcagg tgaatatcag 60
gccgggaatt atgacagcgc ctcgccgcgt ttcgggcagc ttgatctgat ctacggttta 120
ccgtgggggа tgacggccta cggcggcgta ttaatctcta ataattacaa tgcatttaca 180
ttagggatag ggaaaaactt tggttatatc gggggcgattt ccattgatgt gacgcaggct 240
aaaagcgaac tgaataacga tcgcgatagc cagggacaat cttatcgttt cttatattcc 300
aagagcttcg aaagcggcac cgatttccgc cttgcgggct atcggtactc taccagcggt 360
ttctatacct tccaggaagc caccgatgtg cgcagtgacg ctgacagcga ctataaccgt 420
tatcacaagc gcagcgaaat acagggtaac ctgacgcagc aattaggggc ctatggctct 480
gtttatttaa atttaacgca gcaggattac tggaacgacg caggtaaaca gaacacggta 540
tcggcgggtt acaacggacg tattggcaag gtcagttaca gtattgcata tagctggaat 600
aaaagccctg aatgggatga aagcgatcgc ttgtggtctt tcaatatttc cgttccacta 660
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gttggggtca gcggaacgct gcttgaggat cgcaacctga gctacagtgt ccaggaaggc 780
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attagcggaa tgccagagga aggacgggta ttgattaaat ggggtaatga cgcgtcgcag 1380
caatgcgtgg cgccttataa attatccctg gaattaaaac agggcggaat tattcctgtt 1440
tcggccaatt gccagtaa 1458

<212> Type : DNA
<211> Length : 1458
SequenceName : SEQ ID 420
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
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gattatttta atctgttcta cagtaagcgt gatcaggaac aaataagcat ctctcagcag 120
cttggaaatt acggtgcgac atttttcagt gccagtcgcc aaagttactg gaacacgtca 180
cgcagcgacc agcaaatatc atttggatta aatgtgccgt ttggtgatat tacgacttcg 240
ctgaattaca gctattccaa taatatatgg caaaacgatc gggatcattt actcgctttt 300
acgcttaatg ttcccttcag tcattggatg cgtacagaca gtcagtcggc atttcgtaat 360
tcaaacgcca gttacagtat gtcaaacgat ttgaaaggcg gcatgaccaa tctatcgggg 420
gtttatggca ctctgctgcc ggataataac ctgaattata gcgttcaggt cggtaacacc 480
cacggaggta atacatcgtc tggcaccagt ggttacagta ctcttaatta tcgtggagct 540
tacggcaata ctaatgtcgg ttacagtcgg agtggtgaca gcagccagat ttattacgga 600
atgagtggtg ggattattgc tcatgctgat ggcatcacct ttggacagcc gctgggcgac 660
acaatggttc tggttaaggc tcctggcgct gataatgtca aaatagagaa ccagaccgga 720
attcataccg actggcgtgg ctatgccata ttaccatttg cgacagaata tagagaaaat 780
cgtgtcgctc ttaacgcgaa ttcccttgca gataatgttg aactggatga aaccgtggtc 840
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aaagtattaa tgacgttgaa gtacggtaat aaaagcgttc cattcggtgc aattgtcact 960
cacggagaga ataaaaatgg cagcattgtc gcggaaaacg gtcaggttta tctgactgga 1020
cttccacagt cagggaaatt acaggtttca tggggcaatg ataaaaactc aaactgtatt 1080
gtcgattaca agcttcctga agtctctcct ggaaccttgc tgaaccagca gacagcaatc 1140
tgtcgctaa 1149

<212> Type : DNA
<211> Length : 1149
SequenceName : SEQ ID 421
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
atgtctgctt tgtatgaacg ttcacagctg acgcaggtga tgatttcatc tgcccggcg 60
actgctgaaa ccatggagaa ggcggaatat ctgcgcctgg actgcaccat caaggaagtc 120
cagttcaccg ccggtcagaa acaggatatt gatgtgacca cgctctgctc cacagagcag 180
gagaacatca acggtctggg ggcgtcgtcc gagatttcca tgtcgggtaa tttttatctg 240
aatcaggccc agaacgccct gcgtgatgcc tatgacaatg acacggtgta tgcgtttaag 300
gtgcagtttc cgtccggtaa gggctttaag ttcctggcgg aagtgcgtca gcacacctgg 360
tcatccggta ccaacggcgt ggtggctgca acgttttcac ttcgcctgaa gggtaaaccg 420
gtgtcctatg tggtaccgct ggcgtttgtg aaaaatctgg ataagacact taccgtgaat 480
accggtgcgc tgctgacaat gtcagtcagt gtcaacgggg gaacgccgcc ttataaacac 540
gcctggaaga aggatggtca gccggtagag ggacagacta ctgacacttt cagtaagcca 600
ggtgcgcagt caggtgataa gggggcttat acctgcgagg taacggattc tgcagaacag 660
ccgcagagca ttacctctga tgcgtgtaca gtaacggtta atggtgcggg cggataa 717

<212> Type : DNA
<211> Length : 717
SequenceName : SEQ ID 422
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7

<400> PreSequenceString :
atgagaaaca aacctttta tcttctgtgc gctttttgt ggctggcagt gagtcacgct 60
ttggctgcgg atagcacgat tactatccgc ggctatgtca gagataacgg ctgtagtgtg 120
gccgctgaat caaccaattt tactgttgat ctgatggaaa acgcggcgaa gcaatttaac 180
aacattggcg cgacgactcc tgtcgttcca tttcgtattt tgctgtcacc ctgtggtaac 240
gccgtttctg ccgtaaaagt tgggtttacc ggcgttgcag atagccacaa tgccaacctg 300
cttgcacttg aaaatacggt gtcagcggct tcgggactgg gaatacagct tctgaatgag 360
cagcaaaatc agatacccct taatgctcca tcgtccgcga tttcgtggac gaccctgacg 420
ccgggtaaac caaatacgtt gaatttttac gcccggctaa tggcgacaca ggtgcctgtc 480
actgcggggc atatcaatgc cacggctacc ttcactcttg aatatcagta a 531

<212> Type : DNA
<211> Length : 531
SequenceName : SEQ ID 423
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
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atggggagcg aaatctcacc cgcaacaccg tcagatgaag acaactacac ctttgacccg 120
caactcttcc gcggcagcag atttagtcag tcgtcattag caaaactgac aacacgtgag 180
tctgttgcac cgggcaatta taaaatggat atctacacca acaataagtt gtcaggcagt 240
tggaatgtca cgtttaaaga agccgctgat ggtcgcgttc tgccctgcct gacgcctgaa 300
gtcgcggacg cgataggcct caaaacaggg gaagataagg gggaaaaaga tcctgtctgt 360
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aaaggccact tgtcagttcg ctggggtgaa ggtgctaacg atagctgcca attgcccttt 2460
gatatcagcg ggaaggacag caatagccct atcatccgcc tgaatgaaac ctgtcagtct 2520
tga 2523

<212> Type : DNA
<211> Length : 2523
SequenceName : SEQ ID 424
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
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acttctccgg ggttccctgc ctttagcgaa cagggaacgg gaacatttgt cagccacgcg 120
cagttgccca aaggtacgcg tccactcacg ctaaattttg accagcagtg ctggcagcct 180
gcagatgcga taaaactcaa tcagatgctt tccctgcaac cttgtagcaa cacgccgcct 240
caatggcgat tgttcaggga cggcaaatat acgctgcaaa tagaoacccg ctccggtacg 300
ccaacattga tgatttccat ccagaacgcc gccgaaccgg tagcaaacct ggtccgtgaa 360
tgcccgaaat gggatggatt accgctcacg ctggatgtca gcgccacttt cccggaagga 420
gccgccgtac gggattatta cagccagcaa attgcgatag tgaagaacgg tcaaataacg 480
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accggtgaag cctggggcca cggcgtgatg caaagtgact actatcgcca cggcttcgat 1560
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atggatacga cctggcagca aatggcggag aaattgcagg gtttcaacgt gttgagctac 1680
ctctcgtcgc atgatacccg tctgttccgt gaaggggcgg acaaagcagc agagttatta 1740
ctattagcgc caggcgcggt acaaatcttt tatggcgatg aatcctcgcg tccgttcggt 1800
cctacaggtt ctgatccgct gcaaggtaca cgttcggata tgaactggca ggatgttagc 1860
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cccgcaattg gcgcgggcaa acaaacgaca ctttcgctga agcagggcta cggctttgtt 1980
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<212> Type : DNA
<211> Length : 2031
SequenceName : SEQ ID 425
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
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aaacgctgtt tgccgatggt gctcactggc agcggcatgc tttgcactac cgctaacgcc 120
gaagagtatt atttcgaccc cattatgctg gaaaccacaa aaagtggtat gcaaacaacc 180
gatctgtcac gtttttcaaa aaaatacgca caactaccag gaacttatca ggttgatatc 240
tggctgaata aaaagaaggt ttcacagaaa aaaattacat ttaccgccaa tgcagagcaa 300
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cccggtacag ctgctgaatt tgatttcaat catcagcgac ttaatttgag cattccccaa 480
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ccaacgctgt ttaccaacta ctcgtttaca ggttctgata accgttaccg ccagggcaat 600
cgtagccaac gacagtacct aaatatgcaa aatggtgcca attttggccc ctggcgatta 660
cgtaactatt ctacgtggac acgcaacgat caggcgtcaa gctggaacac tatcagtagt 720
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agcggcagta ttttttccag ctacaacttt actggcgtgc aactcgcttc cgacgataat 840
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gcctttgaaa ttaacgatct ctacccctct tccaacagcg gcgatttaga agtcacgatt 1020
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cagcgacctg ggcatctaaa atatagcgcg accgctggac gctatcgcgc tgatgcaaac 1140
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caattcaaca tcagccagac aatatttgat ggggtaagtc tgtatgcctc cggttcacag 1560
caagactatt ggggcaataa cgagaaaaac aggaatatct ctgttggggt ttccggccag 1620
caatggggaa ttggttacag cctgaattat caatacagcc gctacactga tcaaaataat 1680
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caacaaagta tcgtcgatga gggcggcata ctatatctct ctgggatatc gagtaaatca 2400
caaagctgga ctgtacgctg gggaaatcag gcagatcaac aatgtcagtt tgcttttagt 2460
acaccggatt cagaaccaac aacctctgta ttacaaggca cagcgcagtg ccattaa 2517

<212> Type : DNA
<211> Length : 2517
SequenceName : SEQ ID 426
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
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gggtgtcgta ctactgcatc attaaatatt acagatggta ttaatgttgg ggagatttta 120
gcgaatgaaa cttcctttag taaaagtgtc gtgtttactg ggatatcttg tgatacgagc 180
acggataaaa tagtttataa aaatatccaa agtgattggg ttgaagttgg gccttttggt 240
aatggcgaaa aattaaaggt taaaatagag tctttaggta aaaccagcga cacaattggg 300
aaatccagca atgcgcaggc agtattacct tatgtggtta aaatagccag aggcacacct 360
gattttactg gagaaagaaa atctacctgg tttatttcag ataccgtgat tgcaaatatt 420
ggcggtgagt catcgtcatc catcgatttt tggttgggta tttgtaaggc attgaagttt 480
aactggtgtg tgaattatct caccagcaaa ctggcggggg atacatttac gcttgggtta 540
aatatttcct attatcctaa aaatacgacc tgtaagcctg aaaacaccgt tataaaagta 600
gatgatatcg ccttgttcca gctcagaaat cagggaaaga ttgcggcgaa cagtaaggaa 660
ggaacaatta cgttgaaatg tgataatctt ttcggcgaca aaaaacaagc atcgcggaat 720
atggttgtat atcttttctag cagtgactta gttaaaggaa gtaatactat tttgcgtggt 780
aaaacagata atggtgtagg gtttgtgttg gatctaacag aaccaccaaa agggactgag 840
gctgccatta aaatttcggc caacggcgat cagggcgcgg cgacatcatt atggaaaaca 900
gataaaccag gagtttcatt aaatagcaac attattaata taccagtcat ggccagttac 960
tatgtatatg atgaaaaaaa agttaaatct ggcgcactgg aagcaaccgc attaatcaac 1020
gtgaaatacg attaa 1035

<212> Type : DNA
<211> Length : 1035
SequenceName : SEQ ID 427
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
atgattaaaa aagcttcgct gctgacggcg tgttctgtca cagcctttc cgcttgggca 60
caggatacca gcccggatac tctcgtcgtt actgctaacc gttttgaaca gcgcgcagc 120
actgtgcttg caccaaccac cgttgtgacg cgtcaggata tcgaccgctg gcagtcgacc 180
tcggttaatg atgtgctgcg ccgtcttccg ggcgtcgata tcacccaaaa cggcggttca 240
ggtcagctct catctatttt tattcgcggt acaaatgcca gtcatgtgtt ggtgttaatt 300
gatggcgtac gcctgaatct ggcgggggggg agtggttctg ccgaccttag ccagttccct 360

attgcgcttg tccagcgtgt tgaatatatc cgtgggccac gctccgccgt ttatggttcc 420
gatgcaatag gtggggtggt gaatatcatc acgacgcgcg atgaacccgg aacggaaatt 480
tcagcagggt ggggaagcaa tagttatcaa aactatgatg tctctacaca gcaacaactg 540
ggggataaga cacgagtaac gttgttgggc gattatgccc atactcatgg ttatgatgtt 600
gttgcctatg gtaataccgg aacgcaagcg cagccagata acgatggttt tttaagtaaa 660
acgctttatg gcgcgctgga gcataacttt actgatgcct ggagcggctt tgtgcgcggc 720
tatggctatg ataaccgtac caattatgac gcgtattatt ctccgggttc accattggtc 780
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attaaatcac aactcattac cagctatagc catagcaaag attacaacta cgatccccat 900
tatggtcgtt atgattcgtc ggcgacgctc gatgagatga agcaatacac cgtccagtgg 960
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agcacggcac cgggcacagc ttatgttaag gatggatatg atcaacgtaa taccggcatc 1080
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gaaggttatc gcttcattgc ttcctacggg acatcttata aggcaccaaa tctggggcaa 1260
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agtgacttga tcgattatga tgatcacacc ctgaaatatt acaacgaagg gaaagcgcgg 1440
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tatgattatg tcgatgcgcg caatgcaatt accgacacgc cgttgttacg ccgtgctaaa 1560
cagcaggtga aataccagct cgactggcag ttgtatgact tcgactgggg tattacttat 1620
cagtatttag gcactcgcta tgataaggat tactcatctt atccttatca aaccgttaaa 1680
atgggcggtg tgagcttgtg ggatcttgcg gttgcgtatc cggtcacctc tcacctgaca 1740
gttcgtggta aaatagccaa cctgttcgac aaagattatg agacagtcta tggctaccaa 1800
actgcaggac gggaatacac cttgtctggc agctacacct tctga 1845

<212> Type : DNA
<211> Length : 1845
SequenceName : SEQ ID 428
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
atgaaaaaca aattgttatt tatgatgtta acaatactgg gtgcgcctgg gattgcagcc 60
gcagcaggtt atgatttagc taattcagaa tataacttcg cggtaaatga attgagtaag 120
tcttcattta atcaggcagc cataattggt caagctggga ctaataatag tgctcagtta 180
cggcagggag gctcaaaact tttggcggtt gttgcgcaag aaggtagtag caaccgggca 240
aagattgacc agacaggaga ttataacctt gcatatattg atcaggcggg cagtgccaat 300
gatgccagta tttcgcaagg tgcttatggt aatactgcga tgattatcca gaaaggttct 360
ggtaataaag caaatattac acagtatggt actcaaaaaa cggcaattgt agtgcagaga 420
cagtcgcaaa tggctattcg cgtgacacaa cgttaa 456

<212> Type : DNA
<211> Length : 456
SequenceName : SEQ ID 429
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
atgaacattt ttgcatattt actggtactt gtattttcca tgagcatgag cagcagcgcg 60
tttgccagcg tggtaatgac cggaacccgt attattttcc ctggtgacgc aaaggaaaaa 120
accatccagt tgcgaaatac cagcgatcag ccctatatca ttaatatcca tgttgaggat 180
gaacgtggtt ctgacaagaa tgtaccgttt atgccaaccc cgcagacatt tcgcatggaa 240
gctgccgcag gtcaggcgtt acgcctgctc tacactggta ataatttacc gcaggatcgc 300
gagtctgttt tctggtttag tttcagtcaa ctaccttatc tgaataagaa tgataaaagt 360
cagaaccagc tcatcctggc cctgactaat cgagtcaaaa ttttctatcg tcccagctcg 420
attgtcggta aatccagtga cgcacccaaa aacctgactt accaggtaaa acagaaccgc 480
attgaagtga cgaatcccac gggctattac gtcacaattc gcgccgctga actgcttaat 540
aatggtaaaa aagtccccct cgcgaattcg gtaatgattg ctcctcaaag cacaactgaa 600
tggacactac cctctggcat cagtgtcgct cccggtgcgc agatccattt agtgaccgtc 660
aacgactatg gcgtaaatgt tacgtctgag catgccttat aa 702

<212> Type : DNA
<211> Length : 702
SequenceName : SEQ ID 430
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
atgaaaagac ttcacaagag gttcctctta gctacgtttt gcgcgttatt aacagcaact 60
ctccaggccg ccgatgtcac tatcactgtt aatggtcggg tagtcgctaa accctgcact 120
attcaaacca aagaagctaa cgttaatctc ggggatcttt atacgcgcaa tctgcaacaa 180
cctggttctg catctggctg gcacaatatt actttgtcat taaccgattg tccggctgaa 240
acaagtgcag tgacggcaat cgtgacaggt tcaactgaca atacgggtta ttacaaaaat 300
gaaggtactg ccgaaaatat tcagatagag cttagggatg accaggatgc gacgttaaaa 360
aatggcgata gcaaaacggt tattgttgat gagatcactc gtaatgcaca gtttccactt 420
aaggcaagag ctatcacggt gaatggaaac gcaagccagg gaacgatcga ggcgctaatc 480
aatgtgatct acacctggca ataa 504
<212> Type : DNA
<211> Length : 504
SequenceName : SEQ ID 431
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
atgcgggcga aacttctggg aatagtcctg acaaccccta ttgcgatcag ctcttttgct 60
tctaccgaga ctttatcgtt tactcctgac aacataaatg cggacattag tcttggaact 120
ctgagcggaa aaacaaaaga gcgtgtttat ctagccgaag aaggaggccg aaaagtcagt 180
caactcgact ggaaattcaa taacgctgca attattaaag gtgcaattaa ttgggatttg 240
atgccccaga tatctatcgg ggctgctggc tggacaactc tcggcagccg aggtggcaat 300
atggtcgatc aggactggat ggattccagt aaccccggaa cctggacgga tgaaagtaga 360
caccctgata cacaactcaa ttatgccaac gaatttgatc tgaatatcaa aggctggctc 420
ctcaacgaac ccaattaccg cctgggactc atggccggat atcaggaaag ccgttatagc 480
tttacagcca gaggtggttc ctatatctac agttctgagg agggattcag agatgatatc 540
ggctccttcc cgaatggaga aagagcaatc ggctacaaac aacgttttaa aatgccctac 600
attggcttga ctggaagtta tcgttatgaa gattttgagc taggtggcac atttaaatac 660
agcggctggg tggaagcatc tgataacgat gagcactatg acccaggaaa aagaatcact 720
tatcgcagta aagtcaaaga ccaaaattac tattctgttt cagtcaatgc aggttattac 780
gtaacaccta acgcaaaagt ttatgttgaa ggcacatgga atcgggttac gaataaaaaa 840
ggtaatactt cactttatga tcacaatgat aacacttcag actacagcaa aaatggtgca 900
ggcatagaaa actataactt catcactact gctggtctta agtacacctt ttaa 954
<212> Type : DNA
<211> Length : 954
SequenceName : SEQ ID 432
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
ttgtttttta agcgaggaaa gattttgagt gcgggacgcc tgaataaaaa atctctgggt 60
atcgtgatgt tgttatcggt tggactgctt ttggcgggct gttcgggtag caaatcatcc 120
gatacaggaa cgtattccgg ctccgtttac accgtgaaac gggggggatac gctatatcgt 180
atttcgcgca ccacgggaac cagcgtaaaa gagctggcgc gactgaacgg catttccccc 240
ccttacacca ttgaagttgg tcagaaacta aaactgggtg gggcgaaaag tagcagtagt 300
acacgtaaat caaccgccaa atcaacgacc aaaaccgcat cggttacacc gtcatcagcg 360
gtaccgaaat cttcctggcc gccagtaggg caacgttgtt ggttatggcc aacgacaggg 420
aaagttatca tgccgtattc gacagcagat ggcggcaata aagggattga tatctcagct 480
ccacggggta cacctattta cgccgcgggt gcaggaaagg tggtgtatgt gggcaaccag 540
ctgcgtggct acggtaatct catcatgatt aaacacagtg aagattacat tacggcttac 600
gcccataatg acacgatgct ggtaaataat gggcaaagcg tgaaggctgg gcaaaaaatc 660
gccaccatgg ggagcacgga tgcggcatct gttcgcctgc atttccagat tcgttaccgt 720
gcaacggcaa ttgatccgct acgttacttg ccgcctcagg gcagcaagcc aaaatgctga 780
<212> Type : DNA
<211> Length : 780
SequenceName : SEQ ID 433
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
atgccaacac caaatcctct ggcaccggtg aaaggggccg ggaccacact gtgggtttat 60
aacgggaacg gcgacccata tgcaaacccg ctttcagaca atgactggtc gcgtctggca 120
aaggttaaag acctgacgcc cggcgaactg accgctgagt cctatgacga cagttatctc 180
gatgatgaag atgcggactg ggccgcgacc ggacaggggc agaaatccgc tggagatacc 240
agcttcacgc tggcgtggat gcccggagag caggggcagc aggcgctgct ggcgtggttt 300
aatgaaggtg atacccgtgc ctataaaatc cgcttcccga acggcacggt cgatgtgttc 360
cgcggctggg tcagcagtat cggtaaggcg gtgacggcga aggaagtgat cacccgcacg 420
gtgaaagtca ccaacgtggg acgtccgtcg atggcagaag atcgcagcac ggtaacagcg 480
gcaaccggca tgaccgtgac gcctgccagc acctcggtgg tgaaagggca gaggacgacg 540
ctgaccgtgg cattccagcc ggaaggcgca accgacaaga gcttccgtgc ggtgtctgcg 600
gataaaacaa aagccaccgt gtcggtcagt ggtatgacca tcaccgtgaa aggtgttgct 660
gcaggcaagg tcaacattcc ggtcgtatcc ggtaatggtg agtttgctgc ggttgcagaa 720
atcaacgtca ccgccagtta a 741
<212> Type : DNA
<211> Length : 741
SequenceName : SEQ ID 434
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
atgtctgctt tgtatgaacg ctcacagctg acgcaggtga tgatttcatc tgccccggcg 60
actgctgaaa ctatggataa ggcggaatat ctgcgcctgg actgcaccat caaggaagtg 120
cagttcaccg ccgggcagaa acaggatatt gatgtgacca cgctctgctc cacagagcag 180
gagaacatca atggtctggg ggcgtcgtct gagatttcca tgtcgggcaa tttttatctg 240
aatcaggccc agaacgccct gcgtgatgcc tatgacaatg acgcgttgta tgcgtttaag 300
gtgctgtttc cgtccggtaa gggctttaaa ttcctggcgg aagtgcgcca gcacacctgg 360
tcatccggta ccaacggcgt ggtggctgca acgttctcac tgcgtctgaa aggcaaaccg 420
gtgtcctttg tggtaccgct ggcgtttgtg aaaaatctgg ataagacact taccgtgaat 480
accggtgcgc tgctgacaat gtcagtcagt gccaacgggg gaacgccgcc gtataaatac 540
gcctggaaga aggatggtca gccggttgac gggcagacga cagacacctt cagtaagcca 600
ggtgcgcagt ccgctgatgc ggggaaatat acctgtgtgg tgaccgattc ggcagagaaa 660
gcacagagtg tgacgtctgt tgaatgcacc gtgacagtga gcgcagccgc cggataa 717

<212> Type : DNA
<211> Length : 717
SequenceName : SEQ ID 435
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
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gccgcagaaa tatataacaa agacggtaat aaactggatg tctatggcaa agttaaagcc 120
atgcattata tgagtgataa cgacagtaaa gatggcgacc agagttatat ccgttttggt 180
tttaaaggcg aaacacaaat taacgatcaa ctgactggtt atggtcgttg ggaagcggag 240
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ggattgaagt ataaagattt gggttctttc gactatggcc gtaacctggg cgcgttgtat 360
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gacaacttta tgaccaaacg cgccagcggt ctggcgacgt atcggaacac cgacttcttc 480
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gttaaaaagc aaaacggcga tggcttcggc acgtcattga catatgactt tggcggcagc 600
gatttcgcca ttagtggggc ctataccaac tcagatcgca ccaacgagca gaacctgcaa 660
agccgtggca caggcaagcg tgcagaagct tgggctacag gtctgaaata cgatgccaat 720
aatatttatc tggcaacttt ttattctgaa acacgcaaaa tgacgccaat aactggcggc 780
tttgccaata agacacagaa ctttgaagcg gtcgctcaat accagtttga ctttggtctg 840
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gatctggtca attatatcga tgtcgggggt acatattatt tcaacaaaaa tatgtcagcg 960
tttgttgatt ataaaatcaa ccaactggat agcgataaca aattgaatat taataatgat 1020
gatattgtcg cggttggcat gacctatcag ttttaa 1056

<212> Type : DNA
<211> Length : 1056
SequenceName : SEQ ID 436
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
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accatgactt tccagttccg taatccaaac tttggtggta acccaaataa tggcgctttt 120
ttattaaata gcgctcaggc ccaaaactct tataaagatc cgagctataa cgatgacttt 180
ggtattgaaa caccctcagc gttagataac tttactcagg ccatccagtc acaaatttta 240
ggtgggctac tgtcgaatat taataccggt aaaccgggcc gcatggtgac caacgattat 300
attgttgata ttgctaaccg cgatggtcaa ttgcagttga acgtgacaga tcgtaaaacc 360
ggacaaacct cgaccatcca ggtttcgggt ttacaaaata actcaaccga tttttaa 417

<212> Type : DNA
<211> Length : 417
SequenceName : SEQ ID 437
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
atgaaaagaa aagttctggc aatgctggtc ccggcgttat tagttgctgg cgcagcaaat 60
gcggctgaaa tttataataa agatggcaat aaactggatt tgtacggaaa agtagcgggc 120
ctgcactact tctctgatga tgctagcagc gatggcgaca tgtcatatgc ccgtatcggt 180
ttcaaaggtg aaactcagat cgctgaccaa ttcactggtt atggtcagtg ggaatttaac 240
attggcgcaa acggtcctga aagcgacaag ggtaataccg caacgcgtct ggcatttgca 300
ggtttcggct ttggtcagaa tggtactttc gactatggtc gtaactacgg tgtcgtatat 360
gacgtagaag catggaccga tatgctgcca gaatttggtg gagataccta tgctggcgct 420
gacaacttca tgaacggtcg tgctaacagc gtagcaacct atcgtaacaa tggtttcttt 480
ggtcaagttg atggtctgaa ctttgcactc cagtatcagg gtaacaacga gaaaagcgga 540
ttatttgatc aagaaggttc aggtaacggt aatggacgta aacttgctaa agagaacggc 600
gacggttcag tatgtccact tcctatgact ttgactttgg tttaa 645
<212> Type : DNA
<211> Length : 645
SequenceName : SEQ ID 438
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
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gtaaaaattg agaaaaacag caacgcggta attaataaca ccggttccct gtcaacttta 120
caacttcacg atggtacggt gaataacagc ggtattgcgt cggcgcgcgt taacgctcag 180
ggcgatgcgg tattcaataa ccttgcaggc ggcgaggcgc gtaaaggcgc gattctctat 240
aactctgcgg tagtgaataa cgcgggtacc tggaaaatgg gttatcagga tgaaaacaac 300
aatgccggga cgctggatat tgacgataag tcaacgttca acaacagcgg caaactcatc 360
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aacaccggtg aaatgacgct ggatgccgca ttaggtgcgg gcgctattct ctacgacgat 480
ggcgccagcg agtttattaa caagggcgtg gtggatgcga aagtcaccgt ggcggtaagt 540
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gatggtgtaa tgaacatcag cggcaacaac gccgtggcga tggaaggcga taaaaacgca 720
cagctggtta acaacggcgt tatcaatctc ggtaccgaag gcaccaccga taccggattg 780
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ggcgacagcg tgaatgtgga aggggtgaac ggcaacagcg gtaacaatac cgaagtgcat 1020
tacaccgact acacgttgcc ggacatgcca aacacttaca ccacttcacc tttcagtgaa 1080
acgactgata gcggtagtag cgatggcagc agtaacaacc tcaacggcta tatcgtcggt 1140
accaacgttg acggcagcgc cggtaaactg aaggtcaaca acgccagcat gaatggtgtc 1200
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gtggaaggca tcaacctgac cgacgccgat gccatcacct caacgtccgt ggtatggacc 1320
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ctgaagcagg tgagcggtag ccaggcgacc acggtattcc gtgaagcgcg tgtgttaagc 1560
aaccgcttca gcatgctggc ggatgccgcg ccgaaggtgg gcaatggcct ggcctttaac 1620
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aagggcggcg gtatcaacag cctggcgagc gtcggcgtga agtacagtag caaagaaagt 2340
tcgctgaatc tggatgcgta tcactggaaa gaggacggca tcagcgacaa aggcgtgatg 2400
ctgaacttta agaaaacgtt ctaa 2424

<212> Type : DNA
<211> Length : 2424
SequenceName : SEQ ID 439
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
atgcttaatg gaattagtaa cgctgcttct acactagggc ggcagcttgt aggtatcgca 60
agtcgagtga gctctgcggg gggaactgga ttttctgtag cccctcaggc cgtgcgtctt 120
actccggtga aagttcattc ccctttttct ccaggctcgt cgaatgttaa tgcgagaacg 180
atttttaatg tgagcagcca ggtgacttca tttactccct ctcgtccggc accgccgcca 240
ccgacaagtg gacaggcatc cggggcatcc cgacctttac cgcccattgc acaggcatta 300
aaagagcact tggctgccta tgaaaaatcg aaaggtcctg aggctttagg ttttaagccc 360
gcccgtcagg caccgccgcc accgacaagt ggacaggcat ccggggcatc ccgacctttа 420
ccgcccattg cacaggcatt aaaagagcac ttggctgcct atgaaaaatc gaaaggtcct 480
gaggctttag gttttaagcc cgcccgtcag gcaccgccgc caccgacaag tggacaggca 540
tccggggcat cccgaccttt accgcccatt gcacaggcat taaaagagca cttggctgcc 600
tatgaaaaat cgaaaggtcc tgaggcttta ggttttaagc ccgcccgtca ggcaccaccg 660
ccaccgacag ggcctagtgg actaccgccc cttgcacagg cattaaaaga tcatttagct 720
gcctatgagc aatcgaagaa agggtaa 747

<212> Type : DNA
<211> Length : 747
SequenceName : SEQ ID 440
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
atgaacaaga agattcattc cctggccttg ttggtcaatc tggggattta tggggtagcg 60
caggcacaag agccgaccga tactcctgtt tcacatgacg atactattgt cgttaccgcc 120
gccgagcaga acttacaggc gcctggcgtt tcgaccatca ccgcagatga aatccgcaaa 180
aaccccgttg cccgcgatgt ttcggagatc atccgtacca tgccaggcgt taacctgacc 240
ggtaactcca ccagtggtca gcgagggaat aaccgacaga ttgatattcg cggtatgggt 300
ccggaaaaca cgctgatttt gattgacggc aagccggtaa gcagccgtaa ctcggtgcgt 360
cagggctggc gtggcgagcg cgatacccgt ggtgatacct cctgggtgcc acctgaaatg 420
attgaacgta ttgaagttct gcgtggtccg gcagctgcgc gttatggcaa cggcgcggcg 480
ggcggcgtgg ttaacatcat taccaaaaaa ggcagcggcg agtggcacgg ctcctgggac 540
gcatatttca atgcgccaga acataaagag gaaggtgcca ccaaacgcac taactttagc 600
ctgaccggtc cgctgggcga cgaattcagc ttccgcttgt atggcaacct cgacaaaacc 660
caggctgacg cgtgggatat caaccagggt catcagtccg cgcgtgccgg aacgtatgcc 720
acgacgttac cagccgggcg cgaaggggtg atcaataaag atattaatgg cgtggtgcgc 780
tgggacttcg caccattgca atcgctggaa ctggaagcgg gttacagccg ccagggtaac 840
ctgtatgcgg gcgataccca gaacaccaac tctgacgctt acactcgctc gaaatatggc 900
gatgaaacca accgcctgta tcgccagaac tactcgctga cctggaacgg tggctgggat 960

aacggcgtga ccaccagcaa ctgggtgcag tacgaacaca cccgtaactc gcgtattccg 1020
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gacggctggc tggcgggcat cacctggttc cgtaacgatt atcgcaataa gattgaagca 1680
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ttgtcgatca tcccggagta tacgttgaac tcaacgctga gctggcaggc acgagaagat 1920
ttgtcgatgc aaacgacctt cacctggtac ggtaagcagc agccgaagaa gtacaactat 1980
aaaggtcagc cagcggttgg accggaaacc aaagaaatta gtccttacag cattgttggg 2040
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ttcgacaaac gtttgtggcg tgcgggtaat gcccagacca cgggcgattt ggcaggggcc 2160
aactatatcg ccggtgccgg ggcgtatacc tataacgagc cgggacgtac gtggtatatg 2220
agcgtaaaca ctcacttctg a 2241

<212> Type : DNA
<211> Length : 2241
SequenceName : SEQ ID 441
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
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ttggcaggtt gttcttcagt aggcaaccag tcattgaaaa atgagacgca ggaaagtgtg 120
aaaaccaaaa ttgttaaagg caaaactaca aaacaggacg tgttagcatc gttcggtgaa 180
cctgacagcc gttctttgat cgatggtgaa gaacaatggt catacactat gtataacagc 240
cagtccaaag caacctcttt catccccgtt gtgggactgc ttgcaggtgg cgcagactca 300
caaactaaat ctctgacagt ttctttcaaa ggcgaaaaag tcagcacata catctttaat 360
gctggaacaa gcaacgtgaa gactggcatt ttttag 396

<212> Type : DNA
<211> Length : 396
SequenceName : SEQ ID 442
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
atgaaaaaaa ttgcatgtct ttcagcactg gccgcagttc tggctttcac cgcaggtact 60
tccgtagctg cgacttctac cgtaactggc ggttacgcac agagcgacgc tcagggccaa 120
atgaacaaaa tgggcggttt caacctgaaa taccgctatg aagaagacaa cagcccgctg 180
ggtgtgatcg gttcattcac ttacaccgag aaaagccgta ctgcaagctc tggtgactac 240
aacaaaaacc agtactacgg catcactgct ggtccggctt accgcattaa cgactgggca 300
agcatctacg gtgtagtggg tgtgggttat ggtaaattcc agaccactga ataccgacc 360
tacaaacacg acaccagcga ctacggtttc tcctacggtg ctggtctgca gttcaacccg 420
atggaaaacg ttgctctgga cttctcttac gagcagagcc gtattcgtag cgttgacgta 480
ggcacctgga ttgccggtgt tggttaccgc ttctaa 516

<212> Type : DNA
<211> Length : 516
SequenceName : SEQ ID 443
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
atgaagagta tagcaacact ggttgtgtgt gcaatctccg ggattgcctg tgtaaattta 60
tctgcacatg cagcagaagg agagcataca atttctctgg ggtatgcgca ctttcagttt 120

ccgggactga aggattttgt aaaggatgcg actgctcata acagggagac tttcagtcat 180
ttcgtcaaca gaaactactt ttcttcattg ggcgaatata cagatggtcg ggtcagtgga 240
tatgaaggca aggataaaaa tccacagggc attaatatca ggtatcgcta cgagataacg 300
gatgattttg gcgttatcac ctcttttaca tggacgcgtt ctctcactaa ctcacagaca 360
tttattgatg tgcagtcagc cgatcatacc aggaagatta agaatccggc agcttctgcc 420
agaacggata tcagggcgaa ttactggagt ctgttagcgg ggccttcatg gcgggttaat 480
cagtacatga gtttatatgc gatggcaggg atgggcgttg ctaaagttag cgctgacctg 540
aaaattaagg acaatattaa cagtagtggc ggattttctg aaagcaacag cacgaaaaaa 600
acctcccttg cgtgggctgc aggtgcacag tttaacctga atgagagtgt tacactggat 660
gtggcttacg aaggttccgg ctctggcgac tggcgcacga gtggcgttac tgctggcatt 720
ggcctgaaat tctga 735

<212> Type : DNA
<211> Length : 735
SequenceName : SEQ ID 444
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
atgcgtaaac tttatgccgc cattttgtcc gcagccattt gtctgaccgt atccggtgcg 60
cctgcatggg cgtctgagca gcaggccacg ctgagcgcgg ggtatcttca tgtctcgacg 120
aacgctcccg gtagcgataa tcttaacggg attaacgtga aataccgtta tgaattcacg 180
gacacgctgg ggctggtgac gtcattcagc tatgcaggag acaggaatcg ccagattacc 240
cgttacagcg atacccgctg gcatgaagat tccgtgcgta accgctggtt cagcgtaatg 300
gcggggccgt ctgtgcgcgt gaatgaatgg ttcagcgcgt atgcgatggc gggagtggct 360
tacagccgtg tgtcgacttt ctccggggat tatcttcgcg taactgacaa caaggggaaa 420
acgcacgatg tgctgaccgg aagtgatgac ggtcgccaca gcaacacgtc tctggcgtgg 480
ggggctggcg tgcagtttaa cccgaccgaa tccgtggcca ttgatattgc ttatgaaggc 540
tccggcagtg gcgactggcg cactgacggt ttcatcgtgg gtgtcggtta taagttctga 600

<212> Type : DNA
<211> Length : 600
SequenceName : SEQ ID 445
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
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cctgcatggg cgtctgagca gcaggccacg ctgagcgcgg ggtatcttca tgcccggacg 120
agcgctcccg gtagcgataa tcttaacggg attaacgtga aataccgtta tgaatttacg 180
gacacgctgg ggctggtgac gtcattcagc tatgcaggag acaagaatcg ccagcttacc 240
cgttacagcg atacccgctg gcatgaagat tccgtgcgta accgctggtt cagcgtaatg 300
gcggggccgt ctgtgcgcgt gaatgaatgg ttcagcgcgt atgcgatggc gggtgtggct 360
tacagccgtg tgtcgacttt ctccggggat tatcttcgcg taactgacaa caaggggaaa 420
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ggggctggcg tgcagtttaa cccgaccgaa tccgtggcca ttgatattgc ttatgaaggc 540
tccggcagtg gcgactggcg cactgacggt ttcatcgtgg gtgtcggtta taagttctga 600

<212> Type : DNA
<211> Length : 600
SequenceName : SEQ ID 446
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
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cctgcatggg cgtctgagca gcaggccacg ctgagcgcgg ggtatcttca tgcccggacg 120
agcgctcccg gtagcgataa tcttaacggg attaacgtga aataccgtta tgaatttacg 180
gacacgctgg ggctggtgac gtcattcagc tatgcaggag acaagaatcg ccagcttacc 240
cgttacagcg atacccgctg gcatgaagat tccgtgcgta accgctggtt cagcgtaatg 300
gcggggccgt ctgtgcgcgt gaatgaatgg ttcagcgcgt atgcgatggc gggtgtggct 360
tacagccgtg tgtcgacttt ctccggggat tatcttcgcg taactgacaa caaggggaaa 420

acgcacgatg tgctgaccgg aagtgatgac ggtcgccaca gcaacacgtc tctggcgtgg 480
ggggctggcg tgcagtttaa cccgaccgaa tccgtggcca ttgatattgc ttatgaaggc 540
tccggcagtg gcgactggcg cactgacggt ttcatcgtgg gtgtcggtta taagttctga 600

<212> Type : DNA
<211> Length : 600
SequenceName : SEQ ID 447
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
atgcgtaaac tttatgccgc cattttgtcc gcagccatct gtctggccgt atccggcgcg 60
cctgcatggg cgtctgagca gcaggccacg ctgagcgcgg ggtatcttca tgcccggacg 120
agcgctcccg gtagcgataa tcttaacggg attaacgtga aataccgtta tgaatttacg 180
gacacgctgg ggctggtgac gtcattcagc tatgcaggag acaagaatcg ccagcttacc 240
cgttacagcg ataccgctg gcatgaagat tccgttcgta accgctggtt cagcgtaatg 300
gcggggccgt ctgtgcgcgt gaatgaatgg ttcagcgcgt atgcgatggc gggtgtggct 360
tacagccgtg tgtcgacttt ctccggggat tatcttcgcg taactgacaa caaggggaaa 420
acgcacgatg tgctgaccgg aagtgatgac ggtcgccaca gcaacacgtc tctggcgtgg 480
ggggctggcg tgcagtttaa cccgaccgaa tccgtggcca ttgatattgc ttatgaaggc 540
tccggcagtg gcgactggcg cactgacggt ttcatcgtgg gtgtcggtta taagttctga 600

<212> Type : DNA
<211> Length : 600
SequenceName : SEQ ID 448
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
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atctccaccc aggcctggtc ggcaggcttt cagttaaacg aattttcttc ctctggcctg 120
ggccgggctt attcagggga aggcgcaatt gccgatgatg caggtaacgt cagccgtaac 180
cccgcattga ttaccatgtt tgaccgcccg acattttctg cgggtgcggt ttatattgac 240
ccggatgtaa atatcagcgg aacgtctcca tctggtcgta gcctgaaagc cgataacatc 300
gcgcctacgg catgggttcc gaacatgcac tttgttgcac cgattaacga ccaatttggt 360
tggggcgctt ctattacctc taactatggc ctggcaacag agtttaacga tacttatgca 420
ggcggctctg tcggggtac aaccgacctt gaaaccatga acctgaactt aagcggtgcg 480
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acttacgcgt ttaataaaga tgcttcagtc gacgttggtg tttcttatat gcacggtcag 1260
agcgtgaaaa ttaacgaagg cccataccag ttcgagtctg aaggtaaagc ctggctgttc 1320
ggtactaact ttaactacgc gttctga 1347

<212> Type : DNA
<211> Length : 1347
SequenceName : SEQ ID 449
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
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ggcaacaata tcgccaactc cgccacctac ggctttaaat caggcacggc ctcttttgcc 120

gatatgtttg ccggttcgaa agtgggactg ggggtaaaag ttgccggtat cactcaggac 180
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ggtttttcc gtctggtaga tagcaacggt tcggtgttct acagccgtaa cggacaattt 300
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acagccgagc ctgcaatgaa gctggtgttt aatgccaatg gcgttctgac ctcaaatcca 720
acagagaata ttaccaccgg cgcaattaac ggcgcagaac ccgccacgtt tagcctgagc 780
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cagtctaacg cccagaccat caaaacccag gaccagatcc tcaacacgct ggttaactta 1200
cgctaa 1206

<212> Type : DNA
<211> Length : 1206
SequenceName : SEQ ID 450
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
atgtctaaat cgacttttt acacattctg attagctcca tcatattggt ggcactaata 60
caatcatccg cttgggctaa ctgtacaaac acacagatag gtcaaactga agatggtcgg 120
acagcgctta ttgagttcgg aaaaattaat atgaccgaca cctattttgc gccagcaggt 180
tcactcctcg cgacaacggt cgtacctccc actaactaca catcaggtgg cgcgacagga 240
agctccgtat tgtgggaatg tgatgcaaca gatttgccaa acatctattt tctggtcgct 300
accaatggcg acgaccgcgt ggggggcttt tacgatgcag gcgggcctga tggtctgagt 360
gatgtctatg ccacctggtt cgcttttgtc ggtctcaagc agaccatggc gggcgtgacg 420
cttggtcgtt actggaagaa agtgcccatc accagttatg ccactcaggg aactaaaatc 480
cagattcgct tacaggatat ccctcctctt catgctgagc tttatcgcat cagtacgcta 540
cctgatacat cagcaacaac aagttggtgc ggtaataata atacagatag tagtggagtc 600
ggattcgcaa aaccttccgg tacaatctat aactgtgttc agcccaatgc ctatattcag 660
ctttccggta ccagcggcat tttatttggt catgatgagc ccggcgaaga tagttctgtt 720
cattgggatt tctggggtgc tgataatggt tttggttacg gaatgcgttc ggccaatcga 780
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attgcagaag cacaactgaa tgcgggcatg gaaagtaccg gtaattttaa tgtccgcgtc 900
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gtgtctgaag gtgcatatac agcggcgcaa aaactgggga ttatcaatag caacggcggc 1020
gtcagcgccc tggtctctga taattatgac gcagcagaga tggcaaaggg cgttgggatc 1080
tacatttcta acagtgctca ccccgatacg gcgatgacgc tggttggtca accgggcatc 1140
gcgaagttaa ccccggagg aaatgcagcg gggtggtatc ctgtatttga aggggcaaca 1200
ttagaaggtg cgactcaccc cggatactcc agctatagtt actcttttat cgcccggttg 1260
aagaaactgc caaatcagac agtcagtgcg ggaaaagtgc gggcaacggc ttatatattg 1320
gtgaaaatgc aatga 1335

<212> Type : DNA
<211> Length : 1335
SequenceName : SEQ ID 451
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
atggaaaaca atcgcaattt ccctgccaga caatttcatt cgctcacgtt ctttgccggt 60
ctttgtattg gcatcacgcc tgtggctcag gcactcgccg ccgaagggca aactaacgcg 120
gatgacacgc tggttgtcga agcatcaacg ccttcgcttt atgcgccaca acaatctgcc 180
gatccgaaat tctcgcgtcc ggtagcggat actacccgca cgatgacggt gatttctgaa 240
caagtgatta aagatcaggg cgcaaccaac cttaccgatg cgctcaaaaa cgtccccggc 300
gtgggtgcgt tttttgcggg tgagaacggt aactccacca ctggcgacgc catttatatg 360
cgcggtgctg atacctctaa cagtatttat attgatggca ttcgcgatat cggcagcgtc 420

tcgcgcgaca ccttcaatac tgagcaggtc gaagtgatta aagggccttc cggcaccgac 480
tacgggcgca gcgcgccgac gggctcgatc aatatgatca gcaagcagcc gcgcaatgat 540
tccggcattg acgcctccgc cagtattggc agcgcctggt tccgccgcgg cacgctggac 600
gtcaatcagg tcattggtga taccactgcg gtgcgcctga atgtgatggg cgaaaaaacg 660
cacgatgccg gacgcgacaa agtcaaaaat gagcgttacg gcgtcgcccc ttctatcgct 720
tttggccttg gtacagcgaa tcgtttgtat cttaattatc tgcatgtcac ccagcacaac 780
acgccagacg gcggcattcc aaccatcggt ttgccgggct attctgcccc atctgcagga 840
acggcgaccc tgaatcattc cggaaaagtt gatacgcata acttttacgg cacggattcc 900
gattacgacg attcgaccac cgacaccgcc accatgcgtt ttgagcacga tatcaacgat 960
aacaccacca ttcgcaacac tacccgttgg tcgcgcgtga agcaggatta cctgatgacg 1020
gcgattatgg gtggggcgtc gaatattacc cagcccacca gcgatgtgaa tagctggacg 1080
tggtcacgca cggcgaatac caaagatgtg agtaataaaa ttctcaccaa ccagaccaac 1140
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gagctgaacg gcgggatccg tctggataat tatcatactg aatatgacag tgccaccgcc 1440
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gtcaccaccg tcgacaccgc caagtcgggc aatctggtga actggaaagc cggggcgctg 1560
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gatgacggga cttactcgca atacggtaag aaacgcgtcg aaggctatga gatatccgtg 1860
gcagggaata tcactcccgc gtggcaggtg attggcggct atacccagca aaaagcaacc 1920
atcaaaaacg gcaaagatgt tgcccaggat ggttcctcat cgctgccgta tacccggag 1980
cacgccttca ccttatggag ccaatatcag gcaaccgatg atatctctgt tggcgcgggc 2040
gcacgctata tcggcagtat gcataaaggt tcagacggcg cggtgggaac gccagcgttt 2100
accgaaggtt actgggtcgc cgatgccaaa ctggggtata gggttaatcg caatctcgac 2160
ttccagctaa acgtctacaa cctgtttgat accgattacg tcgcctcaat caataagagc 2220
ggctaccgtt atcacccggg cgagccaaga accttcttgc tcacagccaa tatgcatttc 2280
tga 2283

<212> Type : DNA
<211> Length : 2283
SequenceName : SEQ ID 452
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
atgcaaatga agaaattgct ccccattctt atcggcctga gcctttctgg gttcagttcg 60
ttgagccagg ccgagaacct gatgcaagtt tatcagcaag cacgccttag taacccggaa 120
ttgcgtaagt ctgccgccga tcgtgatgct gcctttgaaa aaattaatga agcgcgcagt 180
ccattactgc cacagctagg tttaggtgca gattacacct atagcaacgg ctaccgcgac 240
gcgaacggca tcaactctaa cgcgaccagt gcgtccctgc agttaactca atccattttt 300
gatatgtcga aatggcgtgc gttaacgctg caggaaaaag cagcagggat tcaggacgtc 360
acgtatcaga ccgatcagca aaccttgatc ctcaacaccg cgaccgctta tttcaacgtg 420
ttgaatgcta ttgacgttct ttcctataca caggcgcaaa aagaagcgat ctaccgtcaa 480
ttagatcaaa ccacccaacg ttttaacgtg ggcctggtag cgatcaccga cgtgcagaac 540
gcccgcgcgc agtacgatac cgtgctggcg aacgaagtga ccgcacgtaa taaccttgat 600
aacgcggtag agcagctgcg ccagatcacc ggtaactact atccggaact ggcggcgctg 660
aatgtcgaaa actttaaaac cgacaaacca cagccggtta acgcgctgct gaaagaagcc 720
gaaaaacgca acctgtcgct gttacaggca cgcttgagcc aggacctggc gcgcgagcaa 780
attcgccagg cgcaggatgg tcacttaccg actctggatt taacggcttc tagcgggatt 840
tctgacacct cttatagcgg ttcgaaaacc cgtggtgccg ctggtaccca gtatgacgat 900
agcaatatgg gccagaacaa agttggcctg agcttctcgc tgccgattta tcagggcgga 960
atggttaact cgcaggtgaa acaggcacag tacaactttg ttggtgccag cgagcaactg 1020
gaaagcgcgc atcgtagcgt cgtgcagacc gtacgttcct ctttcaacaa cattaatgct 1080
tctatcagta gtattaacgc ctacaaacaa gccgtagttt ccgctcaaag ctcattagac 1140
gcgatggaag cgggctactc ggtcggtacg cgtaccattg ttgatgtgtt ggatgcgacc 1200
accacgctgt acaacgccaa gcaagagctg gcgaatgcgc gttataacta cctgattaat 1260
cagctgaata ttaagtcagc cctgggtacg ttgaacgagc aggatctgct ggcactgaac 1320
aatgcgctga gcaaaccggt ttccactaat ccggaaaacg ttgccccgca aacgccggaa 1380
cagaatgcta ttgctgatgg ttatgcgcct gatagcccgg cacccgtcgt tcagcaaaca 1440
tccgcacgca ctaccaccag taacggtcat aacccttccc gtaactga 1488

<212> Type : DNA

<211> Length : 1488
SequenceName : SEQ ID 453
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
gtgaccaaac tcaaacttct ggcacttgga gtgcttatcg caacgtctgc aggcgtagcg 60
cacgctgaag gtaaattttc cctgggcgca ggcgtaggtg tcgttgaaca cccatataaa 120
gattacgata ccgatgttta cccagtaccg gtaatcaact atgaaggcga taacttctgg 180
ttccgtggct taggtggtgg ttactacctg tggaatgacg caacggataa actttcaatt 240
accgcttact ggtcgccgct ttacttcaaa gctaaagaca gtggcgatca ccaaatgcgt 300
cacctggatg accgtaagag caccatgatg gctggtctgt cttatgctca ctttacccag 360
tacggttacc tgcgtaccac cctggctggc gataccctgg ataacagcaa cggcatcgtc 420
tgggatatgg cctggttgta tcgttacacc aacggtggcc tgaccgtgac tccgggtatt 480
ggtgtgcagt ggaacagcga aaaccagaac gaatactatt atggcgtatc gcgcaaagag 540
tccgctcgca gcggtctgcg tggctataac tcgaacgaca gctggagccc ttacctggag 600
ctgagcgcca gctacaactt cctcggcgac tggagtgttt acggtaccgc gcgctacacc 660
cgtctgtctg atgaagttac tgacagcccg attgtggata aatcctggac tggcctgatt 720
tctaccggga tcacctacaa attctga 747
<212> Type : DNA
<211> Length : 747
SequenceName : SEQ ID 454
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
atgaaaaaaa cattactggc agccggtgcg gtactggcgc tctcttcgtc ttttactgtc 60
aacgcagctg aaaacgacaa accgcagtat ctttccgact ggtggcacca gagcgttaac 120
gttgtcggaa gctatcacac ccgtttcgga ccgcagatcc gcaacgatac ctaccttgag 180
tacgaagcat tcgctaaaaa agactggttc gacttctatg gttatgcgga tgcgccggta 240
ttcttcggcg gtaactccga tgcaaaaggt atctggaacc acggttctcc tctgtttatg 300
gaaatcgaac cacgtttctc catcgacaag ctgaccaata ctgaccttag cttcggtccg 360
ttcaaagagt ggtacttcgc gaacaactac atttacgaca tgggtcgtaa taaagatggt 420
cgccagagca cctggtacat gggtctgggt accgatatcg acactggcct gccgatgagc 480
ctgtccatga acgtctatgc gaaataccag tggcagaact atggcgcagc gaacgaaaac 540
gagtgggacg gttaccgttt caaaattaaa tactttgtgc cgattaccga tctgtggggc 600
ggtcagctga gctacatcgg cttcaccaac ttcgactggg gttccgattt aggggatgac 660
agcggtaacg caatcaacgg tattaagacc cgtactaata actctatcgc ttccagccat 720
attctggctc tgaactacga tcactggcac tactctgtcg tagctcgtta ctggcacgac 780
ggtggtcagt ggaacgacga tgcagaactg aacttcggca acggcaactt caacgttcgc 840
tctaccggct ggggtggtta cctggtagta ggttacaact tctga 885
<212> Type : DNA
<211> Length : 885
SequenceName : SEQ ID 455
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
atgctttcaa cacaatttaa cagggataat caatatcaag ccatcaccaa accgtcacta 60
cttgccggtt gcatagcact ggcactatta ccttctgccg cttttgctgc accagccact 120
gaagaaacgg tgattgttga gggttcagcc acagctccag atgatggcga aaatgattac 180
agcgtaacgt ctacctctgc gggtaccaaa atgcagatga ctcaacgtga tattcctcag 240
tcggtcacta ttgttagcca gcagcggatg gaagatcagc agttacaaac gctgggcgaa 300
gtgatggaaa acacgctggg gatcagcaaa agtcaggcgg attccgatcg tgctctttat 360
tattcccgcg gattccagat cgataactat atggttgatg gtatccccac ctattttgaa 420
tcgcgctgga atctgggcga cgcactttct gatatggcac tgtttgaacg cgtagaagta 480
gtgcgtggcg cgacaggact catgaccggg acgggtaatc catctgcggc aattaatatg 540
gttcgaaaac acgcgaccag tcgtgaattt aaaggcgatg tctcggcgga atacggtagc 600
tggaacaaag aacggtatgt ggcggattta caaagcccac tcaccgaaga cggtaaaatc 660
cgcgcgcgaa ttgtcggcgg ctaccagaat aacgactcat ggctggaccg ctacaatagt 720
gaaaagacct tcttctccgg cattgtcgat gctgatttag gcgatcttac gacgctttca 780

gccggttacg aatatcagcg cattgatgtt aatagcccaa cctggggcgg tttaccgcgc 840
tggaatactg atggcagcag caacagttac gatcgcgcac gcagtaccgc acctgactgg 900
gcgtacaacg ataaagagat caacaaggtc tttatgaccc tgaagcagcg gtttgctgat 960
acctggcaag cgacactgaa tgccacccac tctgaagtcg aatttgacag caaaatgatg 1020
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ggacctggct ttgattatgt cggcggcacc ggttggaaca gtggcaaacg taaagttgat 1140
gcgctggatt tgttcgctga cggtagttat gaattgtttg gtcgtcagca caatctaatg 1200
tttggtggca gttacagcaa acaaaacaat cgttacttca gttcatgggc caacatcttc 1260
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gtcacccttg ccgatccgct gcatctgatc ctcggcgcac gttataccaa ctggcgggtt 1440
gatacgctga cttacagcat ggagaaaaac cacaccacgc cttacgctgg tctggtgttt 1500
gacatcaatg acaactggtc gacctacgcc agctatacct ctatttttca gccgcaaaat 1560
gatcgtgaca gttcaggcaa atatctggct ccaatcaccg gtaacaacta cgagctgggt 1620
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caggataatg tcgctcagtc caccggtaca cctatccccg gcagcaacgg cgaaaccgcc 1740
tataaagcgg tggatgggac agtcagtaaa ggggtggaat ttgaactcaa cggcgcaatt 1800
accgacaact ggcagctgac atttggcgca acgcgctata ttgcagagga taacgaagga 1860
aacgccgtta atcctaatct gccacgcacc acggttaaaa tgttcaccag ctatcggttg 1920
cctgtcatgc cagagttgac agtcggcggt ggtgttaact ggcaaaatcg cgtgtatacc 1980
gacaccgtga caccgtatgg caccttccgc gccgagcaag gtagctacgc gttggtggat 2040
ctcttcaccc gctaccaggt gacgaaaaac ttctcgttac aggggaacgt caataacctg 2100
ttcgacaaaa cctacgatac caacgtggaa ggttctatcg tctacggcgc accgcgtaat 2160
ttcagcatta ccggcacgta tcaattctga 2190

<212> Type : DNA
<211> Length : 2190
SequenceName : SEQ ID 456
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
atggcgcgat tccagtttaa aaaccgtaaa aataatggac ttatttttt tataagtttt 60
atggtgatgg gagaagctgc aattgctgca ccgctgccac aatgggcgaa tgccccagcg 120
gtaacgccag ttgcccaatt atctttacag gaaagtatat tacgcgcctt tgcgcgaaat 180
cccggtgtca ctcaacaggc ggcgcagata ggtattggcg aagcgcaaat tgatgaagcc 240
aaaagtgcct ggtatccgca cgttggatta accggcaacg cggggccgtc ccgacaaacg 300
gactccagcg gcaggcttga taacaacgtt tcgtatggca taaccctgac acaactggtg 360
tatgactttg gtaaaactaa caacgatatc aatctgcaaa ctgccgcccg tgacagctac 420
cgctttaaat tgatggcaac cttaaccgat gttgcagaga aaacggcgac tgcctacatg 480
gaagtcagtc gttatcaggc tttgtgcgat gcggctcaac gcaatattca ctcgctggaa 540
aacgtctaca acatggcggc attgcgcgct aacgcaggcc tgaactcatc gtcggatgaa 600
ttacaggccc agacgcgtat tgccggaatg cgctcaacgc tggagcaata tcaggcgcag 660
atggcgagcg ccaaagcgca actggcggtg ctcactggcg tacagccgga ggcgatagcc 720
gcgccacctg ctgaattagc cgagcagccg gtatcgctga agaatattga ttaccagtcc 780
atcccgctgg tgctggcggc agaaaactta cgccagtcag cacagtacgg cgtggaaaaa 840
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agcgaccgct cgtattggga tgatcagcta caactgaacg ttaacgcgcc gctgtatcag 960
ggcggcgcgg tttctgccca ggtgcaacag gccgaagggc aacaaaaaat ctctgcctcg 1020
caggtcgaac aggcaaaact ggatgtgctg caacgagcgt ctgtggcata tgcgaactgg 1080
accggcgcac ggggtcgtga agaagccggt ttagcgcaat ccgaaagtgc gcacaaaacg 1140
cgagatgtgt accaaaatga atataaattg ggtaaacgca gtctgaatga tctattaacc 1200
gtcgaacaag atgtctttca ggcgcaatcg gctgaaataa atgccaatta tgatggctgg 1260
gtcgccgccg taaattatgc cgctgcggtg aataacctta ttccattagc gggaattaaa 1320
cagggcttat acaacgactt acccgacttg aaataa 1356

<212> Type : DNA
<211> Length : 1356
SequenceName : SEQ ID 457
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
atggctaagt tcacaccttc attctcagga atcaaaggtc gggcgctctt ttcactgctc 60
tttgcagcac caatgattca tgcaaccgac actgcaacga ccaaagatgg cgaaacaatc 120

actgttacag cggatgcaaa taccgcaact gaggcgaccg atggttatca acctctgagc 180
acttccacgg cgacattaac cgatatgccg atgctggata tcccgcaggt ggtcaatacg 240
gttagcgatc aggttctgga aaatcagaat gcaacgacgc tggatgaagc gctttataac 300
gtcagtaacg tggtacagac caatacatta ggcggaactc aggacgcctt tgtacgtcgt 360
ggttttggtg ctaaccggga tggctccatc atgaccaacg gcctgcgaac tgtacttcct 420
cgcagtttca acgccgccac agaacgtgtg gaagtgctaa aaggtccggc ctccacgctg 480
tatggcattc tcgatcctgg tggattgatt aacgtcgtga ccaagcgccc ggaaaaaaca 540
ttccatggtt ctgtctcagc cacgtcctcc agttttggcg gaggcactgg gcaacttgat 600
atcacaggtc ccattgaagg cactcagctg gcataccgcc tgacgggggа agtgcaggat 660
gaagattact ggcgaaactt cggtaaagag cgcagtacat ttattgcccc gtcactcacc 720
tggtttggtg ataatgcaac agtaaccatg ctctattccc atcgggacta taaaactccg 780
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gcagaatatc atctcaatag ccagtggaca gcgcgctttg attacagcta cagccaggat 960
aaatacagcg acaatcaggc tcgcgttacc gcgtatgatg caacgacagg aacgctgaca 1020
cggcgtgttg atgcaactca gggatctacc cagcgtatgc attctactcg tgcggatctg 1080
caagggaatg ttgatattgc tgggttctat aatgagattc tgggtggggt gtcatatgaa 1140
tattatgatc ttctgcgcac agatatgatt cgctgtaaaa acgctaaaga tttcaatatc 1200
tacaaccccg tttatggcaa taccagcaaa tgcacaacgg tttcggcgtc ggacagtgat 1260
cagacgatca aacaggagag ctactcagct tatgcacagg atgcgctcta tctgaccgat 1320
aactggattg ccgtcgccgg gatccgctat cagtattaca cgcagtatgc gggtaaaggc 1380
cgtcctttta atgtcaatac tgacagccgc gatgaacaat ggacgcccaa actggggtta 1440
gtctacaaac tgacgccatc ggtatcctta tttgctaatt attcgcaaac atttatgccg 1500
caatcgtcaa ttgccagcta catcggagat cttccaccgg aatcatctaa tgcttacgaa 1560
gtcggggcaa aattcgagct gttcgatggt ataaccgcag atattgcgct gtttgatatc 1620
cataaacgta acgtgttgta taccgaaagt attggtgatg aaaccatcgc caaaacggca 1680
ggccgcgttc gttcaagagg ggtagaagtc gaccttgcgg gagcattaac tgaaaacatt 1740
aatatcattg ccagctacgg ctataccgat gctaaggttc tggaagatcc tgattatgca 1800
gggaaaccat tgccgaatgt tcctcgtcat accggttcgc tattcctgac ctatgacatt 1860
cataacatgc caggcaataa cacactgacg tttggcggtg gtggacattg cgtaagccgt 1920
cgttcggcaa ccaatggggc tgactattat ctgccaggct atttcgttgc cgatgccttc 1980
gccgcataca aaatgaaatt gcagtatccg gtcacactgc aattaaacgt caaaaacctg 2040
tttgataaaa cgtattacac ctcttccatc gccacaaata atctggggaa tcagattggc 2100
gatccgcgtg aagtgcaatt cacggtgaaa atggaatttt ga 2142

<212> Type : DNA
<211> Length : 2142
SequenceName : SEQ ID 458
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
atgcggactc tgcagggctg gttgttgccg gtgtttatgt tgcctatggc agtatatgca 60
caagaggcaa cggtgaaaga ggtgcatgac gcgccagcgg tgcgtggcag tattatcgcc 120
aatatgctgc aggagcatga caatccgttc acgctctatc cttatgacac caactacctc 180
atctacaccc aaaccagcga tctgaacaaa gaagcgattg ccagttacga ctgggcggaa 240
aatgcgcgta aggatgaagt aaagtttcag ttgagcctgg catttccgct gtggcgtggg 300
attttaggcc cgaactcggt gttgggtgcg tcttatacgc aaaaatcctg gtggcaactg 360
tccaatagcg aagagtcttc accgtttcgt gaaaccaact acgaacgcga attgttcctc 420
ggttttgcca ccgattaccg ttttgcaggt tggacgctgc gcgatgtgga gatggggtat 480
aaccacgact ctaacgggcg ttcagacccg acctcccgca gctggaaccg cctttatact 540
cgcctgatgg cagaaaacgg taactggctg gtagaagtga agccgtggta tgtggtgggt 600
aatactgacg ataacccgga tatcaccaaa tatatgggtt actaccagct taaaatcggc 660
tatcacctcg gtgatgcggt gctcagtgcg aaaggacagt acaactggaa caccggctac 720
ggcggcgcgg agttaggctt aagttacccg atcaccaaac atgtgcgcct ttatactcag 780
gtttacagcg gctatggcga atcgctcatc gactataact tcaaccagac ccgtgtcggt 840
gtgggggtta tgctaaacga tttgttttga 870

<212> Type : DNA
<211> Length : 870
SequenceName : SEQ ID 459
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :

atggcggttc aaaagaatgt tatcaaaggc atactggcag gtacgtttgc gctaatgctg 60
agcggttgtg tcactgtgcc ggacgccatt aaaggcagca gtcccacgcc gcaacaagat 120
ttagttcggg tgatgagtgc gccgcagctg tacgttggtc aggaggcacg ctttggtggc 180
aaagtggttg cggtacaaaa ccagcaaggg aaaacccgcc tggaaattgc taccgtaccg 240
ctggacagcg gagccagacc gacgctggga gaaccttctc gcggtcgcat ttatgccgat 300
gtgaacggtt ttctggaccc ggtggatttc cgtggacaac tggttacggt agtcgggcca 360
atcactggtg cggttgacgg aaaaatcggc aacacgccct ataaatttat ggtgatgcag 420
gcaacaggtt acaaacgttg gcatttaacc cagcaggtga ttatgccgcc tcagccgatt 480
gatccctggt tttatggcgg tcgtggctgg ccctatggcc acggcggatg gggctggtat 540
aatcccggcc ccgcgagagt acaaacagtt gtaactgaat aa 582

<212> Type : DNA
<211> Length : 582
SequenceName : SEQ ID 460
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
atgcgtaagc agtggctcgg gatctgcatc gcggcaggaa tgctcgcggc atgtacaagc 60
gatgatggtc agcaacagac agtaagtgta ccgcagcctg cggtatgtaa cggccccata 120
gttgaaatta gcggggcgga cccgcgtttc gaaccactga acgcgacggc aaatcaggat 180
taccagcgcg acggtaaaag ctacaaaatc gtgcaggatc cgtctcgatt tatccaggcg 240
ggactggcgg caatctatga tgccgaacca ggcagtaacc tgacggcctc tggcgaagct 300
ttcgatccga cacagctgac ggcggcccat ccaacgcttc cgatccccag ctacgccaga 360
atcactaacc tggctaacgg gcgaatgatc gtggtgcgca ttaatgatcg cggtccttac 420
ggcaacgacc gcgttatttc gctttctcgc gcagcagctg accgtcttaa cacgtcaaac 480
aacaccaaag ttcgtatcga tccgattatt gtcgcccagg atggttcgct ttctggtcct 540
ggtatggctt gtaccacagt cgccaaacag acttacgccc tgcctgcacc tcccgattta 600
agcggtggcg cgggaacaag ttcagtgtct ggcccgcagg gtgacattct tccggtcagt 660
aattcgacgc taaaaagcga agatccgacc ggcgcgccgg taaccagcag cggtttcctc 720
ggcgcaccaa cgaccttagc gccaggtgta ctggaaggca gcgaaccgac gcctgctcca 780
cagcccgttg ttacagctcc gtcgacaacg cctgcaacct cgcctgcaat ggtgacaccg 840
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caggctcgtg cgcaacagta ccaacagcaa ctgggacaga agttcggcgt ccccggtcgc 960
gtaactcaaa atggcgcggt ctggcggatc cagcttggcc cattcgccaa caaagccgaa 1020
gccagtacct tgcagcaacg tttgcaaacc gaagcccaat tacagtcatt tattaccacc 1080
gcgcagtag 1089

<212> Type : DNA
<211> Length : 1089
SequenceName : SEQ ID 461
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
atgattaaac gcgtattggt tgtttcaatg gtaggtctgt ctcttgtcgg ttgtgttaat 60
aacgacaccc tgtcagggga tgtttatacc gcttctgaag cgaaacaagt acagaatgtc 120
agctatggaa ccatcgttaa cgtacgtccg gtacagattc agggcggtga tgattccaac 180
gttatcggtg caattggcgg tgctgttctt ggtggtttcc tgggaaatac tgttggtggc 240
ggaaccgggc gttctctggc tactgcagca ggcgctgttg caggtggcgt agctggtcag 300
ggcgtacaga gtgcaatgaa caaaacgcaa ggtgtcgagc tggaaattcg taaagacgat 360
ggtaatacca tcatggtggt acagaaacaa ggcaacactc gtttctctcc gggccaacgt 420
gtcgtactgg ccagcaatgg cagtcaggtg accgtttctc cgcgctaa 468

<212> Type : DNA
<211> Length : 468
SequenceName : SEQ ID 462
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
gtgtcaaagg caaccgaaca aaacgacaag ctcaagcggg cgataattat ttcagcagtg 60
ctgcatgtca tcttatttgc ggcgctgatc tggagttcgt tcgatgagaa tatagaagct 120
tcagctggag gcggcggtgg ttcgtccatc gacgctgtca tggttgattc aggtgcggta 180

gttgagcagt acaaacgcat gcaaagccag gaatcaagcg cgaagcgttc tgatgagcag 240
cgcaagatga aggaacagca ggctgctgaa gaactgcgtg agaaacaagc ggctgaacag 300
gaacgcctga agcaacttga gaaagagcgg ttagctgctc aggaacagaa aaagcaggct 360
gaagaagccg caaaacaggc cgagttaaag cagaagcaag cggaagaggc ggcagcgaaa 420
gcggcggcag atgctaaagc gaaggccgaa gcggatgata aagctgcgga agaagcagcg 480
aagaaagcgg ctgcagacgc gaagaaaaaa gcagaagcag aagccgccaa agccgcagcc 540
gaagcgcaga aaaaagccga ggcagcagct gcggcgctga agaagaaagc ggaagcggca 600
gaagcagctg cagctgaagc aagaaagaaa gcggcagcag agaaagctgc agccgacaaa 660
aaagcagcag aaaaagcggc tgctgaaaag gcagcagctg ataagaaagc agcggcagaa 720
aaagccgccg cagacaaaaa agcggcagct gcaaaagcag cagctgaaaa agccgctgca 780
gcaaaagctg ccgcggaggc agatgatatt ttcggtgagc taagctctgg taagaatgca 840
ccgaaaacgg ggggaggggc gaaagggaac aatgcttcgc ctgccgggag tggtaatact 900
aaaaacaatg gcgcatcagg ggccgatatc aataactatg ccgggcagat taaatctgct 960
atcgaaagta agttctatga cgcatcgtcc tatgcaggca aaacctgtac gctgcgcata 1020
aaactggcac ccgatggtat gttactggat atcaaacctg aaggtggcga tcccgcactt 1080
tgtcaggctg cgttggcagc agctaaactt gcgaagatcc cgaaaccacc aagccaggca 1140
gtatatgaag tgttcaaaaa cgcgccattg gacttcaaac cgtaa 1185

<212> Type : DNA
<211> Length : 1185
SequenceName : SEQ ID 463
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
gtgatgaaat ttaaaaaatg tcttctgcct gtggcaatgt tagcgtcatt cactctggca 60
ggatgccagt caaatgctga cgatcatgcc gccgatgttt atcaaaccga tcaactgaat 120
accaaacaag aaactaaaac cgttaatatt atttccattc ttcccgcaaa agttgccgta 180
gacaactccc aaaataaacg gaacgcacaa gccttcggcg cgcttattgg cgcagtcgct 240
ggcggtgtta tcggccacaa cgtcgggtct ggcagcaatt ccggaacgac ggcaggtgca 300
gttggcggcg gagctgtagg cgcggcagcg ggttctatgg tgaatgataa aaccttagtg 360
gaaggtgttt ctttaacgta taaggaaggc accaaagtgt atacctctac tcaggtgggt 420
aaagagtgcc agtttacgac aggtttagcc gttgttatta ccacgacgta taacgaaacg 480
cgtattcagc caaataccaa atgtcctgaa aagagctaa 519

<212> Type : DNA
<211> Length : 519
SequenceName : SEQ ID 464
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
atgttgctta gcataatcac tgtcgcgttt cgtaacctcg aagggatagt caaaacacat 60
gcctcgctgg cgcatctggc gcaggcggaa gatatcagct tcgaatggat tgttgtcgat 120
ggcggttcca atgacggcac tcgtgagtac ctggaaaatc tcaatggtat ctataaccta 180
cgctttgtca gcgagccaga taacggtatc tacgacgcca tgaacaaggg cattgcgatg 240
gcacaaggca agttcgcgtt gtttctcaac tcgggcgata tttttcatca ggatgccgca 300
tattttgtcc gtaagttaaa aatgcaaaaa gataacgtga tgatcaccgg cgatgcgctg 360
ctggattttg gcgacgggca taaaattaaa cgtagcgcca aaccgggctg gtatatttat 420
cacagcctgc ccgccagtca tcaggcgata tttttcccgg tatccggttt gaaaaaatgg 480
cgttatgacc tggaatataa agtttcttct gattacgcgc tggcagccaa aatgtataaa 540
gcaggttatg catttaaaaa actcaatggc ctggtgtctg aattttctat gggtggggta 600
tctaccacca ataatatgga attgtgtgct gacgcgaaaa aagtccaacg gcaaatatta 660
catgtgcctg gcttttgggc tgaattatcc tggcatttac gccagcgtac tacctcaaag 720
acgaaagcct tatataacaa aagctga 747

<212> Type : DNA
<211> Length : 747
SequenceName : SEQ ID 465
SequenceDescription :

Sequence

<213> OrganismName : Haemophilus influenzae Rd
<400> PreSequenceString :
atgaaattaa caacactgca aaccttgaaa aaagggttta cattaatcga gctaatgatt 60

gtgattgcaa ttattgctat tttagccacc atcgcaattc cttcttatca aaattatacc 120
aaaaaagctg cggtatccga attactgcaa gcgtctgcgc cttataaggc tgatgtggaa 180
ttatgtgtat atagcacaaa tgaaacaaca agctgtacag ggggaaaaaa tggtattgca 240
gcggatataa agacagcaaa aggctatgta gcctcagtta tcactcaatc aggtggtatt 300
acagtaaaag ggaatggcac attggcaaat atggaatata ttttgcaagc taaaggtaat 360
gctgcagcag gtgtaacttg gacaacaacc tgcaaaggaa cggatgcctc tttatttcca 420
gcaaattttt gcggaagtgt cacaaaatga 450

<212> Type : DNA
<211> Length : 450
SequenceName : SEQ ID 466
SequenceDescription :

Sequence

<213> OrganismName : Haemophilus influenzae Rd
<400> PreSequenceString :
atgctaaata aaaaattcaa actcaatttt attgcgctta ctgtcgccta cgcattaacc 60
ccttatacag aagctgcgtt agtgagagac gatgtggatt atcaaatatt tcgtgatttt 120
gcagaaaata aagggagatt ttctgttggt gcaacaaatg tggaagtgag agataaaaat 180
aaccactctt taggcaatgt tttacctaat ggcattccga tgattgattt tagtgttgtg 240
gatgtagata aacgcatcgc cacattgata aatccacaat atgtagtagg tgtaaaacac 300
gttagtaacg gcgtgagtga actacatttt gggaacttaa atggcaatat gaataatggc 360
aatgctaaat cgcaccgaga tgtatcttca gaagaaaata gatattttc cgttgagaaa 420
aatgagtatc caactaaatt gaatggaaaa gcagtaacta ctgaagatca aactcaaaaa 480
cgccgtgaag actactatat gccacgtctt gataaatttg ttaccgaagt tgcaccaata 540
gaggcttcaa ctgcaagtag tgatgctggc acatataatg atcagaataa atatcctgct 600
tttgtaagac taggaagtgg tagtcaattt atttataaaa aaggagataa ttacagctta 660
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tatggtattg caggcacacc ttataaagta aaccacgaaa ataatggact aattggtttt 780
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aatcaatatg attttgctta caacgtggaa aaccaacagc aatataacgc agggcttaaa 4980
ttgaaatatc ataatgtgaa attaagtcta ataggcggat taacaaaagc gaaacaagcg 5040
gaaaaacaaa aaactgcaga attaaaacta agttttagtt tttaa 5085

<212> Type : DNA
<211> Length : 5085
SequenceName : SEQ ID 467
SequenceDescription :

Sequence

<213> OrganismName : Haemophilus influenzae Rd
<400> PreSequenceString :
atggcattag taaacaaaat taaaacatta tcatcagtag gtattctagc ggctacatta 60
tttcttgcag gctgccaagc acaatcaaat atattagcat ttacaccgcc tgcaccaagt 120
gcttcaatga atgttaatcg aactgccgtt gtatctgtga caacaaaaga tagccgtgca 180
atacaagaga ttgcgagtta tacgaaacac ggggaactga ttaaattaaa tgcatcccca 240
agtgttacac aattatttca gcaagtgatg cagcaaaatt taattagtaa aggttttaga 300
gttgggcaat taaatggttc aaatgcgtgg gtaactgtgg atgtgcgtga atttggtacg 360
caagtagaac aaggtaatct tcgttataaa cttaatacca aaattcaagc gacagtttat 420
gtacaaggtg cgaaaggttc gtataataaa tcatttaatg tcacgcactc acaagagggc 480
gtatttaatg cgggcaatga tgaaattcat aaagtgctat ctcaaacttt taatgatatt 540
gtgaacaata tttatcaaga tcaagaagtt gcggctgcga taaaccaata ttctaattaa 600

<212> Type : DNA
<211> Length : 600
SequenceName : SEQ ID 468
SequenceDescription :

Sequence

<213> OrganismName : Haemophilus influenzae Rd
<400> PreSequenceString :
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ccttggctga atccgtcaaa gtgcggcgta atttttgatg gttttcaact tgtgggcgat 120
gatttcaatt cagatcaaac ggctgaaaat acatcgccag cttggcaagt gctttacaca 180
acccatttac aaagttgctc gccgattcat agtggagaaa atttcgcacc catccctttg 240

tataaacaac taaaaaatca accgcaccta agccaagatc tgattaaatg gcaagaaaat 300
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gaaatttccg atcatcaaag tacgctttca aaacacggac gatatttagc tcaagaaata 420
gaaaaagaaa ctggcatacc gacttactat tatttatatc gtgtaggtgg gcaatcttta 480
gaatctgaaa aatcccgttg ctgcccttct tgtggtgcaa attgggcgtt aaaagacgcg 540
atttttgata cctttcattt taaatgcgat acctgtcgat tagtttcgaa tctatcgtgg 600
aatttttgt aa 612
<212> Type : DNA
<211> Length : 612
SequenceName : SEQ ID 469
SequenceDescription :

Sequence

<213> OrganismName : Haemophilus influenzae Rd
<400> PreSequenceString :
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ggtttatctc aaactaaagc aaacggtagt aacaatacaa gagttggacc tcgcgtatcc 120
gtgggttata aagtaggaaa tacacgtgtt gcgggtgatt atactcatca tggaaaagtt 180
gatggcacaa aaattcaagg tttaggtgca tcagtattat atgattttga cacgaattct 240
aaagtgcaac cttatgttgg tgctcgtgta gcgactaatc aatttaaata caccaatcgc 300
gcagaacaaa agtttaaaag ttcttctgat attaagctcg gatatggggt tgtagcaggt 360
gcaaaatata agttagatgg caactggtac gcaaatggtg gagttgagta caatcgttta 420
ggtaattttg atagtaccaa agttaataac tatggtgcaa aagttggtgt ggggtacgga 480
ttctaa 486
<212> Type : DNA
<211> Length : 486
SequenceName : SEQ ID 470
SequenceDescription :

Sequence

<213> OrganismName : Haemophilus influenzae Rd
<400> PreSequenceString :
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<212> Type : DNA
<211> Length : 2388
SequenceName : SEQ ID 471
SequenceDescription :

Sequence

<213> OrganismName : Haemophilus influenzae Rd
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<211> Length : 405
SequenceName : SEQ ID 472
SequenceDescription :

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<213> OrganismName : Haemophilus influenzae Rd
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<212> Type : DNA
<211> Length : 3033
SequenceName : SEQ ID 473
SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori, strain J99
<400> PreSequenceString :
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<212> Type : DNA
<211> Length : 7200
SequenceName : SEQ ID 476
SequenceDescription :

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<213> OrganismName : Helicobacter pylori, strain J99
<400> PreSequenceString :

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<212> Type : DNA

<211> Length : 3867

SequenceName : SEQ ID 477

SequenceDescription : .

Sequence

<213> OrganismName : Helicobacter pylori, strain J99

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<212> Type : DNA

<211> Length : 2235

SequenceName : SEQ ID 478

SequenceDescription :

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<213> OrganismName : Helicobacter pylori, strain J99

<400> PreSequenceString :

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tcgcaaacct tacggcagct tttaggggat aaaaccttct ttatggtgca acaaaagctc 3060
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gaatttggga tcaaggtgcc tctcatcaat caagcgtatt tgaatagtgc tggggctgat 3660
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<212> Type : DNA
<211> Length : 3714
SequenceName : SEQ ID 479
SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori, strain J99
<400> PreSequenceString :
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aaagtaagat tcttagcccc tttgagccta gcgttaagct tgagcttcaa tccagtgggc 120
gctgaagaag atgggggctt tatgaccttt gggtatgaat taggtcaggt ggtccagcaa 180
gtgaaaaacc cgggtaaaat caaagccgaa gaattagcgg gcctgttaaa ctctaccacg 240
acaaacaaca ccaatatcaa tattgcaggc acaggaggga atgtcgccgg gactttgggc 300
aacctttta tgaaccaatt gggcaatttg attgatttgt atcctacttt gaaaactaat 360
aatcttcacc aatgcggtag cactaatagc ggtaatggcg ctactgctgc cgctgctact 420
aacaatagcc cttgtttcca aggtaacctg gctctttata acgaaatggt tgactctatc 480
aaaactttga gtcaaaacat cagcaagaac atctttcaag gcgacaacaa caccacgagc 540
gctaatctct ccaaccagct cagtgagttg aacaccgcta gcgtttattt gacttacatg 600
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gcttacgaga atggtgttac cgctcaacaa atcgcttatg tcctaaagca agcttgaatc 720
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gacctaaaaa gccataacca gcattctata gaaatcggtg tgcaaatccc tacgatttac 1500
aacacttact ataaagctgg tggcgctgaa gtgaaatact tccgcccttа tagcgtgtat 1560
tgggtctatg gctacgcctt ctaa 1584

<212> Type : DNA
<211> Length : 1584
SequenceName : SEQ ID 480
SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori, strain J99
<400> PreSequenceString :
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ggcttttacg caagcgcggg aattcggatc ggtgaagccg ctcaaatggt gaaaaacacc 120
aaaggcattc aacagctttc agagaattat gaaaagttga acaatctttt aaataattac 180
aacaccctaa acactcttgt aaagctgtcc tccgatccga gtgctgtcaa cgacgcaagg 240
gataatctag gctcaagcac taggaatttg ctagatgtca aagccaattc ccccgcctat 300
caagcggtgc ttttagcatt gaacgctgca gtgggcttgt ggcaagttac aagctatgcc 360
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aatgtgccag gacaaaacac gacgaccatc acttgtaatt cgtattatga gccaggacat 480
ggcgggccaa tatccactaa aaattatgcg atcatcaaca aggcttatca aatcattcaa 540
aaggctttga cagccaatgg agaagggatc ccagttttaa gcaacaccac tacaaaactt 600
gatttcacta tcaatggaga caaaagaacg ggtggcgaac caaataaaaa attagtatac 660
ccatggagtc atgggaaagc tatttcaacc tcgtggaatg caaccataac agcaccaaca 720
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aaatccagct tcttcaactc ggcttctgac gtgtggactt atggctttgg agcggacgct 1740

ctttataatt tcatcaacga taaagccacc aatttcttag gcaaaaacaa caagctttct 1800
gtgggggctt ttgggggtat tgcattagcc gggacttcat ggcttaattc tgagtatgtg 1860
aatttagcca ccatgaataa cgtctataac gctaaaatga acgtggcgaa tttccaattc 1920
ttattcaaca tgggagtgag gatgaattta gccaggccta agaaaaaaga cagcgatcat 1980
gcggctcagc atgggattga gttagggctt aaaatcccca ccatcaacac gaactactac 2040
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ttcgcttact aa 2112

<212> Type : DNA
<211> Length : 2112
SequenceName : SEQ ID 481
SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori, strain J99
<400> PreSequenceString :
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gccgaagatg atggagggtt tttcaccgtc ggttatcagc ttgggcaggt catgcaagat 120
gtccaaaacc caggcggcgc taaaagcgac gaactcgcca gagagcttaa cgctgatgta 180
acgaacaaca ttttaaacaa caacaccgga ggcaatgtcg caggggcgtt gagtaacgct 240
ttctcccaat acctttattc gcttttaggg gcgtatccca cgaaactcaa tggtaacgac 300
gtgtctgcga acgctctttt aagtggtgcg gtaggcagtg ggacttgcgc ggctgcaggg 360
acggctggtg gcacaactct taacactcaa agcgcttgca ccgctgcggg ctattactgg 420
ctccctagct tgactgatag gattttaagc acgatcggca gccagactaa ctacggcacg 480
aacaccaatt tccccaacat gcaacaacag ctcacctact tgaatgcggg gaatgtgttt 540
tttaatgcga tgaataaggc tttagagaag aatgggactg ctactgctaa tagcactagt 600
agcactagcg gtgcgactgg ttcagatggt caaacttact ctcaacaagc tattcaatac 660
cttcaaggcc aacaaaatat cttaaataac gcagcgaact tgctcaagca agatgaattg 720
ctcctagaag ctttcaactc tgccgtagct gctaacattg ggaataagga attcaattca 780
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gatgacccca atgtgaaatt gcatgggaaa atcaataaca cgcacttcca gttcctcttt 1380
gacttcggta tgagaatgaa cttcggtaag ttggacggga aatccaaccg ccacaaccag 1440
cacacggtgg aatttggcgt agtagtgcct acgatttata acacttatta caaatcagca 1500
gggactaccg tgaagtattt ccgtccttat agcgtttatt ggtcttatgg gtattcattc 1560
taa 1563

<212> Type : DNA
<211> Length : 1563
SequenceName : SEQ ID 482
SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori, strain J99
<400> PreSequenceString :
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gaagacaacg gctttttttgt gagcgccggc tatcaaatcg gtgaatccgc tcaaatggtg 120
aaaaacacca aaggcattca agatctttca gacagctatg aaagattgaa caacctttta 180
acgaattata gcgtcctaaa cgctctcatc aggcagtccg ccgaccccaa cgccatcaat 240
aacgcaaggg gcaatttgaa cgcgagcgcg aagaatttga tcaatgataa aaagaattcc 300
ccggcgtatc aagccgtgct tttagccttg aatgcggcag cggggttgtg gcaagtcatg 360
agctatgcga tcagccttg tggtcccggt aaagacacaa gcaaaaatgg gggcgttcaa 420
actttccaca acacgccttc aaatcaatgg ggaggcacta ccattacttg tggcactact 480
ggttatgaac caggaccata cagcatttta tccactgaaa attacgcgaa aatcaataaa 540
gcttatcaaa tcatccaaaa ggcttttggg agcagcggaa aagatattcc tgccttaagc 600
gacaccaaca cagaactcaa attcacaatc aataaaaata atggaaacac gaatacgaat 660
aataatggag aagaaattgt tacaaaaaat aacgctcaag ttcttttaga acaggctagc 720
accattataa ctacccttaa tagcgcatgc ccatggatca acaatggtgg tgcaggtggt 780
gcgagtagtg gtagtttatg ggaaggaata tatttgaaag gcgatgggag cgcttgcggg 840
atttttaaaa atgaaatcag cgcgattcaa gacatgatca aaaacgctgc aatagccgta 900

gagcaatcca agatcgttgc tgcaaacgcg caaaaccagc gcaacctaga caccgggaag 960
acattcaacc cctataaaga cgccaacttc gcccaaagca tgttcgctaa cgccaaagcg 1020
caagcggaga ttttaaaccg cgcccaagca gtggtgaaag actttgaaag aatccctgca 1080
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gatgtctgga cctatggcgt ggggagcgat ttgttagtga atttcatcaa cgataaagcc 1740
actaaacaca ataagatttc ttttggcgcg tttggcggta tcgccttagc cgggacttca 1800
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aacacggcga atttccaatt cttattcaat ctgggtttga gaatgaacct cgctaggaaa 1920
aagcatagag cgaccgataa cgcggcccaa catggcattg aactaggcac aaagatcccc 1980
acgatcaaca cgaattacta ttctttgcta ggcactacct tgcaatacag aaggctttat 2040
agcgtgtatc tcaactatgt gttcgcttac taa 2073

<212> Type : DNA
<211> Length : 2073
SequenceName : SEQ ID 483
SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori, strain J99
<400> PreSequenceString :

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gctgaagatg acggatttta catgagtgtg ggctatcaaa tcggtgaagc ggtccaaaaa 120
gtgaaaaaca ctggagcatt acaaaatctt gcagacagat acgataactt gagcaacctt 180
ttaaaccaat acaattactt aaattcctta gtcaatctag ccagcacgcc tagcgcgatt 240
accggtgcga ttgacaatct aagctcaagc gcgatcaatc tcactagcgc taccaccact 300
tctccggcct atcaagctgt ggctttagcg ctcaatgcgg ctgtgggcat gtggcaagtc 360
atagcctttg gcatcagctg tggccctggc cccaatcttg gcccagaaca tttagaaaat 420
gggggcgttc gatcgtttga caacacgcca aactacagct acaacaccgg tagcggaacg 480
accaccacca cttgtaatgg agccagtaat gtagggccca atggtatcct atctagcagc 540
gaataccagg ttctcaatac cgcttatcaa actatccaaa ccgctttaaa ccaaaaccaa 600
ggaggcggga tgcctgcctt gaatagctcc aaaaatatgg tagtcaatat caatcaaact 660
ttcacaaaaa accctaccac agaatacact taccccgatg ggaatggcaa ttattattca 720
ggcggttcat caatcccaat ccagctaaag attagtagcg tcaatgacgc tgaaaacctt 780
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ttgggcgtga aaatccccac cattaacacg gattattatt ctttcatggg ggctgaactc 2040
aaatacagaa ggctctatag cgtgtatctc aattatgtgt ttgcttacta a 2091

<212> Type : DNA
<211> Length : 2091

SequenceName : SEQ ID 484
SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori, strain J99
<400> PreSequenceString :

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gctgaagatg acggatttta catgagtgtg ggctatcaaa tcggtgaagc ggtccaaaaa 120
gtgaaaaaca ctggagcatt acaaaatctt gcagacagat acgataactt gagcaacctt 180
ttaaaccaat acaattactt aaattcctta gtcaatctag ccagcacgcc tagcgcgatt 240
accggtgcga ttgacaatct aagctcaagc gcgatcaatc tcactagcgc taccaccact 300
tctccggcct atcaagctgt ggctttagcg ctcaatgcgg ctgtgggcat gtggcaagtc 360
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gaataccagg ttctcaatac cgcttatcaa actatccaaa ccgctttaaa ccaaaaccaa 600
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ttgggcgtga aaatccccac cattaacacg gattattatt ctttcatggg ggctgaactc 2040
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<212> Type : DNA
<211> Length : 2091
SequenceName : SEQ ID 485
SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori, strain J99
<400> PreSequenceString :

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gactattctg ggcaggtcaa tttgggttat agcgggatta ccgcgcctaa gagttggcaa 180
gatgaagaag tgaaaaaata cacaggaagc cgcacggtga tctctaacaa agcgctcacc 240
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atcatcacta aacctatccc taatcaatgg gaaaaccaag cggctgaaag gatcacttat 600
tgggctaagg ctagaaacgc tgggtttgcc gctccccctg ataaaaccgg cgatccttct 660
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ttctaa 2526

<212> Type : DNA
<211> Length : 2526
SequenceName : SEQ ID 486
SequenceDescription :

Sequence.

<213> OrganismName : Helicobacter pylori, strain J99
<400> PreSequenceString :

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ggcgaattga aaaaactttc agacacttat gagaatttga gcaacctttt aaccaatttt 180
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<212> Type : DNA
<211> Length : 2007
SequenceName : SEQ ID 487
SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori, strain J99
<400> PreSequenceString :
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<212> Type : DNA
<211> Length : 2007
SequenceName : SEQ ID 488
SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori, strain J99
<400> PreSequenceString :
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tatttagggg ttgggtatca gcttagcgcg atcaacacgt cttttagcac cagttctata 180
gataaatcgt atttcatgac cggcaatggt tttggcgtgg tgttgggggg gaaatttgtg 240
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tag 663
<212> Type : DNA
<211> Length : 663
SequenceName : SEQ ID 489
SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori, strain J99
<400> PreSequenceString :
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caagccacgc ttttagcatt gagatcggcg ttagggttat ggaatagcat gggctatgcg 360
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<212> Type : DNA
<211> Length : 1932
SequenceName : SEQ ID 490
SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori, strain J99
<400> PreSequenceString :
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<212> Type : DNA
<211> Length : 1452
SequenceName : SEQ ID 491
SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori, strain J99
<400> PreSequenceString :
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aaaatcaata aagaaagagg catctaccct atgcagcaat tcgcaacgat tgcgggctat 180
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<212> Type : DNA
<211> Length : 1416
SequenceName : SEQ ID 492
SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori, strain J99
<400> PreSequenceString :
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gtttttgctt cctcttttgg ggtgtttggg gggttaaggg gcttatacaa tagctactat 2040
gtcttcaatc aagtcaaagg aagcggtaat ttagatatag taaccgggtt taattaccgc 2100
tacaagcatt ctaaatattc cataggcgtt agcgttcctt taatccaaag cggtattaag 2160
atcgcttcta ataatggtat ctatgcagac tctgttgttt tgaatgaagg gggtagccat 2220
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<212> Type : DNA
<211> Length : 2256
SequenceName : SEQ ID 493
SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori, strain J99
<400> PreSequenceString :
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tttcttaacc ctttaatggc agaagacgat gggtttttta tgggggtgag ttatcaaact 120
tctttggccg ttcaaagggt ggataactca gggcttaacg ccagtcaaga cgcatccact 180
tatatccgcc aaaacgctat cgctctagaa tctgcggcgg tgcctttagc ctattattta 240
gaagcgatgg gccaacaaac gagagtctta atgcaaatgc tctgccctga tccttctaaa 300
agatgtttgc tctatgcagg gggctatcaa aacggacaaa ataataacgg cgatacaggc 360
aacaaccccc caagaggcaa tgtcaatgcc acctttgata tgcaatctct agtcaataat 420
ttaaacaagc tcacccaact catcggcgaa actttaatcc gtaaccctga aaatcttcct 480
aactccaaag tctttaacgt caaatttggc aatcaaagca ctgttattgc attgcctgag 540
ggtctagcca ataccatgga cgctttaaac aatgacatca ccaacgcttt aaccacgctc 600
tggtataacc aaaccttaac gaataaatct tttagcaccc ctagtaacac ttctgtgaat 660
tttagccccc aagtcttgca acacctttta caagacggct tagccacagc aaataataat 720
caaaccattt gcagcactca aaaccaatgc accgccacta atgaagctaa atctatcgct 780
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gtggatggca accatcttaa acctaaggac acttctttcc aattcctttt tgatttgggc 1920
ataaggacca atttttccaa aatcgctcat caaaaaagat cccgtttttc tcaagggata 1980
gaatttggcc ttaaaatacc ggtgctttat cacacctatt accaatcaga aggcgttaca 2040
gcgaagtata gaagagactt tagtttttat gtgggctaca acataggctt ttga 2094

<212> Type : DNA
<211> Length : 2094
SequenceName : SEQ ID 494
SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori, strain J99
<400> PreSequenceString :
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gaagacaacg gctttttgt gagcgcgggc tatcaaatcg gcgaagcggt gcaaatggtc 120
aaaaacaccg gtgaattgaa aaacttgaac gaaaaatacg agcaattaag ccagtattta 180
aatcaagtgg cttcgttgaa gcaaagcatt caaaacgcca acaacattga gctggtcaat 240
agctctttaa actatttaaa aagctttacc aacaacaact acaacagcac cacccaatcg 300
cccatcttta acgccgtgca agccgttatc acttcggtat tgggtttttg gagtctttat 360
gcggggaact atctcacttt ttttgtggtt aataaggata ctcaaaaacc cgctagtgtc 420
cagggtaacc ctccttttc aactattgtt caaaactgct caggaattga aaactgcgcg 480
atgaatcaaa ccacttatga taagatgaaa aagctcgctg aagatctcca agcagcccaa 540
caaaacgcta ccactaaagc gaacaatctt tgcgctttat ccggatgcgc cacaacacaa 600
ggccaaaacc caagctcaac cgtaagcaac gctcttaact tagcgcaaca gcttatggat 660
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gctaagaaaa aagacagcga acgttccgcg caacatggcg ttgaactggg cattaaaatc 1860
cctaccatta acaccaatta ttattctttt ctaggcacta agctagaata cagaaggctt 1920
tatagcgtgt atctcaatta tgtgtttgct tattaa 1956
<212> Type : DNA
<211> Length : 1956
SequenceName : SEQ ID 495
SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori, strain J99
<400> PreSequenceString :
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gaagcctttc aaaaacacca aaaagacggc ttttttcatag aagccggctt tgaaaccggg 120
ctattacaag gcacacaaac ccaagaacaa accatagcca ccactcaaga aaaacccaaa 180
cccaaaccca aaccaaaacc cattacccct caaagcacct atgggaaata ctacatctcc 240
caaagcacca ttttaaagaa tgcgactgag ttgtttgcag aggataatat caccaactta 300
acctttttact ctcaaaaccc tgtgtatgta accgcttata accaagaaag cgctgaagaa 360
gctggctatg gtaataacag cttgattatg atacaaaact tcttgcctta taacttgaac 420
aacattgagc tgagttacac ggacgatcaa ggcaatgtgg tcagtttggg cgtgatagag 480
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cagaatctgt ttaacaagct cagcaaggtt acaaccaatc ttcaaatgac ttatatcaat 660
tacaaccaat tttctagcgg taacggcagt ggctctaaac ccccatgccc cccatacgaa 720
aaccaagcaa attgtgtggc taaagtgccg cctttcacct ctcaagacgc taaaaatttg 780
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cttacatgcg tgaatcctta caacgatggg cttgttgatc ctaaattgat cgccaaaaat 960
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ctagggttgt cttcttatgg cattatcaaa tacaactacg ctcaagccaa caacgaaaaa 1860
atccagcaat taagctatgg cgtgggaatg gatgtgctgt ttgatttcat caccaattac 1920
actaacgaaa agaaccccaa aagcaatcta accaagaaag ttttcacttc ctctcttggg 1980
gtgtttgggg ggttaagggg cttatacaac agctattatt tgttgaacca atacaaaggg 2040
agcggtaatt taaatgtgac cggtgggttg aattaccgct acaagcattc caaatattct 2100
ataggcatta gcgttccttt ggtccagttg aaatctagga tcgtttctag cgatggtgct 2160
tataccaatt ctatcaccct caatgaaggg ggcagtcatt ttaaagtgtt ttttaattac 2220
gggtggattt tctaa 2235

<212> Type : DNA
<211> Length : 2235
SequenceName : SEQ ID 496
SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori, strain J99
<400> PreSequenceString :
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ggctttttca tagaagccgg ctttgaaact gggctattag aaggcacaca aacgcaagaa 120
aaaagacaca ccaccacaaa aaacacttac gcaacttaca attatttacc cacagacacg 180
attttaaaaa gagcggctaa tttattcacc aatgccgaag cgatttcaaa attaaaattc 240
tcatctttat cccctgttag agtgttgtat atgtataatg gtcaattaac tatagaaaac 300
ttcttgcctt ataatttaaa taatgttaag cttagtttta cagacgctca aggcaatgtg 360
atcgatctag gcgtgataga gactatcccc aaacactcta agattgtttt gcccggagag 420
gcatttgata gtctaaaaat tgacccctat actttatttc ttccaaaaat tgaagccact 480
agcacttcta tttctgacgc taacacgcag agggtgtttg aaacgctcaa taagattaag 540
acaaatttgg tcgtaaatta taggaatgaa aacaaattta aagatcacga aaatcattgg 600
gaagccttta ccccacaaac cgcagaagaa ttcactaatt taatgttgaa catgatcgct 660
gttttagact cccaatcttg gggcgatgcg atcttaaacg ctccttttga gttcactaac 720
agcccaacag attgcgataa tgatccttca aaatgcgtaa atcctgggac aaacgggctt 780
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agtgatatta cccctagcaa caatgatgat ggcaagcatt atggccagtt aggggtagta 960
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aagccaaaag attctgatgg cctcccctat aatgtgtgtt cgctttatgg gggatccaat 1200
cagcccgctt tccctagcaa ctaccctaat tccatctatc acaattgtgc ggatgtcccg 1260
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gttaccaacc accatttttc aaacgcatcg caaagtttta gaagccctat ttttaggggtt 1500
aacgctaaaa taggctatca aaactacttt aatgatttca tagggttggc ttattatggc 1560
atcatcaaat acaattacgc taaagctgtt aatcaaaaag tccagcaatt gagctatggt 1620
gggggatag atttgttatt ggatttcatc accacttact ccaataaaaa tagccctaca 1680
ggcattcaaa ccaaaaggaa tttttcttca tcttttggta tctttggggg gttaaggggc 1740
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accgggttga actaccgcta taagcattct aaatattctg tagggattag catcccttta 1860
atccaaagaa aagctagcgt cgtttctagc ggtggcgatt atacgaactc ttttgttttc 1920
aatgaagggg ctagccactt taaggtgttt ttcaattacg ggtgggtgtt ttag 1974

<212> Type : DNA

<211> Length : 1974
SequenceName : SEQ ID 497
SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori, strain J99
<400> PreSequenceString :
atgagtctag ctacgagtta caatgtgagt aataattttt ctaagtttaa tattaagaga 60
gtcagaggat atttgatttg tcttgtttgt aacacaccta aaatgataca aagaggattg 120
aatggtgtct cattttatgg ttgctctgat tatgtaaata aaggcgactg taagggcgtt 180
ttacgagaaa taaatggctc aatgaaaatg gtctgcttac attgtgaaaa cacgcccata 240
atggaaaaag tagaaagtgg taggggagga gcttacgctt gtaagaattg caataggaag 300
ttttacttta tcgatcttgc aaaacaaaac gaacgaaaaa aagatttaga aaaagaagaa 360
aaagaattgc ttaataagat tgaaaagcaa aaaatcaaac accttgagcg tttcattttg 420
gctggtgtaa aagctaatat taaagaaaat tctttttctt taggatgtaa aaattatcct 480
aagtgcgaat ggactgctag tatggattca caagatctta aatgtcccaa atgcaacaga 540
ttaatgaaaa gaaaaaagaa tttcaaaaac aatgagtttt ttacagctac atcgcttacc 600
ttaaatgcaa tagaattttg tctctatatt aatttgaaaa aaaaggaaac caatgtttag 660

<212> Type : DNA
<211> Length : 660
SequenceName : SEQ ID 498
SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori, strain J99
<400> PreSequenceString :
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ttatccaaac ttcaagctta taaattcaac atgagtattg ttggaaaggt gagcagctat 120
actaagtttg gctttaacaa ccaaagatac cagccttcta aagacattta tcctacaggt 180
agttatactt ctttactcgg cgaattgaat ttgagcatgg gattatacaa gggcttgagg 240
gcagaagtag gggctatgat ggcagcgctt ccctatgact ctaccgccta tcaaggcaat 300
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caatacattg gctggtatgc aggacatagc ggtttaaacg tgcaaaaacc tcgtttggct 420
atggtgcata acgcttttct gagctacaac tacaagaaag acaaattcag ttttggcgtg 480
aaaggggggc gctatgatgc tgaagagtat gattggttca cttcttacac tcaaggggtt 540
gaaggctttg tcaaatacaa agacaccagg ttaagggtga tgtattcaga cgctagggct 600
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atgattgcgg atttgaaata cgaaaaagac aacctaaaaa tcaaccctta tttttatgcg 720
atctttcaaa gaatgtatgc gccaggcatt aatatcactt acgacaccaa ccctaatttc 780
aacaataagg gctttcgttt tgtaggcact ttcgtggggt ttttccccat ttttgccact 840
ccggctaatc aaaatgatat tatcctattc caacaagtgc cattaggaaa gagcgggcaa 900
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aaaaatatcg gtaacgctaa tggcgatata ggtatttatg gcgaccctct agggtataac 1020
atttggacga atagtattta tgacgcagaa attaacaata tcgttggcgc tgatgttatt 1080
aacgggtttt tatatgtagg ctcgcagtat agggggttta gttggaaaat tttaggccgt 1140
tggacggata gcccaagggc tgatgaaagg agtctcgcgc tctttttgag ttatttttct 1200
aataagtata atattagaat ggatttgaaa ctagaatatt atggcaatat caccaaaaaa 1260
ggctattgta ttgggtattg tggcatgtat gttccagttg atcctaatgg gcctggcacg 1320
caacctttaa cacacaacgt gtattctgac aggagccata tcatgtttaa cattacttat 1380
ggttttagga tttactag 1398

<212> Type : DNA
<211> Length : 1398
SequenceName : SEQ ID 499
SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori, strain J99
<400> PreSequenceString :
atgaaaaaga caattctact ctctctctct ctctctctcg cttcatcgct cttgcatgct 60
gaagacaacg gctttttttgt gagcgcgggc tatcaaatcg gcgaagcggt gcaaatggtc 120
aaaaacaccg gcgaattgaa aaacttgaac gacaaatacg agcagttaag ccaatcttta 180
gcccaactgg cttcgttaaa aaaaagcatt caaacggcga acaacattca ggctgtcaac 240
aatgctttaa gcgatttaaa aagctttgcg agtaacaacc acacaaacaa agaaacatcg 300

cccatctaca acaccgcgca agctgttatc acttcagtat tggctttttg gagtctttat 360
gcagggaacg ctctcagttt tcatgtgacc ggtttgaatg atggatctaa ttctccttta 420
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acttatgata aaatgaagac acttgccgaa aacctccaaa aagctcaagg caatctctgt 540
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cttcaaaccg cgcaacagct catggactta atcgaacaga ccaaggtttc tatggtgtgg 660
aaaaatatcg tcatcgcagg tgttacaaac aaacccaatg gtgctggcgc tatcacatcc 720
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ttagcggcga tgagcaataa ccccttaaa aaagtgggca tgatcagctc tcaaaacaat 1380
aacggcgctt tgaacgggct tggcgtgcaa gtgggttata aacaattctt tggcgaaagc 1440
aaaagatggg ggttaaggta ttatggtttc tttgattaca accacggcta tatcaaatcc 1500
agctttttta attcttcttc tgatatatgg acttatggcg gtgggagcga tttgttagtg 1560
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ttgaggacga atctcgctac agctaagaaa aaagacagcg aacgttccgc gcaacatggc 1800
gttgaactgg gcattaaaat ccctaccatt aacaccaatt attattcttt tctaggcact 1860
aagctagaat accgaaggct ttatagcgtg tatctcaatt atgtgtttgc ttattaa 1917

<212> Type : DNA
<211> Length : 1917
SequenceName : SEQ ID 500
SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori, strain J99
<400> PreSequenceString :
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ttgttcacta cgggttcatt aggggcggtt acttatgaag tgcatgggga ttttatcaac 120
ttctccaaag tgggttttaa ccgttcgcct attaaccctg ttaaaggtat ctatcctaca 180
gaaacttttg ttaaccttac gggtaagcta gaggggtctg tgcatttagg taggggatgg 240
accgtgaatg taggcggtgt tttgggcgga caagtttatg ataacactag gtatgatagg 300
tgggcaaagg attttacccc cccaagctat tgggataaaa cttcttgcgg cactgattct 360
ttgagccttt gtatgaatgc gactaaaatg tggcaacagc aagggccagg tggtatcatt 420
gaccctaggg gtattggcta tatgtatatg ggtgagtgga acggcttgtt ccctaattac 480
tatccggcta acgcctactt gcccgggcat tcaaggcgct atgaagttta taaagcgaat 540
cttacctatg acagcgacag agtccatatg gtaatggggc gctttgatgt taccgagcag 600
gagcaaatgg attggattta ccaattgttc caaggttttt atgggacttt caagcttact 660
aagaacatga aattcttgct ctttagctct tggggtcgtg gtatcgctga tggtcaatgg 720
ttgttcccta tctatcgtga aaagccttgg ggtattcata aggcgggtat tatttatcgc 780
cctacaaaga atctaatgat ccacccttat gtgtatctca tcccaatggt aggtacattg 840
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aaaacgactt tctatgtgtt gtatgactat cgttggaata acgctgaata cggccgttac 960
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caaggtcctg gtggtgcgac gctctatttg caccaccaca tagacattaa caactacttt 1080
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aaccctgtgg ctcttgatgg tatcgaacaa tgggtcggtg gcatctacag cttaggcttt 1200
gcggggattg acaacattac cgatgctgat gcgttcactg agtatgttaa aggtggaggt 1260
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caaggccctc aaaacatggg tggtatcgca aaaagcatta ctcaagacag aagccatttg 1560
atgacacaca tcagttatag tttctaa 1587

<212> Type : DNA
<211> Length : 1587
SequenceName : SEQ ID 501

SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori, strain J99

<400> PreSequenceString :

atgaaaaact tttccccact ctattgtctt aaaaagctca aaaaacgcca tttaatcgct 60
ctgagtctgc ccttgctttc ttatgcgaat ggctttaaaa tccaagagca aagcttgaat 120
ggcacggctt taggctcggc gtatgtcgct ggggctaggg gtgctgacgc ttctttttac 180
aacccggcta acatgggctt tactaacgat tggggcgaaa acagaagcga atttgaaatg 240
accaccaccg tgatcaatat cccggccttt agctttaaag tccctacgac caatcaaggc 300
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aacactatag ggttaggcaa tatccttaaa gcgcttggca atacggccgc taccaatggc 420
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gttttaccta aattctttta taaaacgcgc acgcataacg gcttcacttt tggggggagt 600
tttaccgctc ctagtgggtt gggtatgaaa tggaatggta agggggggga atttttgcat 660
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gcctctttag gctatcgctg gtaa 1764

<212> Type : DNA

<211> Length : 1764

SequenceName : SEQ ID 502

SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori, strain J99

<400> PreSequenceString :

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gcggctgatg acgcatcagg catgacggtg gcggattctt tgcgttcgca agcgagcagt 180
ttgggtcaag cgattgccaa cacgaatgac ggcatgggga ttatccaggt tgcggataag 240
gctatggatg agcaattaaa aatcttagac accgttaagg ttaaagcgac tcaagcggct 300
caagatgggc aaactacgga atctcgtaaa gcgattcaat ctgacatcgt tcgtttgatt 360
caaggtttgg ataatatcgg taacacaacg acttataacg ggcaagcgtt attgtctggt 420
caattcacta acaaagaatt ccaagtaggg gcttattcta accaaagcat taaggcttct 480
atcggctcta ccacttccga taaaatcggt caggttcgta tcgctacagg cgcgttaatc 540
acggcttctg gggatattag cttgactttt aaacaagtgg atggcgtgaa tgatgtaact 600
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atcaataaaa actctaaccg aacaggggtt aaagcttatg cgagcgttat caccacgagc 720
gatgtggcgg tccagtcagg aagtttgagt aatttaacct taaatgggat tcatttgggt 780
aatatcgcag atattaagaa aaacgactca gacggaaggt tagtcgcagc gatcaatgcg 840
gtcacttcag aaaccggtgt ggaagcttat acggatcaaa aagggcgctt gaatttgcgc 900
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cgcgatgtta ctgggaattt taacgctaat gtcaaatcag ccagtggcgc gaactataac 1200
gccgtgatcg ctagcggtaa ccaaagcttg ggatctgggg ttacaacctt aagaggcgcg 1260
atggtggtga ttgacattgc cgaatcagcg atgaaaatgt tggataaagt ccgctctgac 1320

ttaggttctg tgcaaaatca aatgattagc actgtgaata acatcagcat cactcaagtg 1380
aatgttaaag cggctgaatc tcaaatcagg gatgtggatt tcgctgaaga gagcgcgaat 1440
ttcaacaaaa acaacatttt ggcgcaatca ggcagctatg cgatgagtca agccaatacc 1500
gttcaacaaa atatcttaag gcttttaact tag 1533

<212> Type : DNA
<211> Length : 1533
SequenceName : SEQ ID 503
SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori, strain J99
<400> PreSequenceString :
atggcaggca caeaagctat atatgaatca tcttctgcag gattcttatc gcaagtctcc 60
tcaatcatct caagcacaag tggtgtcgca gggccatttg caggaatagt agcgggcgct 120
atgacagcag cgattattcc tattgttgtg ggatttacta atccgcaaat gaccgctatc 180
atgacccaat acaatcaaag catcgctgaa gctgtaagcg tgcctatgaa agccgctaac 240
caacaataca accaattgta tcaaggtttt aacgatcaaa gcatggctgt ggggaacaat 300
atcttaaata tcagcaaatt aacaggggaa tttaacgcgc aaggcaacac gcaaagcgcg 360
caaattagtg ctgtcaatag tcagattgca agcattttag cgagtaacac tacccctaaa 420
aatcctagcg ctattgaagc ttatgcgacg aatcaaatcg ctgttcctag cgtgccaaca 480
acggttgaaa tgatgagcgg tatattaggc aatattacaa gcgcagcacc aaaatacgcc 540
ctagctctac aagagcaact gcgttctcaa gcaagcaaca gctcaatgaa tgatacagcc 600
gattcccttg atagctgtac cgctttaggc gcacttgttg gctcatcaaa agtgtttttc 660
agttgcatgc aaatttctat gactcctatg agtgtttcta tgcccactgt ttatgccaaa 720
taccaagcgg ttgccactaa agccctaact tcaggcgtta atcctatgac cactcctgca 780
tgccctattg gggacaaggt tcttgccgtt tattgctatg ctgaaaaagt agcagaaatt 840
ttgagagaat actatataga atttgtgaaa aacaatacca atttgttgca gaacgcttct 900
caaatgatac ttaatcaatc aggattagct actagcacct atgacactca agcgatttct 960
aacataagct cgctatataa ttacaatata gtagcgaata aatctttttt gaaatcgcat 1020
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gaaagggtgc agactaaaat aatcgtgaag tga 1113

<212> Type : DNA
<211> Length : 1113
SequenceName : SEQ ID 504
SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori, strain J99
<400> PreSequenceString :
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tttatcaata atcttcaagt ggcttttatt aaagttgata atgttgtcgc ttcatttgat 120
cctaatcaaa aaccaatcgt tgataagaat gatagggata ataggcaagc ttttgagaaa 180
atctcgcagc taagggagga attcgctaat aaagcgatca aaaatcctac caaaaagaat 240
cagtattttt caagctttat cagtaagagc aatgatttaa tcgacaaaga caatctcatt 300
gatacaggtt cttccataaa gagctttcag aaatttggga ctcagcgtta ccaaattttt 360
atgaattggg tgtcccatca aaacgatccg tctaaaatca acacccaaaa aatccgaggt 420
tttatggaaa atatcataca acccccatc tctgatgata aagagaaagc ggagtttttg 480
aggtctgcca aacaagcttt tgcaggaatt atcataggaa accaaatccg atcggatcaa 540
aaattcatgg gcgtgtttga tgaatctttg aaagagaggc aagaagcaga aaaaaatgga 600
gagcctaatg gagatcctac tggtggggat tggcttgata ttttttatc atttgtgttt 660
aacaaaaaac aatcttccga tctcaaagaa acgctcaatc aagaaccagt tcctcatgtc 720
caaccagatg tagccactac caccactgac atacaaagct taccgcctga agctagggat 780
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aagggtgtgg gtgctacgaa tggcgtttcc catttagaag caggctttag caaggtagct 1620
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aaaggtggtt tccaaaaatc ttaa 3504

<212> Type : DNA
<211> Length : 3504
SequenceName : SEQ ID 505
SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori, strain J99
<400> PreSequenceString :
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gtggtggctt tattagtggg gtgtagcccg catattattg aaaccaatga agttgctttg 120
aaattgaatt accatccagc tagcgagaaa gttcaagcgt tagatgaaaa gattttactt 180
ttaaggccag ctttccaata cagcgataat attgctaaag agtatgaaaa caaattcaag 240
aatcaaacca cgcttaaagt tgaagagatc ttgcaaaatc agggctataa ggttattaat 300
gtggatagca gcgataaaga cgatttttct tttgcgcaaa aaaaagaagg gtatttggct 360
gtcgctatga atggcgaaat tgttttacgc cccgatccta aaaggaccat acagaaaaaa 420
tcagaacccg ggttattatt ctccactggt ttggataaaa tggaaggggt tttaatcccg 480
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catagcggag ggttagttag cactatggtt aaggggacgg ataattctaa tgacgcaatt 660
aagagcgctt tgaataagat ttttgcaagt atcatgcaag aaatggataa gaaactcact 720
caaaggaatt tagaatctta tcaaaaagac gccaaggaat taaaaaacaa gagaaaccga 780
taa 783

<212> Type : DNA
<211> Length : 783
SequenceName : SEQ ID 506
SequenceDescription :

Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
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acgttgtcac tagccaacac ctacctcctc caagaccaca acaccctcac cccctacacg 120

ccctttacga caccgctcaa tgggggctg gatgtcgtgc gcgccgccca tttacacccc 180
tcatacgaac tcgtggactg aaagcgggtg ggggatacca agttggtggc gctggtccgc 240
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<212> Type : DNA
<211> Length : 3657
SequenceName : SEQ ID 507
SequenceDescription :

Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :

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<212> Type : DNA
<211> Length : 4884
SequenceName : SEQ ID 508
SequenceDescription :

Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
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<212> Type : DNA
<211> Length : 3903
SequenceName : SEQ ID 509
SequenceDescription :

Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
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aaaagcccag aagttgtttg aacagctcat taa 453

<212> Type : DNA
<211> Length : 453
SequenceName : SEQ ID 510
SequenceDescription :

Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
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<212> Type : DNA
<211> Length : 2181
SequenceName : SEQ ID 511
SequenceDescription :

Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
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actaatgatg attttttcgc gaagattcaa agcgaagttt ttgatcaatg ggctgagtac 660
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<212> Type : DNA
<211> Length : 714
SequenceName : SEQ ID 512
SequenceDescription :

Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
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gctaaattgc cttatgttag aacaaatggt aattacgaaa aactcaacaa ttacttcact 180
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atcttagaag acattcaaaa gaaggttcaa gaatttgtta aaaacaagct taaaccaacc 360
ttagcaccac gacaaactta cagtaatgta attttgttaa acgttaacaa cgataaggtt 420
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<212> Type : DNA
<211> Length : 1719
SequenceName : SEQ ID 513
SequenceDescription :

Sequence

<213> OrganismName : Mycoplasma pneumoniae
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aaattgctca aatag 3735

<212> Type : DNA
<211> Length : 3735
SequenceName : SEQ ID 514
SequenceDescription :

Sequence

<213> OrganismName : Mycoplasma pneumoniae
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<212> Type : DNA
<211> Length : 969
SequenceName : SEQ ID 515
SequenceDescription :

Sequence

<213> OrganismName : Mycoplasma pneumoniae
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<212> Type : DNA
<211> Length : 1158
SequenceName : SEQ ID 516
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
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<212> Type : DNA
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SequenceDescription :

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<213> OrganismName : Mycobacterium tuberculosis H37Rv
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<212> Type : DNA
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SequenceDescription :

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<213> OrganismName : Mycobacterium tuberculosis H37Rv
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<212> Type : DNA
<211> Length : 4983
SequenceName : SEQ ID 521
SequenceDescription :

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<213> OrganismName : Mycobacterium tuberculosis H37Rv
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<212> Type : DNA
<211> Length : 4146
SequenceName : SEQ ID 522
SequenceDescription :

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<213> OrganismName : Mycobacterium tuberculosis H37Rv
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<212> Type : DNA
<211> Length : 3921
SequenceName : SEQ ID 523
SequenceDescription :

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<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :

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<212> Type : DNA
<211> Length : 4311
SequenceName : SEQ ID 524
SequenceDescription :

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<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
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<212> Type : DNA
<211> Length : 7572
SequenceName : SEQ ID 527
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
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<212> Type : DNA
<211> Length : 2337
SequenceName : SEQ ID 528
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
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<212> Type : DNA
<211> Length : 3240
SequenceName : SEQ ID 529
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
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<212> Type : DNA
<211> Length : 4617
SequenceName : SEQ ID 530
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
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<212> Type : DNA
<211> Length : 2772
SequenceName : SEQ ID 531
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
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<212> Type : DNA
<211> Length : 2250
SequenceName : SEQ ID 532
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
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<212> Type : DNA
<211> Length : 2562
SequenceName : SEQ ID 533
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv

<400> PreSequenceString :
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<212> Type : DNA
<211> Length : 1857
SequenceName : SEQ ID 534
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
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<212> Type : DNA
<211> Length : 3162
SequenceName : SEQ ID 535
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
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attggttcgg cgatcagcac ggcaaatggt gcggcggcac tcccgactgt tgaggtggtg 120
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<212> Type : DNA

<211> Length : 1848

SequenceName : SEQ ID 536

SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv

<400> PreSequenceString :

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gctgctgtct ctttcggctc ggtgacagcc gggctggtcg gcgggtcgtg gcagggtcgg 180
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ttcttccaga gcaccacgcc ataa 2964

<212> Type : DNA

<211> Length : 2964

SequenceName : SEQ ID 537

SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
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gccgcgggtg ctgatgaggt ttccgcggca atcgcgtcgc tgtttggggc gcatggtcag 180
gcgtatcagg cggtgagcgc ccaaatgtcg gcgtttcacg cccagttcat gcaggcgttg 240
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ggcgagccgg gggcgaacgg gtag 2304
<212> Type : DNA
<211> Length : 2304
SequenceName : SEQ ID 538
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
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atccggtcgg cgatcagcgc cgcgaccgcg gcggccgcgg ccccgacgat ccaggttgcc 120
gcggccggcg ccgacgaggt gtcgctggcc atctcggcgc tgtttggcca gcacgcccag 180
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<212> Type : DNA
<211> Length : 2196
SequenceName : SEQ ID 539
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :

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accaacgtgg gcagcggcaa catcggcagc accaacgtgg gcagcggcaa catcggcgac 120
acgaacttcg gtaacggcaa caacggcaac ttcaactttg gtagcggcaa taccggcagt 180
aacaacatcg gcttcggaaa caccggcagc gggaatttcg gtttcggaaa cacgggcaac 240
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<212> Type : DNA
<211> Length : 1065
SequenceName : SEQ ID 540
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :

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gggttgccgt ag 2352

<212> Type : DNA
<211> Length : 2352
SequenceName : SEQ ID 541
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
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<212> Type : DNA
<211> Length : 2085
SequenceName : SEQ ID 542
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
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gccgcgggtg ccgatgaagt ctcgacggcg gttgcggcgc tgttcggcgc ccacggccag 180
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<212> Type : DNA
<211> Length : 2514
SequenceName : SEQ ID 543
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :

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gccgccggtg ccgatgagat ctcggcggca atcgctgcgt tgttcggcgc gcacggccgg 180
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<212> Type : DNA
<211> Length : 2745
SequenceName : SEQ ID 544
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
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gccgcgggcg ccgatgaggt gtcggcggcg atcgcgacgc tgtttggcag ccatgctcgg 180
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atctga 2226

<212> Type : DNA
<211> Length : 2226
SequenceName : SEQ ID 545
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
atgtcgtttg tcacggcagc tccagagatg ctggcgacgg cggcgcagaa tgtcgcgaat 60
atcggcacat cgctgagtgc ggcaaacgcg acggcagcgg cgtccacgac ctcggtgctg 120
gcggccggag ccgacgaggt atcgcaggct atcgcaaggc tgttcagtga ttacgccacg 180
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ggaccgtcgt ag 1632

<212> Type : DNA
<211> Length : 1632
SequenceName : SEQ ID 546
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
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ggcgcagcgt ttggcggtaa cggcaacacc ggcggcaacg gcggcaacgg cggcgccccc 1620
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<212> Type : DNA
<211> Length : 1821
SequenceName : SEQ ID 547
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
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<212> Type : DNA
<211> Length : 1731
SequenceName : SEQ ID 548
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
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<212> Type : DNA
<211> Length : 1920
SequenceName : SEQ ID 549
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
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gcctaccagg cggcgagcgc acaggcggcg gcgttttacg cccagttcgt gcaggccctg 240
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<212> Type : DNA
<211> Length : 2406
SequenceName : SEQ ID 550
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
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<212> Type : DNA
<211> Length : 1305
SequenceName : SEQ ID 551

SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :

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ggttcggcgc cgatgcttca ggcggcggcg gcctgggacg ggctggccgc ggagttggga 120
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<212> Type : DNA
<211> Length : 1659
SequenceName : SEQ ID 552
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :

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ccgtag 1086

<212> Type : DNA
<211> Length : 1086
SequenceName : SEQ ID 553
SequenceDescription :

Sequence

<213> OrganismName : Rickettsia prowazekii strain Madrid E

<400> PreSequenceString :

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ggagggcgtg aaattaaaat atcggcagat aaagcaaatg ctatcattgg aggaatcaat 240
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cctcttaatg caggagaaga tcttaatact aattttggcc ctcttaaatt tattagtaat 360
aatgttacgt caattattac aggagtcggt actaaaacat ttagtaatat cgattttgct 420
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acagtagccg gaaataatgg ttcaataaca tttgaaggta gcggtattat atcaaatcac 540
ataggctaca ctaactctct tttaggaata aatgtaggaa acggagaagc caagatttat 600
gccccagaag caaataatat tacaattaat gctaaaaata taaatcttac tcacaataac 660
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<212> Type : DNA
<211> Length : 7023
SequenceName : SEQ ID 554
SequenceDescription :

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<213> OrganismName : Rickettsia prowazekii strain Madrid E
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<212> Type : DNA
<211> Length : 4932
SequenceName : SEQ ID 555
SequenceDescription :

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<213> OrganismName : Porphyromonas gingivalis W83
<400> PreSequenceString :

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<212> Type : DNA
<211> Length : 6318
SequenceName : SEQ ID 556
SequenceDescription :

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<213> OrganismName : Porphyromonas gingivalis W83

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<212> Type : DNA
<211> Length : 6615
SequenceName : SEQ ID 557
SequenceDescription :

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<213> OrganismName : Porphyromonas gingivalis W83
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<212> Type : DNA
<211> Length : 2823
SequenceName : SEQ ID 558
SequenceDescription :

Sequence

<213> OrganismName : Porphyromonas gingivalis W83
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<212> Type : DNA
<211> Length : 5121

SequenceName : SEQ ID 559
SequenceDescription :

Sequence

<213> OrganismName : Porphyromonas gingivalis W83
<400> PreSequenceString :
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ctaagtgaag ccgatgtgga gtgtacaatc aaaatagaag ccgaggatgg ctatgccaac 180
gacatttggg cagacctcaa cggaaacggc aagtacgatt cgggggagag gctcgattca 240
ggtgagtttc gtgatgttga gttcagacaa acaaaggcca tcgtctatgg caaaatggcc 300
aaattcttgt ttagaggttc ttctgcaggg gactatggtg ctacctttat agatattagc 360
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caggtatata ccgtgggagg aagcatgatg tactcatctg tcgcttccgg atcagccatg 1380
gaaatacagc tcccgagagg tgcagcctat gtagtacgta tcggcagcca tgcgatcaaa 1440
accgcgatgc cgtaa 1455
<212> Type : DNA
<211> Length : 1455
SequenceName : SEQ ID 560
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
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tcattcgcct gtaaaaccgc caatggtacc gctatcccta ttggcggtgg cagcgctaat 120
gtttatgtaa accttgcgcc tgtcgtgaat gtggggcaaa acctggtcgt agatctttcg 180
acgcaaatct tttgccataa cgattatccg gaaaccatta cagactatgt cacactgcaa 240
cgaggctcgg cttacggcgg cgtgttatct aatttttccg ggaccgtaaa atatagtggc 300
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gatgattttc agtttgtgtg gaatatttac gccaataatg atgtggtggt gcccactggc 540
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taa 903
<212> Type : DNA
<211> Length : 903
SequenceName : SEQ ID 561
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
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tccccctgc tgatagctgc tgatacagga agtcaatatg gcaccaatat tactattaat 180
gatggtgaca gaattacagg agataccgcc gatccatcag gaaacctcta tggtgtaatg 240
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gctaaccgac tcacagtaga tgttgttggt caaacctctg ccatcggcat taacttaatt 420
ggtgactata cccatgctga cttaggcaca ggcagcacca ttaagagtaa cgatgacggc 480
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atcaagaccg atggaagtac aggtgtttat atcggtggtc tcaacggcaa taacgccaat 660
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agtgcacagt ataacaaaca gcacacattc tatctcgaag cggattacac gcagggtaac 2820
ctctttgatc agaagcaagt caacggagga tatcgcttca gctttaa 2868

<212> Type : DNA
<211> Length : 2868
SequenceName : SEQ ID 562
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 24 57T
<400> PreSequenceString :
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acggcaacaa tcgctgcggg taacaacggt actgcacgtt tttacggcac cattgaagac 120
tcagtgtgtt ctatcgttcc ggacgatcac aaactggaag ttgatatggg tgatatcggt 180
gccgaaaaac tgaaaaataa cggcaccacc acgccgaaaa gtttccagat tcgtctgcaa 240
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gcaaatagcg gcaattatta caccatttcc aataccgata ccggtgcggc atttaacaat 360
gttagcctgg cgatcggtga ctctctgggt acctcttaca aaagcggcat gggtattgac 420
cagaaaatag tgaaagacac ttctaccaac aaaggcaaag cgaagcagac actgaacttt 480
aacgcctggc tggtcggcgc agctgatgcg ccagatctgg gtaatttga agcaaatacc 540
accttccaga ttacttacct gtaa 564
<212> Type : DNA

<211> Length : 564
SequenceName : SEQ ID 563
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
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gctctggccg atactacgac ggtaaatggt gggaccattc actttaaagg ggaagttgtt 120
aacgccgctt gcgcagttga tgcaggctct gttgatcaaa ccgttcagtt gggacaggtt 180
cgtaccgcta gcctgaagca ggctggagca accagctctg ccgttggttt taacattcag 240
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attgatgcta cgcgtactga tgtactggct ctgcagagtt ctgctgcagg tagtgcaaca 360
aacgttggcg tgcagatcct agacagaaca ggcaatgctc tgacgctgga cggtgcgaca 420
tttagtgcac aaacaaccct gaataacggt accaacacca ttccgttcca ggcgcgttat 480
tatgcaatcg gcgaggcaac cccgggtgca gctaatgcgg atgcaacctt caaggttcag 540
tatcaataa 549
<212> Type : DNA
<211> Length : 549
SequenceName : SEQ ID 564
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
atggcaagta tttcatcgct gggagtcggg tcaggtctgg atttaagttc aatccttgat 60
agcctcaccg ccgcgcaaaa agcgacgcta acccctattt caaatcagca atcgtcgttt 120
accgctaaac ttagcgccta cggtacgctg aaaagcgcgc tgacgacttt ccagaccgcc 180
aatactgcat tgtctaaagc cgatcttttt tccgccacca gcaccaccag cagcaccacc 240
gcgttcagtg ccaccaccgc gggtaacgcc atcgccggga aatacaccat cagcgtcacc 300
catctggcgc aggcgcaaac cctgaccacg cgcaccacca gagatgatac gaaaacggcg 360
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acccaactgg acgttttaat gacctcgtta aacagcacca gcagctactt aacgcagcag 1380
ttcgaaaaca acagtaattc caagtaa 1407
<212> Type : DNA
<211> Length : 1407
SequenceName : SEQ ID 565
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
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ggacacacag ccactaatac ccgcgtggat gatggcggaa cgctggatgt ccgcaacggt 120
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cgcggtacag ccctgaagct gaccggcagc actgtgctga acggtgccat tgaccccacg 660
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gcaaccggaa aaaccatcct gaacctggtg aacgccggca acagtgcgtc ggggctggcg 960
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gcctttatcc aggggaataa gctgcaggcc ggtgccttta actactccct caaccgggac 1080
agtgatgaga gctggtatct gcgcagtgaa aatgcttatc gtgcagaagt ccccctgtat 1140
gcctccatgc tgacacaggc aatggactat gaccggattc tggcaggctc ccgcagccat 1200
cagaccggtg taagcggtga aaataacagc gtccgtctca gcattcaggg cggtgatctc 1260
ggtcacgata acaacggcgg tattgcccgt ggagccacgc cggaaagcag cggcagctat 1320
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aacgcctccg gcctgtgggc tgacattgtg gcccagggaa cccgccacag catgaaagcc 1560
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aaaggcacct catcccgtga cacccgcgc ggcagtgcca aacacagtgt gcgtgaactg 1860
ccggtgaact ggtgggtaca gccttctgtt atccgcacct tcagctcccg gggggacatg 1920
agcatgggta cagccgcagc cggcagtaac atgacgttct caccgtcaca gaatggtacg 1980
tcactggacc tgcaggccgg actggaagcc cgtgtccggg aaaatatcac cctgggcgtt 2040
caggccagtt atgcccacag catcaacggc agcagcgctg aaggttataa cagtcaggcc 2100
acactgaatg taaccttctg a 2121

<212> Type : DNA
<211> Length : 2121
SequenceName : SEQ ID 566
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
atggcctttt ctcaagcggt tagcggatta aacgctgccg ccaccaacct cgatgttatt 60
ggcaacaata tcgccaactc cgccacctac ggctttaaat caggcacggc ctcttttgcc 120
gatatgtttg ccggttcgaa agtgggactg ggggtaaaag ttgccggtat cactcaggac 180
tttaccgatg gcacgaccac caacaccggg cgaggtctgg acgttgctat cagccagaac 240
ggtttttttcc gtctggtaga cagcaacggt tcggtgttct acagccgtaa cggacaattt 300
aagctggatg aaaaccgtaa cctgttgaat acgcaaggtt tacagctgac gggttacccg 360
gtaaccggta cgccgccgac tattcagcaa ggggcgaatc cgaccaatat ttcgatcccg 420
aatacctga tggcagcgaa aactaccacc acggcgtcga tgcagatcaa cctgaattcc 480
agtgatccgc ttcctactgt tacgccattc agcgccagca atgcggatag ctataacaaa 540
aaaggttcgg tgactgtttt cgacagtcag ggtaatgctc atgacatgag cgtctatttt 600
gtgaagaccg gggataataa ctggcaggtc tacacccagg atagcagtga tccaaacagc 660
attgcgaaga cagcgacaac actggaattt aatgctaatg gcacattagt ggatggtgcg 720
atggcgaata atatcgcaac cggcgcaatt aacggtgcag aacccgccac gtttagtctg 780
agcttcctca actccatgca gcaaaatacc ggcgctaaca acattgtggc aaccacccag 840
aatggctaca aaccgggcga tctggtgagt tatcaaatca atgatgacgg tacggttgtc 900
ggcaacaatt ccaacgaaca aacccaactg ctggggcaga ttgtactggc gaactttgcc 960
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gaagcgtcca acgtcgatct cagtaaagaa ctggtcaata tgatcgttgc ccagcgtaac 1140
tataagtcta acgcccagac catcaaaacc caggaccaga tcctcaacac gcgggttaac 1200
ttacgctaa 1209

<212> Type : DNA
<211> Length : 1209
SequenceName : SEQ ID 567
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T

<400> PreSequenceString :
atgaaactcg tgcacatggc cagtggttta gcggttgcga ttgcgttggc ggcttgcgca 60
gataaaagcg cggatattca gacgccagcc ccggctgcaa atacgtctat ttcagcaaca 120
caacaacctg ctatccagca accgaatgtc tccggtactg tctggatccg tcagaaagtc 180
gcactgccgc ctgatgctgt gctgaccgtg acactttctg acgcgtcgtt agccgatgca 240
ccgtcaaaag tgctggcgca gaaagcggtg cgtactgaag gtaaacagtc accattcagc 300
tttgttctgc catttaaccc ggcagatgtt cagccgaacg cgcgtattct gttgagtgcg 360
gcgattaccg tgaatgacaa actggtattt atcaccgata ccgttcagcc ggtgatcaac 420
cagggcggaa ctaaagccga cctgacattg gtgccggtac agcaaaccgc cgtgccggtt 480
caggccagcg gtggcgcaac gactaccgta ccttcgactt caccaactca ggtgaatccg 540
tcttcggcag ttcccgctcc tacgcaatat taa 573
<212> Type : DNA
<211> Length : 573
SequenceName : SEQ ID 568
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
atgatcataa aaaaagcgg tggtcgctgg cagctaagcc tgctggcgag cgtggtaatc 60
agtgcctttt ttctcaacac agcttacgcc tggcaacaag aatatatcgt tgatacgcaa 120
cccggacatt ccacagagcg ttacacctgg gatagtgatc atcaacctga ttacaacgat 180
attttgtcgc aacgtattca aagtagccaa agggcgctgg gactggaagt caatctggcg 240
gaagaaactc ctgtggatgt gaccagcagt atgagtatgg gctggaattt tcctttatat 300
gaacaggtta caaccggccc ggtcgcggca ttacattacg atggcacaac cacctcgatg 360
tataacgagt ttggcgacag tactaccacg ctgaccgatc cgttatggca tgccagcgtg 420
agtagcttag gctggcgtgt tgactcccgg cttggcgatc tccgaccctg ggcgcaaatc 480
agctataacc agcaatttgg cgagaatatc tggaaggcgc aatcaggcct gagccggatg 540
acggcgacaa accagaacgg caactggctg gatgtcaccg taggcgctga tatgttgctc 600
aatcaaaata ttgccgccta tgctgcgcta actcaggcag aaaataccac taataatagc 660
gactatctgt atacgatggg ggttagcgcc agattttaa 699
<212> Type : DNA
<211> Length : 699
SequenceName : SEQ ID 569
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
atgaaatggt gcaaacgtgg gtatgtattg gcggcaatgt tggcgctcgc aagtgcgacg 60
atacaggcag ccgatgtcac catcacggtg aacggtaagg tcgtcgccaa accgtgtacg 120
gtttccacca ccaatgccac ggtagatctc ggcgatcttt attctttcag tcttatgtct 180
gccggggcgg catcggcctg gcatgatgtt gcgcttgagt tgactaattg tccggtggga 240
acgtcgaggg tcactgccag cttcagcggg gcagccgaca gcaccggata ttataaaaac 300
caggggaccg cgcaaaacat ccagttagag ctacaggatg acagtggcaa cacattgaat 360
actggcgcaa ccaaaacagt tcaggtggat gattcctcac aatcagcgca cttccgtta 420
caggtcagag cattgacggt aaatggcgga gccactcagg gaaccattca ggcagtgatt 480
agcatcacct atacctacag ctga 504
<212> Type : DNA
<211> Length : 504
SequenceName : SEQ ID 570
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
atgaaaagag cgcctcttat aacaggactt ttgttgatat ccacatcctg cgcttatgcc 60
tcctcaggag ggtgtggagc cgacagcact agcggtgcga caaattacag cagtgtggtt 120
gatgatgtta cggtgaacca gacagataac gtgacaggac gggagtttac ctctgcaacg 180
ctaagtagca ctaactggca atacgcctgt tcctgctctg cgggtaaggc agttaaactt 240
gtctatatgg tcagccccgt acttaccacc actggacatc agacaggata ttacaaactc 300
aatgacagcc tggatattaa aaccacatta caggcaaacg acattccagg actcacaacc 360
gaccaggttg tctctgttaa cacccgattc acacagataa aaagcagcac cgtatatttct 420
gctgcaaccc aaacgggtgt ttgccagggt gacacgtctc gttatggacc cgttaatatt 480

ggtgcaaata ccacctttac cctgtatgtc accaagccat ttctcggctc gatgaccatt 540
ccgaaaacgg atattgccgt cattaaaggc gcgtgggtcg atggaatggg aagcccgtct 600
acaggtgact tccatgattt agtcaagtta tcgattcagg gaaatctcac cgccccacag 660
tcgtgcaaaa ttaatcaggg cgatgttatt aaagttaatt ttggattcat caatggtcag 720
aagtttacca cccgcaatgc catgccagac ggttttactc cagtagactt tgatatcact 780
tatgactgtg gtgatacttc aaagattaaa aactcgttgc aaatgcgcat cgacggtaca 840
actggggtag tagaccagta caacctggtc gccaggcgaa gaagttcaga caatgtgccc 900
gatgtcggta ttcgtattga aaatctcggc ggcggagttg caaatattcc ttttcagaac 960
ggtatccttc ccgttgatcc ttccgggcat ggcaccgtca atatgcgcgc ctggccagtt 1020
aatctggtcg gtggtgagct ggaaacagga aaatttcagg gcacagccac cattaccgtc 1080
atggtgcggt aa 1092

<212> Type : DNA
<211> Length : 1092
SequenceName : SEQ ID 571
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
atgcaaaaaa acgctgcgca tacttatgcc atttccagct tgttggtgct ttcactaacc 60
ggctgcgcct ggatacctc cacgccgctg gtgcaggggg cgaccagtgc acaaccggtt 120
cccggtccga cgcccgtcgc caacggttct attttccagt ctgctcagcc gattaactat 180
ggctatcaac cgctgtttga agatcgtcga ccacgcaata ttggcgatac gctgaccatc 240
gtgttgcagg agaacgtcag cgccagcaaa agctcctctg cgaatgccag ccgtgacggt 300
aaaactaatt ttggctttga tactgtgccg cgctatttgc aggggctgtt tggtaacgct 360
cgtgccgatg tcgaagcctc cggtggtaac acgttcaacg gaaagggcgg ggccaatgcc 420
agcaatacct ttagcggcac gttgacggtg acggttgacc aggtactggt caacggcaac 480
ctgcatgtgg tgggtgaaaa acagattgcc attaatcagg gtaccgaatt tattcgcttc 540
tcgggcgtgg ttaatccacg cactatcagc ggcagcaata ccgtaccgtc tactcaggtg 600
gcggatgcgc gtattgaata cgtaggcaat ggctacatta acgaagcgca aaatatgggc 660
tggttgcagc gtttcttcct taacctgtcg ccaatgtaa 699

<212> Type : DNA
<211> Length : 699
SequenceName : SEQ ID 572
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
atgaaacgac atctgaatac ctgctacagg ctggtatgga atcacattac gggcgctttc 60
gtggttgcct ccgaactggc ccgcgcacag ggtaaacgtg gcggtgtggc ggttgcactg 120
tctcttgccg cggtcacgtc actcccggtg ctggctgctg acatcgttgt gcacccgggt 180
gaaacagtga atggcggaac actggtaaac catgacaacc agtttgtatc cggaacagct 240
gatggcgtga ctgtcagtac cgggcttgag ctggggccgg acagtgacga aaacaccggc 300
gggcaatgga taaaagcggg tggcacaggc agaaacacca ctgtcaccgc aaatggtcgt 360
cagattgtgc aggcaggagg aactgccagt gatacggtta ttcgtgatgg cggagggcag 420
agccttaacg gactggcggt gaacaccacg ctggataaca gaggtgagca gtgggtacac 480
gggggaggga aagctgccgg tacaattatt aaccaggatg gttaccagac cataaaacat 540
ggcggactgg caaccggaac catcgtcaac accggtgcag aaggtggtcc ggagtctgaa 600
aatgtgtcca gcggtcagat ggtcggaggg acggctgaat ccaccaccat caataaaaat 660
ggccggcagg ttatctggtc ttcggggatg gcacgggaca ccctcattta cgccggtggt 720
gaccagacgg tacacggaga ggcacataac acccgactgg agggggtaa ccagtatgta 780
cacaacggtg gcacggcaac agagacgctg ataaaccgtg atggctggca ggtgattaag 840
gaaggaggaa ctgccgcgca taccaccatc aaccagaaag aaagctgcag gtga 894

<212> Type : DNA
<211> Length : 894
SequenceName : SEQ ID 573
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
atgatgatga aaactattaa acatcttctg tgctgtgcca ttgccgccag cgcattaatt 60

tccaccgggg tgcatgctgc gtcctggaaa gatgcgctct ccagcgccgc cagcgaactt 120
ggcaaccaaa acagcacgac acaggaaggc ggttggtcgc tcgcgtcatt aactaacttg 180
cttagcagcg gaaaccaagc cttaagcgca gataacatga acaatgccgc aggcattctg 240
caatactgcg cgaagcaaaa gctggcttcg gtaaccgatg ccgaaaacat caagaaccag 300
gtgctggaaa agctgggcct gaacagtgaa gagcaaaaag aagacaccaa ctatctggac 360
ggtattcagg gtttgctgaa aacaaaagat ggtcagcaac tcaatctgga taacatcgga 420
acgactccgc tggcagaaaa ggtgaaaacc aaagcctgcg atctggtgtt aaagcagggg 480
ctgaacttca tttcctga 498

<212> Type : DNA
<211> Length : 498
SequenceName : SEQ ID 574
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
atgtttaaag gacaaaaaac attggccgca ctggccgtat ctctgctgtt cacagcacct 60
gtttatgcgg ctgatgaagg atccggtgaa attcacttta aaggtgaagt tattgaagca 120
ccgtgtgaaa tacatcagga tgatattgat aaagaggttg aactcggtca ggtgaccacc 180
agccacatta atcagtcaca tcacagcgat gccgttgctg tcgacctgct cttagtcaac 240
tgtgatctgg aaaactccag caacggttcc ggtggcaaga tttctaaagt tgcagtcacc 300
tttgatagct cagcgaaaac caccggcgca gatccgattc tcaacaacac cagcacgggt 360
gaagccaccg gcgtcggcgt acgtttaatg aataaagatc aaagcaatat cgttttaggc 420
accgctactc cagatatcga cctggctccg acctccagcg aacaaacgct gaatttcttt 480
gcctggatgg aacaaattga tcaggctaca cctgtaacgc caggcgcagt tacggcgaat 540
gcaacctacg tgctggatta taaataa 567

<212> Type : DNA
<211> Length : 567
SequenceName : SEQ ID 575
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
atgagcgcgg gaagcccaaa attcaccgtt cgccgcattg cggctttgtc actggtttcg 60
ctatggctgg caggctgttc tgacacttca aatccaccgg caccggtcag ctccgttaat 120
ggcaatgcgc ctgcaaatac taattctggt atgttgatta cgccgccgcc gaaaatgggg 180
acgacgtcta cagcgcagca accgcaaatt cagccggtac agcagccaca aattcaggct 240
actcaacaac cgcaaatcca gccagtgcag ccagtagctc agcagccggt acagatggaa 300
aacggacgca tcgtctataa ccgtcagtat gggaacattc cgaaaggcag ttatagcggc 360
agtacctata ccgtgaaaaa aggcgacaca cttttctata tcgcctggat tactggcaac 420
gatttccgtg accttgctca gcgcaacaat attcaggcac catacgcgct gaacgttggt 480
cagaccttgc aggtgggtaa tgcttccggt acgccaatca ctggcggaaa tgccattacc 540
caggccgacg cagcagagca aggagttgtg atcaagcctg cacaaaattc caccgttgct 600
gttgcgtcgc aaccgacaat tacgtattct gagtcttcgg gtgaacagag tgctaacaaa 660
atgttgccga acaacaagcc aactgcgacc acggtcacag cgcctgtaac ggtaccaaca 720
gcaagcacaa ccgagccgac tgtcagcagt acatcaacca gtacgcctat ctccacctgg 780
cgctggccga ctgagggcaa agtgatcgaa acctttggcg cttctgaggg gggcaacaag 840
gggattgata tcgcaggcag caaaggacag gcaattatcg cgaccgcaga tggccgcgtt 900
gtttatgctg gtaacgcgct gcgcggctac ggtaatctga ttatcatcaa acataatgat 960
gattacctga gtgcctacgc ccataacgac acaatgctgg tccgggaaca acaagaagtg 1020
aaggcggggc aaaaaatagc aaccatgggt agcaccggaa ccagttcaac acgcttgcat 1080
tttgaaattc gttacaaggg gaaatccgta aacccgctgc gttatttgcc gcagcgataa 1140

<212> Type : DNA
<211> Length : 1140
SequenceName : SEQ ID 576
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
gtgattaaat ttctctctgc attaattctt ctactggtta cgacggcggc tcaggctgag 60
cgtattcgcg atctcaccag tgttcagggg gtaaggcaaa actcactgat tggctatggc 120

ttggtagtgg ggctggatgg cactggtgac cagacaaccc agacgccgtt taccacacaa 180
acgcttaata acatgctctc acagctggga attaccgttc cgacgggcac caatatgcag 240
ctaaaaaacg tcgctgcggt aatggtgaca gcgtcacttc ctccgtttgg acgtcagggg 300
caaaccatcg atgtggtggt ttcttccatg ggtaatgcca aaagcttgcg tggaggtacg 360
ttgttgatga caccgcttaa gggcgttgac agtcaggtgt atgcgctggc gcagggcaat 420
attctggttg gcggcgcagg agcctccgca ggcggtagca gtgttcaggt taaccaactg 480
aacggtggac ggatcaccaa tggtgcggtt attgaacgtg aattgcccag ccagtttggc 540
gtcgggaata cccttaattt gcaacttaac gacgaagatt tcagcatggc gcagcaaatc 600
gctgacacca tcaaccgcgt gcgtggatat ggcagcgcca ccgcgttaga tgcgcggact 660
attcaggtgc gcgtaccaag tggcaacagt tcccaggtcc gtttccttgc cgatatccag 720
aatatgcagg ttaatgtcac cccgcaggac gctaaagtag tgattaactc gcgcaccggt 780
tcggtggtga tgaatcgcga agtgaccctc gacagctgcg cggtagcgca gggaaatctc 840
tcagtaacag ttaatcgtca ggccaatgtc agccagccag atacaccgtt tggtggtgga 900
cagactgttg ttactccaca aacgcagatc gatttacgcc agagcggcgg ttcgctgcaa 960
agcgtacgtt ccagcgccag cctcaataac gtggtgcgtg cgctcaatgc gctgggcgct 1020
acgccgatgg atctgatgtc tattttgcaa tcaatgcaaa gtgcgggatg tctgcgggca 1080
aaactggaaa tcatctga 1098

<212> Type : DNA
<211> Length : 1098
SequenceName : SEQ ID 577
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
atgaaacgtt caattattgc tgccgctgtc ttttcttctt tttttatgag cgctggagta 60
tttgctgcag acgttgatac cggaacatta accattaaag gaaatattgc agaatctccg 120
tgtaaattcg aagcgggtgg tgattcagta agtattaata tgccgactgt accaaccact 180
gtctttgaag gtaaagctaa atattctacc tatgatgatg cagtcggtgt aaccagcagc 240
atgttaaaaa ttagctgccc gaaagaagtt gctggtgtaa aactctcgtt gatcacaaac 300
gacaaaataa ccggtaacga taaggcgata gccagtagca acgataccgt aggtgataac 360
agcgatgtcc tagatgtttc tgcacctttt aacattgaga gttataaaac agcggaaggt 420
caatatgcta ttccgtttaa agcaaaatac ctgaaactga cagataactc agtgcaatca 480
ggtgatgtgt tatcttctct ggttatgcgt gtggcgcagg attaa 525

<212> Type : DNA
<211> Length : 525
SequenceName : SEQ ID 578
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
atggcggttc aaaagaatgt tatcaaaggc atactggcag gtacgtttgc gctaatgctg 60
agcggttgtg tcactgtgcc ggacgccatt aaaggcagca gtaccacgcc gcaacaagat 120
ttagttcggg tgatgagtgc gccgcagctg tacgttggtc aggaggcacg ctttggtggc 180
aaagtggttg cggtacaaaa ccagcaaggg aaaacccgcc tggaaattgc taccgtaccg 240
ctggacagcg gagctaggcc gacgctggga gaaccttctc gcggtcgcat ttatgccgat 300
gtgaacggtt ttctggaccc ggtggatttc cgtggacaac tggttacggt agtcgggcca 360
atcaccggtg cggttgacgg caaaatcggc aatacgccct ataaatttat ggtgatgcaa 420
gtaacgggtt acaaacgttg gcatttaacc cagcaggtga ttatgccgcc tcagccgatt 480
gatccatggt tttatggcgg tcgtggctgg ccctatggct acggcggatg gggctggtat 540
aatcccggcc ccgcgagagt acaaacagtt gtaaccgaat aa 582

<212> Type : DNA
<211> Length : 582
SequenceName : SEQ ID 579
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
atgagaaaca aacttttta tcttctgtgc gcttttttgt ggctggcggt aagtcgcgtt 60
ttggctgcgg atagcacgat tactatccgc ggctatgtca gagataacgg ctgtagtgtg 120
gccgctgaat caaccaattt tactgttgat ctgatggaaa acgcggcgaa gcaatttaac 180
aacattggcg cgacgactcc tgtcgttcca tttcgtattt tgctgtcacc ctgtggtaat 240

gccgtttctg ccgtaaaagt tgggtttacc ggcgttgcag atagccacaa tgccaacctg 300
cttgcacttg aaaatacggt gtcagcggct gcgggactgg gaatacagct tctgaatgag 360
cagcaaaatc aaataccgct taatgctcca tcgtctgcga tttcgtggac gaccctgacg 420
ccgggtaaac caaatacgct gaatttttac gcccggctaa tggcgacaca ggtgcctgtc 480
actgcggggc atatcaatgc tacggctacc ttcactcttg aatatcagta a 531

<212> Type : DNA
<211> Length : 531
SequenceName : SEQ ID 580
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
atgaaaaagt taacagtggc ggctttggca gtaacaactc ttctttctgg cagtgccttt 60
gcgcatgaag caggcgaatt ttttatgcgt gcaggttctg caaccgtacg tccaacagaa 120
ggtgctggtg gtacgttagg aagtctgggt ggattcagcg tgaccaataa cactcaactg 180
ggcttgacgt ttacttatat ggcgaccgac aacattggtg tggaattact ggcagcgacg 240
ccgttccgcc ataaaatcgg cacccgggcg accggcgata ttgcaaccgt tcaccatctg 300
ccgccaacac tgatggcgca gtggtatttt ggtgatgcca gcagcaaatt ccgtccttac 360
gttggggccg gtattaacta caccaccttc tttgataatg gatttaacga tcatggcaaa 420
gaggcggggc tttccgatct cagtctgaaa gattcctggg gagctgccgg gcaggtgggg 480
gttgattatc tgattaaccg tgactggttg gttaacatgt cagtgtggta catggatatc 540
gataccaccg ccaattataa gctaggcggt gcacagcaac acgatagcgt acgcctcgat 600
ccgtgggtgt ttatgttctc agcaggatat cgtttttaa 639
<212> Type : DNA
<211> Length : 639
SequenceName : SEQ ID 581
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
ttgtttttta agcgaggaaa gattttgagt gcgggacgcc tgaataaaaa atctctgggt 60
atcgtgatgt ttttatcggt tggactgcta ttggcgggct gttcgggtag caaatcatcc 120
gatacaggaa cgtattccgg ctccgtttac accgtgaaac ggggggatac gctatatcgt 180
atttcgcgca ccacgggaac cagcgtaaaa gagctggcgc gactgaacgg catttccccc 240
ccttacacca ttgaagttgg tcagaaacta aaactgggtg gggcgaaaag tagcagtagt 300
acacgtaaat caaccgccaa atcaacgact aaaaccgcat cggttacacc gtcatcagcg 360
gtaccgaaat cttcctggcc gccagtaggg caacgttgtt ggttatggcc aacgacaggg 420
aaagttatca tgccgtattc gacagcagat ggcggcaata aagggattga tatctcagct 480
ccacggggta cacctattta cgccgcgggt gcaggaaagg tggtgtatgt gggcaaccag 540
ctgcgtggct acggtaatct catcatgatt aaacacagtg aagattacat tacggcttac 600
gcccataatg acacgatgct ggtaaataat gggcaaagcg tgaaggctgg gcaaaaaatc 660
gccactatgg ggagcacgga tgcggcatct gttcgcctgc atttccagat tcgttaccgt 720
gcaacggcaa ttgatccgct acgttacttg ccgccgcagg gcagcaagcc aaaatgctga 780

<212> Type : DNA
<211> Length : 780
SequenceName : SEQ ID 582
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
atggcacaag tcattaatac caacagcctc tcgctgatca ctcaaaataa tatcaacaag 60
aaccagtctg cgctgtcgag ttctatcgag cgtctgtctt ctggcttgcg tattaacagc 120
gcgaaggatg acgccgcggg tcaggcgatt gctaaccgtt ttacttctaa cattaaaggc 180
ctgactcagg ctgcacgtaa cgccaacgac ggtatttctg ttgcacagac cactgaaggc 240
gcgctgtccg aaatcaacaa caacttacag cgtatccgtg agctgacggt tcaggcttct 300
accgggacta actctgattc ggatctggac tccattcagg acgaaatcaa atcccgtctc 360
gacgaaattg accgcgtatc cggtcagacc cagttcaacg gcgtgaacgt actggcaaaa 420
gacggttcga tgaaaattca ggttggtgcg aatgacggcc agactatcac tattgatctg 480
aagaaaattg actctgatac gctggggctg aatgggttta atgtgaatgg tggcggggct 540

gtggctaata ctgctgcatc taaagctgac ttggtagctg ctaatgcaac agtggtcggc 600
aacaaatata ctgtgagtgc gggttacgat gctgctaaag cgtctgattt gctggctgga 660
gttagtgatg gtgatactgt tcaggcaacc attaataacg gcttcggaac ggcggctagt 720
gcaacgaatt acaagtatga cagtgcaagt aagtcatact cttttgatac cacaacggct 780
tcagctgccg atgttcagaa atatttgacc ccgggagttg gtgataccgc taagggcact 840
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gatcccctga aagctctgga tgaagccatc agctccatcg acaaattccg ctcctccctg 1440
ggtgcggtgc aaaaccgttt ggattccgca gtcaccaacc tgaacaacac cactaccaac 1500
ctgtctgaag cgcagtcccg tattcaggac gccgactatg cgaccgaagt gtccaacatg 1560
tcgaaagcgc agattatcca gcaggccggt aactccgtgc tggcaaaagc caaccaggta 1620
ccgcagcagg ttctgtctct gctgcagggt taa 1653

<212> Type : DNA
<211> Length : 1653
SequenceName : SEQ ID 583
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
atgaaaaaaa ttgcatgtct ttcagcactg gccgcagttc tggctttcac cgcaggtact 60
tccgtagctg cgacttctac cgtaactggc ggttacgcac agagcgacgc tcagggccaa 120
atgaacaaaa tgggcggttt caacctgaaa taccgctatg aagaagacaa cagcccgctg 180
ggtgtgatcg gttctttcac ttacaccgag aaaagccgta ctgcaagctc tggtgactac 240
aacaaaaacc agtactacgg catcactgct ggtccggctt accgcattaa cgactgggca 300
agcatctacg gtgtagtggg tgtgggttat ggtaaattcc agaccactga atacccgacc 360
tacaaacacg acaccagcga ctacggtttc tcctacggtg ctggtctgca gttcaacccg 420
atggaaaacg ttgctctgga cttctcttac gagcagagcc gtattcgtag cgttgacgta 480
ggcacctgga ttgccggtgt tggttaccgc ttctaa 516

<212> Type : DNA
<211> Length : 516
SequenceName : SEQ ID 584
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
atgaagcgta atattatagg cggtgcattc actctggcat ctctaatgct ggccgggcat 60
gcactggcag aagatggtgt tgttaacttc gtcggtgaaa ttgtcgacac tacttgtgaa 120
gttacctccg atacagccga tcaaattgtc ccactgggta aagtcagtaa aaatgcattt 180
tcaggtgtag gtagtctggc gtcgccacag aagttcagta ttaaacttga aaattgcccg 240
gcaacgtaca ctcaagcagc cgttcgtttt gatggtacag aagcgcctgg cggcgacggc 300
gacctgaaag tgggtacgcc gcttacagca ggcaaccctg gtgattttac cggtacagga 360
caagcgattg cggcaaccgg cgttggtatt cgtattttta accagtccga taattcgcag 420
gttaaacttt ataacgactc tgcttatacc gctatcgatg ctgaaggcaa ggctgaaatg 480
aagtttattg cacgctatgt ggcaaccaat gcgaccgtaa cggctggtac ggcgaacgct 540
gattcacaat ttactgtcga atataagaaa taa 573

<212> Type : DNA
<211> Length : 573
SequenceName : SEQ ID 585
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
atgaaaaaga gcactctggc attagtggtg atgggcattg tggcatctgc atctgtacag 60
gctgcagaaa tatataataa agacggtaat aaactggatg tctatggcaa agttaaagcc 120

atgcattata tgagtgataa cgccagtaaa gatggcgacc agagttatat ccgttttggt 180
tttaaaggtg aaactcaaat taacgatcaa ctgactggtt atggtcggtg ggaagcggag 240
tttgccggaa ataaagcgga gagtgatact gcacagcaaa aaacgcgtct cgcttttgcc 300
gggttgaaat ataaagattt gggttctttc gattatggtc gtaacctggg cgcgttgtat 360
gacgtggaag cctggaccga tatgttcccg gaatttggtg gcgattcctc ggcgcagacc 420
gacaacttta tgaccaaacg cgccagcggt ctggcgacgt atcggaacac cgacttcttc 480
ggcgttatcg atggcctgaa cttaaccctg caatatcaag ggaaaaacga aaaccgcgac 540
gttaaaaagc aaaacggcga tggcttcggc acgtcattga catatgactt tggcggcagc 600
gatttcgcca ttagtggggc ctataccaac tcagatcgca ccaacgagca gaacctgcaa 660
agccgtggca caggcaagcg tgcagaagca tgggcaacag gtctgaaata cgatgccaat 720
aatatttatc tggcaacttt ctattctgaa acacgcaaaa tgacgccaat aactggcggc 780
tttgccaata agacacagaa ctttgaagcg gtcgctcaat accagtttga ctttggtctg 840
cgtccatcgc tgggttatgt cttatcgaaa gggaaagata ttgagggcat cggtgatgaa 900
gatctggtca attatatcga cgtcggtgct acgtattatt tcaacaaaaa tatgtcagcg 960
tttgttgatt ataaaatcaa ccaactggat agcgataata agctgaatat taataatgat 1020
gatactgtcg cggttgggat gacgtatcag ttttaa 1056

<212> Type : DNA
<211> Length : 1056
SequenceName : SEQ ID 586
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
atgcgtaagc agtggctcgg gatctgcatc gcggcaggaa tgctcgcggc atgtacaagc 60
gatgatggtc agcaacagac ggtaagtgta ccgcagcctg cggtatgtaa cggccccata 120
gttgaaatta gcggggcgga cccgcgtttc gaaccactga acgcgacggc aaatcaggat 180
taccagcgcg acggtaaaag ctacaaaatc gtgcaggatc cgtctcgatt tagccaggcg 240
ggactggcgg caatctatga tgccgaacca ggcagtaacc tgacggcctc tggcgaagct 300
ttcgatccga caaagctgac ggcggcccat ccaacgcttc cgatccccag ctacgccaga 360
atcactaacc tggctaacgg gcgaatgatc gtggtgcgca ttaatgatcg cggcccttac 420
ggcaacgacc gcgttatttc gctttctcgc gcggcagctg accgtcttaa cacgtcaaac 480
aacaccaaag ttcgtatcga tccgattatt gtcgcccagg atggttcgct ttctggtcct 540
ggtatggctt gtaccacagt cgccaaacag acttacgccc tgcctgcacc tcccgattta 600
agcggtggcg cgggaacaag ttcagtgtct ggcccgcagg gtgacattct tccggtcagt 660
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ggcgctccaa cgaccttagc gcctggtgta ctggaaggca gcgaaccgac gcctgcgcca 780
cagcccgttg ttacagcttc gtcgacaacg cctgcaacct cgcctgcaat ggtgacaccg 840
caagccgcct cgcaaagcgc cagcggcaac tttatggtgc aagtcggggc cgtaagcgat 900
caggctcgtg cgcaacagta ccaacagcaa ctgggacaga agttcggcgt ccccggtcgc 960
gtaactcaaa atggcgcggt ctggcggatc cagcttggcc cattcgccag caaagccgaa 1020
gccagtacct tgcagcaacg tttgcaaacc gaagcccaat tacagtcatt tattactacc 1080
gcgcagtag 1089

<212> Type : DNA
<211> Length : 1089
SequenceName : SEQ ID 587
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
atgaagaaaa aaacgatata tcagtgcgtt attttgttct ttagccttct taacatccat 60
gtcgggatgg ctgggcctga acaagtcagt atgcatattt atgggaatgt ggtcgatcag 120
ggctgtgatg tcgccaccaa aagtgcatta caaaatattc atattggtga ttttaatatc 180
agtgattttc aggccgcgaa taccgtaagc actgctgctg atttgaatat tgatatcacc 240
ggttgtgccg ctggtattac tggcgcggac gtccttttta gcggcgaggc tgacaccctt 300
gcgccgacac tgctcaaact aactgacaca ggcggaagcg gtggtatggc aacggggatt 360
gccgtgcaaa ttcttgatgc gcaaagtcag caagaaatcc cgctcaatca ggtccagcct 420
cttacgccct taaaagccgg ggataacaca ctcaaatatc aacttcgtta taagtccaca 480
aaggcgggag caacgggcgg taatgcgacg gcggttctct attttgatct ggtttaccag 540
tga 543

<212> Type : DNA
<211> Length : 543
SequenceName : SEQ ID 588
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
atgaaaaaca aattgttatt tatgatgtta acaatactgg gtgcgcctgg gattgcagcc 60
gcagcaggtt atgatttagc taattcagaa tataacttcg cggtaaatga attgagtaag 120
tcttcattta atcaggcagc cataattggt caggctggga ctaataatag tgctcagtta 180
cggcagggag gctcaaaact tttggcggtt gttgcgcaag aaggtagtag caatcgggca 240
aagattgacc agacaggaga ttataacctt gcatatattg atcaggcggg cagtgccaac 300
gatgccagta tttcgcaagg tgcttatggt aatactgcga tgattatcca gaaaggttct 360
ggtaataaag caaatattac acagtatggt actcaaaaaa cggcagttgt agtgcagaga 420
cagtcgcaaa tggcaattcg cgtgacacaa cgttaa 456
<212> Type : DNA
<211> Length : 456
SequenceName : SEQ ID 589
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
gtgatgaaat ttaaaaaatg tcttctgcct gtggcaatgt tagcgtcatt cactctggca 60
ggatgccagt caaatgctga cgatcatgcc gccgatgttt atcaaaccga tcaactgaat 120
accaaacaag aaactaaaac cgttaatatt atttccattc ttcccgcaaa agttgccgta 180
gacaactccc aaaataaacg gaacgcacaa gccttcggcg cgcttattgg cgcagtcgct 240
ggcggtgtta tcggccacaa cgtcggttct ggcagcaatt ccggaacgac ggcaggggca 300
gttggcggcg gagctgtagg cgcggcagcg ggttctatgg tgaatgataa aaccttagtg 360
gaaggtgttt ctttaacata taaggaaggc accaaagtgt atacctccac ccaggagggt 420
aaagagtgcc agtttacgac aggtttagcc gttgttatta ccacaacgta taacgaaacg 480
cgtattcagc caaataccaa atgtcctgaa aagagctaa 519
<212> Type : DNA
<211> Length : 519
SequenceName : SEQ ID 590
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
atgcaaacga aaaaaaatga aatttgggtg ggtatctttt tattagcagc actgctggcg 60
gcgctgtttg tttgcctgaa ggcggcgaac gtgacgtcca tacgtactga atcgacctac 120
acgctttatg cgacgttcga taacattggc ggcctgaaag cgcgctctcc ggtcagcatt 180
ggtggtgttg ttgtgggccg ggtggcggat attacgctgg acccgaaaac ctatctgccg 240
cgcgtaacgc tggaaattga acaacgttat aaccacattc ctgataccag ttcgctgagc 300
attcgtactt ccggcctgct gggagaacaa tatctggcat taaacgtcgg ttttgaagac 360
ccggaactgg ggactgctat cctgaaggat ggcgatacaa ttcaggacac caagtctgcg 420
atggtgctgg aagatctcat tggtcagttc ctttacggta gtaaaggcga tgacaataag 480
aatagtggcg atgcgccagc tgctgcgcca ggtaataatg aaaccactga acctgtgggt 540
acaacgaaat aa 552
<212> Type : DNA
<211> Length : 552
SequenceName : SEQ ID 591
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
atggcaccgt tagccttttc tgcacaatca ttggctgaat cattaacggt ggaacaacgc 60
cttgagttat tagaaaaagc gttaagagaa acgcaaagcg aactcaaaaa gtataaagat 120
gaagagaaga aaaaatatac gccagcgacg gtgaatcgta gcgtaagtac gaatgatcaa 180
gggtatgccg ccaatccgtt cccgaccagt agtgccgcaa aacctgatgc tgtactggtc 240
aaaaatgaag agaaaaatgc cagtgagaca ggctcgattt attcttccat gactctgaaa 300
gatttcagta agtttgtgaa agatgaaatt ggctttagtt acaacggcta ttaccgttct 360
ggttgggga ccgcctctca tggttcacct aaatcatggg cgattggttc tctgggccgc 420
tttggtaacg aatactccgg ctggtttgat ttgcagttaa aacaacgtgt ctacaacgaa 480

aacggcaaac gggttgatgc cgttgtgatg atagatggta acgttggtca gcagtactct 540
accggctggt ttggcgataa tgccggtggc gagaacttta tgcagttctc cgatatgtac 600
gttaccacca aaggtttcct gccctttgcg ccagaggctg atttctgggt gggtaaacac 660
ggtgcgccga aaattgaaat ccagatgctg gactggaaaa cgcagcgtac tgatgctgca 720
gcgggtgtag gtctggaaaa ctggaaagtc ggtccgggta aaattgatat cgcgctggtt 780
cgcgaagatg tcgatgatta cgatcgcagc ctgcaaaaca aacagcagat taatacccat 840
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ggtcgttatg tcacggcaaa cgaaagcgca tcggaaaaag ataatcagga taataacggg 960
tattatgact ggaaagatac ctggatgttc ggcacatctt taacgcagaa atttgataaa 1020
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aaatttaatg agtctggtta taaaaccacg ctcttccata cctttaaagt caataccagt 1440
atgttgacct cgcgtctgga aattcgtttc tacgccacgt atatcaaagc cctggaaaac 1500
gaactggatg gcttcacctt cgaagacaat aaagacgccc agtttgctgt cggtgcccag 1560
gctgaaatct ggtggtaa 1578

<212> Type : DNA
<211> Length : 1578
SequenceName : SEQ ID 592
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
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acattatcag ctgtaaaagc tgatgacttt gatgcgcaga ttgcgtcaca agattctaaa 120
atcaacaact tgaccgcaca acagcaagca gcacaagcac aagttaatac gattcaagga 180
caagtaagtg ctttacagac acaacaagct gaattacaag ctgaaaatca aagacttgaa 240
gctcagtctg ctactttggg tcaacaaatt caaacacttt caagcaaaat tgttgcacgt 300
aatgaatctt tgaagcaaca agctcgtagt gctcaaaaaa gtaacgcagc taccagctat 360
attaatgcta tcattaattc aaaatcagtt tctgatgcta ttaatcgtgt ttcggctatt 420
cgtgaagttg tatctgctaa tgaaaaaatg cttcaacaac aagagcaaga taaagcagct 480
gttgagcaaa agcaacaaga aaatcaagca gcaattaata ctgttgcagc taatcaggag 540
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ctaaacttgc aagctgaatt gactactgca caagatcaaa aagctacttt agttgctcaa 660
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aaggccgcag cagaagcgaa agctttacaa gaacaagcag cgcaagcaca agcagcagca 780
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caagcagcac aaacaggtga ttcaactgag cagtcagcag cacaagcagt aaataattct 900
gatcaagaaa gtactacagc aacagaagca caaccatcag cttctagtgc ttcgacagct 960
gctgtagcag ctaatacttc ttctgctaat acatatccag cagggcaatg tacttggggt 1020
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agtgcagcag cggcaggata tagagttggt tctacacctt cagctggagc tgtagctgta 1140
tggaatgatg gcggttatgg acacgttgct tatgttacag gtgttcaagg tggccaaatt 1200
caagttcaag aagctaacta tgcaggtaac caatctattg gtaactaccg tggttggttt 1260
aatccaggta gtgtaagcta tatctatcca aactaa 1296

<212> Type : DNA
<211> Length : 1296
SequenceName : SEQ ID 593
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
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gctgttctag gaacagtagc agcagtctct gtagcaggac aaaaggtttt tgccgatgaa 120
acgaccacta ctagtgatgt agatactaaa gtagttggaa cacaaactgg aaatccagcg 180
accaatttgc cagaggctca agggagtgcg agtaaggaag ctgaacaaag tcaaaaccaa 240
gctggagaga caaatggttc aataccagtt gaagtaccta aaactgatct tgatcaagca 300
gcaaaagatg ctaagtctgc tggtgtcaat gttgtccaag atgccgatgt taataaagga 360
actgttaaaa cagctgaaga agcagtccaa aaagaaactg aaattaaaga agattacaca 420
aaacaagctg aggatattaa gaagacaaca gatcaatata aatcggatgt agctgctcat 480

gaggcagaag ttgctaaaat caaagctaaa aatcaggcaa ctaaagaaca gtatgaaaaa 540
gatatggcag ctcataaagc cgaggttgaa cgcattaatg ctgcaaatgc tgccagtaaa 600
acagcttatg aagctaaatt ggctcaatat caagcagatt tagcagccgt tcaaaaaacc 660
aatgctgcca atcaagcagc ctatcaaaaa gcccttgctg cttatcaggc tgaactgaaa 720
cgtgttcagg aagctaatgc agccgccaaa gccgcttatg atactgctgt agcagcaaat 780
aatgctaaaa atacagaaat tgccgctgcc aatgaagaaa ttagaaaacg caatgcaacg 840
gccaaagctg aatatgagac taagttagct caatatcaag ctgaactaaa gcgtgttcag 900
gaagctaatg ccgcaaacga agcagactat caagctaaat tgaccgccta tcaaacagag 960
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aaagattga 4689

<212> Type : DNA
<211> Length : 4689
SequenceName : SEQ ID 594
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
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ggcaaagtat ctgatttacc tgttgcagtt gttaataaag ataaaacggc aacttatgaa 180
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gactatcatt ttgttgatag cgaaaaagct caaaagggac ttgaaaaagg tgattactat 300
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ttgttaatcg ctcgaaggag gattaggtct gtcaaagtag cctaa 2505

<212> Type : DNA
<211> Length : 2505
SequenceName : SEQ ID 595
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
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aatagaatta atctcctatt ttttttgatt gtcgctttgt ttactgtttt gcttttgagg 120
ttagctcaga tgcagcttta tgatgcaaag ttttacaaat ctaaattgac agagtcaaca 180

acatatacta taaaaacctc cagccctcgc ggacaaattt atgacgctaa aggggtggct 240
ttagttgaaa acgaggttaa agaggttgtt gcctttacaa gaagcaatac catgactgcc 300
aaggatatta aagcaaatgc aaaaaagtta gcagatatgg tgactttaac tgaatctaag 360
gtaaccaaac gtcagaaaaa agattactat ctggcagatc caaaaaatta tcaaaaaatc 420
gttaaaaaat taccaaataa taaaaaatat gataactttg gaaataacct aacggaatcg 480
aagatctatg caaatgctgt taaagcagtt ccaaacagtg ctattgatta ttctgaagat 540
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gatttaaagg gaatttctgt taagactgac tgggaacgta aaacagataa aaattccatt 720
acttctatta tcggtaaagt ttccagtcaa aaaaccggtc tgcctgctga agaagccaat 780
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gtcttgccac atgagacaga ccttcatgga accactagtc atgctattac gagagatatc 2040
atcaatcttt atcaaaagat gtatccaatg aatcagtga 2079

<212> Type : DNA
<211> Length : 2079
SequenceName : SEQ ID 596
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
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ggtgctgaaa agcgcgaaag tatttcttca gacagtattc caatgaagtt agtaaatgcc 240
gttacctcta ttgaagatca ccgtttcttt aaacatcgtg gtgtcgacat ttatcgtatt 300
attggtgcag cttggagtaa tttacttcat aaatcaactc aaggggatc cactcttgat 360
cagcagctta tcaagctggc ctatttctct actaaagagt ctgatcagac cttaaaacgt 420
aaagctcaag aagtttggct gtctctacaa atggagaaaa aatacacgaa agaagagatt 480
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gcaggtattc cgcaagcacc gacacaatat gatccttacg ctcagccaaa ggcagctaca 660
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gcagctcctg caacttcatc gtcatcttct tcatcatctt cttctgattc aaacaataac 2040
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gctacgacat cttctaatcc ataa 2124

<212> Type : DNA
<211> Length : 2124
SequenceName : SEQ ID 597
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
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gcaacgaatg cttttgcaga tgaagcatca actcaattaa attctgatac tgttgcagca 120
cctactgctg atacacaagc atcagaaccg gctgcaacag aaaaagaaca gtctcctgtt 180
gtagctgttg tcgaaagtca cacacaagga aatacaacaa cgacaacatc tcaagttact 240
tctaaagaat tggaagatgc taaggctaat gctaatcagg aaggtttaga agtcactgaa 300
actgaagctc aaaaacagcc ttcggtagaa gctgcagatg cagataacaa agcacaggca 360
caaacaatta atacagcggt agctgattat caaaaggcaa aagctgaatt tcctcaaaaa 420
caagaacaat ataataaaga ttttgaaaag tatcagtctg atgtcaagga gtatgaagct 480
caaaaggcag cttacgagca atataaaaaa gaagttgcac aaggtttggc atctgggcgt 540
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cagcaatata atactgataa ttatacagct tctgatttta cccaagcaaa tccatatgat 720
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aaagaaaact ag 1752

<212> Type : DNA
<211> Length : 1752
SequenceName : SEQ ID 598
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
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gaacagcctg tcgcagctga gactgtctcg caagctgatg gggacaatcc cgaacaaaca 180
acaagcgttc aacaagaaac tgctcctcaa caaacgaaaa cttctcaaag ctcagacgca 240
accgtagata gtgaagagtc agcaacttcc ccatctgatg aacagaccgt aagtcaaaat 300
gattcaaact catcatctca aattgatcaa acgatagctg atacgaatcg ctctgactct 360
gatcatattt caaaaacatc agccgctaca actgaagatc aagaagagaa agttaattct 420
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gcttatggca attccaattt taacaagaca ttaactgaat ttggaaaaaa tgctaatgtt 540

gctgatgtaa cctataatgg cgtgagggat gaatatattg tagttaacga tcctagtgct 600
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ggtaataaag accaaaattc tcttttctgct caactacctg atacaggagt tcaaaaaaat 1440
aatcaattag ccttgatagc tttaggaaca ggcttgattt tactttccgg acttcttctt 1500
tcaaaaagaa aatccttaaa ataa 1524
<212> Type : DNA
<211> Length : 1524
SequenceName : SEQ ID 599
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
atgacatttg aaaagcaaaa acactttagt ttacgtaaac taaaatttgg tttagtttca 60
gttgcgatca tagctttctt atttgctgta acaaagactg cagaagctga cgagacagtg 120
ataactgaac aaaggcaaac aagtaagatt aacgctagtt ctcaaaaagt ggagaatcag 180
acttcaaatc aggtggaagc aaaaacggat agtgcaaaca aggatcctca agaaaaaaca 240
ggaagtgttg caactgatgc cccttcaatg aattcagcta ataatatgag tcagtctgac 300
aaacaaaata ctgttaatga aatatcttca gatagtcagc aaacaaaaac agatgaacaa 360
actgatttac cgcaaaacag ctttaaacaa caatctgctc atgttaaaat gactactgaa 420
gcagagaaga ccccatcaca ttcgattaat acctttgtta atgatggtaa tggtaattgg 480
tattaccttg gtgctgatgg tagaaatgtt acaggcagtc atacgattgg tggcaagact 540
atgtattttg ctcaagatgg taagcaagtt aaaggtgctt ttgctcaaga ttcggatgga 600
aataaacatt attatgatag agatagtggt gagatgtgga ccaatcgctt tgtcaatgat 660
caaggcaatt ggtattatct taataatgat ggtgtccctg tcaccggtag tattactgtc 720
aatggtcagt ctctgtattt taattcggat ggtagtcagg ttaaagggaa ttttgttgaa 780
gaagatggat ctttgcgtta ttatgataaa aattctggag atttactgag aaagacaagc 840
cgaaccatta atggtgttaa ctaccaattt gataatgatg gaaatgcaag ggcgattgac 900
aaaattgagg ttgttaagac cagtcttgta gttgatagtt atgaatttgg tccttctgtt 960
tcaaagatta ttcttgagtt caatcataag gtaactcctg ctgttgttca tgctggtgca 1020
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ggacatgtgg tttactttga tagtagccat tatgtgacac ttgaattaga tattccttat 1140
gatccaaatg atagcagccg aaatgcatca ccttttattt ttgactcagc agcctttcgt 1200
aataactggg tcaacagtta tactgtcaaa gtagataatt tgcaggtgca agcagatggt 1260
tctaatagca gtcaaattat cagttcagag caagatgcta tcaataatcg tttcttgcct 1320
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ccagaagcag ctattggcgg tgagaagaat ccattgattg tctggttgca tggtatagga 1440
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gatcctattc aaagccattt cacttctaca ggtagtggtg gtcaaaaggg agcctatgtg 1560
ctagttcctc aaagttcaat tccttggtct caaaatcaaa cagctagctt aatggcgctc 1620
attaaagcct atgtagcaag ccatccagac atcgatagcc gacgcattta tttggcaggt 1680
gtttctaatg gtggcggtat gactctggat atgggagtcg cttatcctaa ctattttgca 1740
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caaaataaat ggctttccta ttatgaaact aatgttggta aacatcactc tggagtcact 1980
tataacggtc actggtcttg gatttatttc ttgaatgatc aagtaactgg cactcaaaat 2040
actgataacg ccaagaattg gtctggactt tctggcatgg ttgcgaccaa tccaacctat 2100
ggtggtgatg ctaaggctac tgtcaatggc agaacttata gtaatgtctt tgattggcta 2160
aatggtcagc gaagaaggta a 2181
<212> Type : DNA
<211> Length : 2181
SequenceName : SEQ ID 600
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
atgaaaattt ttataaaaaa acaccaacaa agtattcttt actatagtct tagttttctg 60
ctaccaagtt ttataatgtt tctcgttcta ttctccaaaa atatttattg ggggagtagc 120
acaactattt tagctagtga tggttttcat caatatgtga tttttgatgc tctttttcgt 180
aatattctcc atggaacgga tagtttgttt tactctttta aggctgggct tggttttaat 240
atttttgctc tgacaagtta ttacttggga agtttttttaa caccttttac ttacttttt 300
aatgtaaaaa atatggcaga tgcttttttat ctcttcactt taatcaaatt tggtctaata 360
ggtttatctg ctttttacag tcttgggcaa atttatacta aaatctctaa atcactcgtt 420
ttgatgctgt caacatctta tgctttaatg agctttacta gcagtcagtt agaattaaac 480
aattggttag atgtttttat cctgctacca cttattatgc ttggtttaca gcgtttagta 540
gaaaaaaggg ggatttttct ttattttcta actcttactt gtttatttat tcaaaattac 600
tattttggtt tcatgacagc tattttctta actctttggt tttttacgca agtctcgtgg 660
gatattagaa acagaatgaa acgattaagt gattttgtgc tcgtatcaat ctttgcaacg 720
ctgacaagtg cttttatgct gcttccaaca tttcttgatt taaagagcca tggtgaagta 780
ttaacagaac aaattagtct attttcatca gacatttggt atttcgattt ttttgctaaa 840
agtcttcttg gtagttatga tacgacaaaa tatggctcta ttccaacgat ttatatcggt 900
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aaagtagctt attttctttt attggctatt attattgcaa gttttatctt tcaaccactt 1020
gatttatttt ggcaaggaat gcattcacct aatatgtttt tgcatcgtta ttcttgggct 1080
ttctccttag ttattgtcat aatggcagct gaaacgttaa ctcggataaa ggatataaaa 1140
ttgaaaaatt tttatccagc ctttaccttc ttgggagtag gacttttagc aacttttttа 1200
ttcaaggact attataatta tctgacacaa gttaatttta tattaacaac tatcttttta 1260
gttagttatt ttattattct ttttacttttt tttaatcaat tagtttctta taaagttatt 1320
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gaaggtattc aaactgactg gaatttccct tcaagagagg tttatgaaga taatgtaaag 1440
gaaattgaca actatgttaa gaaaactaaa aaagataact tagaattttt tcgaacagaa 1500
aaacaaattc cccaaactta caatgatggt atgaaattta attataatag catttctcag 1560
ttctcatctg tcaaaaataa cttatcagca caattattga attctctagg ctactattca 1620
caaggaaatc attctaccat tagttatcct aataatacta ttttgatgga tagtcttttt 1680
tcaattaaat acaatattaa taatcaaaat cctcataaat ttggattcca tttaaaacag 1740
aaaaacaata agctgcaact ttacaaaaac ttctattctc ttcctttagc acttatgtca 1800
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gtcggaatgc aagttttaga taatcgtgtt actattaatg gttcaaaagg aaataaggca 1980
caagtttact atactgtaaa gtgtcctgca aatagtcaac tttatatcag ccttcctaac 2040
ttgacagtta ataataaaga cgaaaatgtc tttataacaa ctaacaagca cacaagttct 2100
tatatcatag acgaaagtta ttatcttttt aatttaggaa attataaaaa aactcaaaca 2160
ttaatattta agcttagttt tccaaaaaat aaaacggtta gttatgattt accacatatt 2220
tatgctctcg atttaactgc ctatcaaaaa agtataaagc aattaaaaag tcaaactgtt 2280
aaaacaacaa ctaagaaaaa taaaattttt actacctatg ttgccaaaaa gagaacttcc 2340
ttgatttaca ctttaccata tgataaaggt tggtttgcta aacaaaatgg aaaagcaatt 2400
aaaatatcta aagcacaaaa tggactaatg aaaattgatg tttctaaagg tagtgggaag 2460
attataatga cttttgtgcc ccaaggacta tatcaaggaa ttcttcttac ctgtctaggt 2520
atctttctct ttgtatttta ccaactttat tacaaaaaat ttaatttaaa ataa 2574

<212> Type : DNA
<211> Length : 2574
SequenceName : SEQ ID 601
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
atgaaattga aacatatttt aagaattgga gcggttgctt ttgcctcaat tcttttgtta 60
actgcttgcg gatcaaaaac atctaaaaaa acagtaaccc ttgcgactgt tggaacaaca 120
aatccatttt cttatgagaa aaagggaaaa ttgacgggat atgatatcga agttgctaag 180
gaagttttca aagcttctga taaatacgat gtcaaatatc aaaaaacaga gtggaccagc 240
attttctctg gtctagatag tgacaaatat caaatcggag ctaacaatat cagttatact 300
aaagagcgtg ccaataaata tctttattct aatccaacgg cttccaatcc attggtatta 360
gtggttccaa aagatagtga tattaagtct tataacgata ttgctgggca tagcactcaa 420
gttgttcaag gaaatacaac agtgtctatg ctgcagaaat tcaataaaaa ccatgaaaac 480
aatcaagtta aactaaactt taccagtgaa gatcttgcgc atcaaatccg gaatgtcagt 540

gatggtaagt atgattttaa aatttttgaa aaaatttcag cagaaacgat catcaaagag 600
caaggacttg ataatttgaa agttattgat cttccttcag accaaaaacc atatgtttac 660
tttatttttg cgcaagacca aaaagactta caaaagtttg tcaataaacg tctcaaaaaa 720
ctttacgaga atggtacact tgaaaaatta tcgaaaaaat accttggagg aagctatctt 780
ccagataaaa aagatatgaa ataa 804

<212> Type : DNA
<211> Length : 804
SequenceName : SEQ ID 602
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
atgcgatttc ttgtctttct catcgcattt tttgctgctt tctataaatt tatcgagact 60
gaacggattg attcaaatac agttgctgta aaccctgatt cgctcatttt aaagcgattt 120
ttaaaaacaa atcaattaaa tgggatcatg attgtgacgg ggccagatgg taaggctcaa 180
gtattttcaa atcaaagcaa ggtagatggc agtcctgttt caattaagga ttattttcct 240
cttgcttctt tacaaaaatt gataacaggg gtggctatcc aacaattaat tgataaagga 300
aaactgtctt taaacacacc tttaagcaaa tattatcctc aaattgaaaa tagtgaaaat 360
atcacgatac aaaatttact tacccacaca agcggtttgg cagatcgaaa agaagttcct 420
cagcaagtgc tgacaactca agagcagcaa ttggattttt cattgaccaa ttatcgcgta 480
acttatcgaa aaaaatggaa gtatgctaac attaattatg ctttgctagc tggcattatc 540
agtcaaatta gcggtcaaaa ttatgcgact tatgttcgtc aacacttctt aacagctggt 600
aaggggtggc attttaaaaa gtatattcaa ataaaagata agtccaagtt agctgccttg 660
tcagtgatgg atcaaagtac gacttgggat aagctgtcaa aagaagtgac atctaccttt 720
ggagctggtg attatgcttc taggccagtg gattattgga aatttatgat ggcttttatt 780
aatgaccaat ttgttcctgt cagcgaatac caacgttcta tgaaaatgac ttctaagagc 840
tattatggcg gcctctatat cagccaaaag atgctgcatg caaatggtgg tggctttgat 900
acttactctt gttttgctta ttcaaatcct aaaaccaaac aggtcatggt tttgtttatc 960
acaaacggta agtataaacg ggtcaaatcc ttagcagcta aagcctttaa actatatgca 1020
gattcgtatg cgctgaggaa aaatgaaacg tcaaaataa 1059

<212> Type : DNA
<211> Length : 1059
SequenceName : SEQ ID 603
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
atgaagaaaa aaatagctct agcagctctt tcttttgtca gtgcagctgt tcttgcagct 60
tgcagctcag cacctggtgg ttcatcagat gcagctggta ataaaattgg agatactgta 120
aaaattggtt acaatcttga attatcagga gatgtagccg cttatggaca agctgaaaag 180
aacggtgcta accttgctgt tgaagagatt aataaggcag gcggcattga tggcaaaaag 240
attaaagtta tctcaaaaga taataaatct gataacggtg aagcatcaac aatctcaact 300
aatcttgcta cccaaagtaa agtaaatgct atcttgggac cagcaacatc tggtgctaca 360
gcggctgctg ctcccaatgc caacgatgct gcagtaccac tcgtaacgcc ttctggaaca 420
caagataatt tgacctattc aaaaggcaaa gttcaagatt acatcttccg tacaactttt 480
caagatagct tccaaggaaa gatcattgcc aaatatgcaa cagataattt gaaagctaaa 540
aaagtagcgc tttactatga taagtcaagt gattacgccc aaggtattgc tgatgcattc 600
aaaaaagcat ataaagggaa gattactgtt gaagatacct ttcaagctaa agaccaagat 660
ttccaagcag ctctgaccaa gtttaaaaat aaagactttg atgccattgt gataccaggt 720
tattatactg aaactggtct gattacaaag caagcacgtg atatggggct tacccagcct 780
atcttaggac ctgatggttt taatgatgaa aaatatgttg aaggtgctgg tgcagccaat 840
accaataatg ttcattatgt atctggttac tcaacaaaag ttgctttaac aaataaggct 900
gaaaaattcc tgaaagatta taaggctaag tatggtgaag agccaaatat gtttgccgct 960
cttgcttatg attccgttta tatgattgct gatgctgcaa aagatgccaa aacatctaag 1020
gatattgcaa caaacctagc taaattgaaa aactttaaag gtgtgacagg taaaatgaca 1080
attgataaga aacataaccc tgttaaatca gccgttatgg ttggtcttaa agatggtaaa 1140
gaagacacag ctactgctgt tgaagcaaaa taa 1173

<212> Type : DNA
<211> Length : 1173
SequenceName : SEQ ID 604
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
atgaagaaat taagcttatt attactagtt tgtttatctt tattaggctt atttgcctgt 60
acttctaaaa aaacagccga caaaaaattg actgttgtgg ctaccaattc tattattgct 120
gatattacta agaatatcgc tggtaataag gttgtcttac atagtatcgt tcctgttggt 180
cgagatcctc acgaatatga gcctcttcct gaagatgtta aaaagacctc tcaggctgat 240
gtcatttttt ataatgggat taatcttgaa aatggaggca atgcttggtt taccaaacta 300
gttaaaaatg ctcataaaaa gacagacaag gattattttg cagtgagcga tagtgttaag 360
accatttatt tggaaaatgc aaaagaaaaa ggaaaggaag atcctcatgc ttggcttgac 420
cttaaaaatg gtattattta tgctaaaaat atcatgaaac gtctatctga aaaagatcct 480
aaaaacaaga gttattatca gaaaaatttt caagcctaca gcgccaaact tgaaaaacta 540
cacaaagtag ccaaagaaaa aatcagtcgt atcctactg agaagaaaat gatcgtaact 600
agtgaaggtt gtttcaagta tttctctaag gcttacgata ttccttctgc ctatatatgg 660
gaaattaata ccgaagaaga gggaacacca aatcaaatta aggctttagt gaaaaaatta 720
aggaaaagtc gggtgtctgc gctttttgta gaaagcagtg ttgatgatcg tccaatgaaa 780
actgtttcaa aagatacagg tatcccaatt gccgctaaaa tttttacaga ttcagttgct 840
aaaaaaggac aggctggaga tagttactat gcgatgatga agtggaatat agataaaatt 900
gcaaatggtc tgtcacaatg a 921
<212> Type : DNA
<211> Length : 921
SequenceName : SEQ ID 605
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
atgtttgttc atactaagac taagaaaaaa agaaagtggc aaaggaaagt gtttctactg 60
ctgcttcttt ttttattgcc tattgtgtca gtattggctt ttattgtgtt atttattggc 120
ggtggtacag ctgagtctca tgatgtggaa gcgacgacag ggggcgttaa gctttcagct 180
aagcaatttg cagataagac aaagttagga atttcagaag aggaagctaa aaatgcctta 240
gcttttgcgg ataggttgat gtctcgtcat cattttacag ctcaagcaac tgctggagta 300
ttggctgttg gctttcgtga aagtggcttt gatgtcaaag cagttaataa ttctggtggt 360
gtagctggct ttttccaatg gtctggctgg ggtagttctg ttaatggtga tcgttggaaa 420
gtagctagta aaagagagtt aactctagag gttgaggtag atttgatgag cactgaacta 480
gatggtcgat atgctgatgt tgtcaaaaaa gttggttctg cgactgatga aaaacaggct 540
gctaaggatt ggtctcagta ttatgaaggt gttgcggtta gtgatggtca aacgaaagct 600
gataaaattg agagttgggc aacaactatt tgtgaggctt taaagtctgg tggtacaaat 660
tatgctaaag tgaataatac gggaacaagt tctactgcta tcccgcaggg ttgggaaaat 720
attagtgctt ttgatggcca tgcttatgaa ggtagtgaaa attatcctca aggacaatgc 780
acttggtatg tttataatcg tgctaaacag ttgggtgtta gcttcagtcc ttatatgggg 840
aatggcggtc agtggtatca agtgcaaggc taccattcta gtcatacacc taaagcacat 900
acggctttat cttttgtcaa tggtcaggca ggttctgatc caacttatgg tcatgttgct 960
tttgtagagg ctgttaaaga tgatgggagt attctaatca gtgagatgaa cgtttatggt 1020
caaccagcta tgacggttgc ctatcggaca tttgatgctg aaactgctaa acaattttgg 1080
tatgtagagg gaaaataa 1098
<212> Type : DNA
<211> Length : 1098
SequenceName : SEQ ID 606
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
atgaaaatga aacgtaaact attaagcttg gtttcagtcc ttactatttt attgggagct 60
ttttgggtaa cgaagattgt aaaagctgac caagtcacaa attatacaaa tacggcttct 120
atcacaaaat cagatggtac agcactttct aatgatccat ctaaggctgt taattattgg 180
gaaccacttt ctttcagtaa ttctattact ttcccagatg aagtcagtat taaggctggg 240
gatactttaa ccattaagtt gccagagcaa ttacaattta cgactgctct aacttttcgat 300
gttatgcata ccaatgggca attagctggt aaagcaacaa ctgatcctaa tacaggagaa 360
gtaacagtta cctttactga tatttttgaa aaactgccta atgataaggc tatgacatta 420
aattttaatg cacaattgaa tcataacaat atttctattc ctggtgttgt aaactttaac 480
tataataatg ttgcttatag ctcttatgtt aaagacaaag atattacgcc aataagtcca 540
gatgttaaca aagtgggtta tcaggataaa agtaatcctg gtttgattca ctggaaagtt 600
ctcattaaca acaaacaagg tgctattgat aatttgactt tgactgatgt tgtcggagaa 660

gatcaagaaa tcgtaaaaga ttccttggtt gctgcacgct tgcagtacat tgctggtgat 720
gatgttgaca gtttagatga agctgcttcg cgaccttatg ctgaggattt ttcaaaaaat 780
gttacttatc aaactaatga tttaggattg acaacaggat ttacctatac aattccagga 840
tccagtaaca acgctatctt tatctcttat actactcgtt taacttcttc tcaatctgct 900
ggtaaagatg tcagcaacac tattgctatt tcaggaaata atattaatta ttccaatcaa 960
acaggctacg ctcgtattga atccgcatat ggtagagcta gttctagagt aaagaggcaa 1020
gcagaaacaa caactgttac tgaaacaaca acttcgtcat cttctgaaac gacaactagt 1080
gaagcgacaa cagaaacaag tagtacaaca aataataatt caactactac agaaacagct 1140
actagcacaa caggagcttc aacaacacaa acaaaaacga ctgcttctca aacgaatgtt 1200
ccgacaacaa caaacataac aacaacttca aaacaagtaa ccaagcaaaa agcgaaattt 1260
gttttaccat caacaggtga acaagcaggg cttttgttaa ctactgtagg tcttgtaatt 1320
gttgctgtgg caggtgtcta tttctataga acacgtcgtt aa 1362

<212> Type : DNA
<211> Length : 1362
SequenceName : SEQ ID 607
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
atgacattta aaaagttagt tttaggtttg ttgagttttg tggctgtatt tactttagta 60
gcttgcagtt cttctaattc aaaaaattta caggatgata ttaaagaaaa gaaaaagtta 120
gttgttgctg ttagtccgga ctatgctcct tttgagttca aggctcttgt gaacggtaag 180
gatactgttg ttggtgctga tattgatttg gcaaaagcaa ttgctaaaga attgggagtg 240
aaactggaat tatcttccat gagttttgat aatgtcttgt ccagtttaaa aacaggaaaa 300
gcagacatag ctatctctgg tttatcttat accaaggaac gtgctcaagc ctatgacttt 360
tcagaagctt attataaaac ggaaaatgct attcttatta aaaagtctga tttgaacaaa 420
tatacaatga tttcttcttt taataataag actaaagtag ctgttcaaaa aggaacgatt 480
gaagaaggat tagctaaaaa tcaattaaaa caatcaaaca ttacctcttt gacttcgatg 540
ggcgaagctg ttaatgagct caaatctggt caggttgatg ctattgatct tgaaaaacca 600
gtggcagaag gttatgtgtc tcaaaatagt gatttggttc ttgccaaagt tgccttaaaa 660
acgggtgaag gggatgccaa agcagttgct ctgcctaaag acagtggtca attagttaag 720
acggtgaata aggttattaa gaaactcaaa aaagaagata aatacaagca gtttatcagc 780
gatgctgtta aattaactgg tcagcaagtg gattga 816

<212> Type : DNA
<211> Length : 816
SequenceName : SEQ ID 608
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
atgaaaaagc atttttcat gacttttagc ctcttgctag cggctgtttt tctagttgct 60
tgttccaatc tttccgattc tggacagagg aattgggata agataaataa gagaggaatg 120
cttaaaattg ctactgcagg aacgctttat ccgcaatctt atcatgatga tcataataaa 180
ttgacgggtt atgatgttga aattctaaaa gaaataggaa aacgtttggg attgaaagtt 240
cagtttactg aaatgggtgt cgatggtatg ctgacagcca tcaagagcgg tcagatcgat 300
gttgctaatt attccctaga agacggcaac aaaaatatca gtaagttttt gagaacctct 360
ccctataaat attcttttac gtcaatggtt gtccgctcta aagatgattc aggtattcat 420
tcttggtcag accttaaggg aaaaaaagct gccggagctg ccagcactaa ttatatgaag 480
attgctaaaa aattaggagc aaaattagtt gtctatgata atgtcaccaa cgatgtttat 540
atgaaagatt tagttaatgg tcgtacagat gtcattatca atgattatta tctgcaaaag 600
atagctgttg cagcagtcaa agacaaatac gctatcaaaa taaaccaagg actttatgcc 660
aatccttaca gcactagttt tacattgtct ttgaaaaaca aagtactgca aaagaaaatc 720
aataaggctg tgaaagacat gcgcaaggat ggcaccctaa ccaagctatc taagaagttt 780
ttccaaggag aagacgtcac taaaaaacat tataatagct ataaaaaaat tgatatttct 840
gacgttgatt aa 852

<212> Type : DNA
<211> Length : 852
SequenceName : SEQ ID 609
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pneumoniae R6

<400> PreSequenceString :
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agaacctact acaaaaaggg ggctctaaaa gaaacctact ggagagtgat agatgggaag 180
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tggttttatt ttggtcaaga tggtgtctta caagaatttg ttggcaagca agttttagaa 360
gcaaaaactg ctacgaatac caacaaacat catggggaag aatatgatag ccaagcagag 420
aaacgagtct attattttga agatcagcgt agttatcata ctttaaaaac tggttggatt 480
tatgaagagg gttattggta ttatttacag aaggatggtg gctttgattc tcgcatcaac 540
agattgacgg ttggagagct agcacgtggt tgggttaagg attaccctct tacgtatgat 600
gaagagaagc taaaagcagc tccatggtac tatctagatc cagcaactgg ctggcaaaac 660
cttgggaaca aatggtacta tctccgttca tcaggagcta tggcaactgg ttggtatcag 720
gaaggttcga cttggtacta tctaaatgca agtaatggag atatgaaaac aggctggttc 780
caagtcaatg gtaactggta ctatgcctat gattcaggtg ctttagctgt taataccaca 840
gtaggtggtt actacttaaa ctataatggt gaatgggtta agtaa 885
<212> Type : DNA
<211> Length : 885
SequenceName : SEQ ID 610
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pneumoniae R6
<400> PreSequenceString :
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aaatattatg taaaagatga tcataaagca atctattggc ataaaataga cggtaaaact 180
tactattttg gtgatattgg agagatggtt gtcggttggc aatacttaga aattcctgga 240
acaggttatc gtgataattt attcgataac caaccagtta atgaaattgg ccttcaggag 300
aagtggtact attttggaca agatggtgct ttgctagaac aaacagataa acaagtacta 360
gaggcaaaaa cgtctgaaaa tacaggaaaa gtatacggtg aacaatatcc tctatctgct 420
gaaaagagaa cttattattt tgataataat tatgctgtaa agacaggctg gatttatgaa 480
gacggcaatt ggtattattt aaataagcta ggaaattttg gcgatgattc ttacaatcca 540
ctaccaattg gtgaagttgc taagggttgg actcaagatt ttcatgttac tattgacatt 600
gatagaagca aacctgctcc atggtactac ctagatgctt caggtaagat gcttacagat 660
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<212> Type : DNA
<211> Length : 1017
SequenceName : SEQ ID 611
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pneumoniae R6
<400> PreSequenceString :
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aaagctgaga aagactatga tgcagcgaag aaagatgcta agaatgcgaa aaaagcagta 180
gaagatgctc aaaaggcttt agatgatgca aaagctgctc agaaaaaata tgacgaggat 240
cagaagaaaa ctgaggagaa agccgcgcta gaaaaagcag cgtctgaaga gatggataag 300
gcagtggcag cagttcaaca agcgtatcta gcctatcaac aagctacaga caaagccgca 360
aaagacgcag cagataagat gatagatgaa gctaagaaac gcgaagaaga ggcaaaaact 420
aaatttaata ctgttcgagc aatggtagtt cctgagccag agcagttggc tgagactaag 480
aaaaaatcag aagaagctaa acaaaaagca ccagaactta ctaaaaaact agaagaagct 540
aaagcaaaat tagaagaggc tgagaaaaaa gctactgaag ccaaacaaaa agtggatgct 600
gaagaagtcg ctcctcaagc taaaatcgct gaattggaaa atcaagttca tagactagaa 660
caagagctca aagagattga tgagtctgaa tcagaagatt atgctaaaga aggtttccgt 720
gctcctcttc aatctaaatt ggatgccaaa aaagctaaac tatcaaaact tgaagagtta 780
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gaaaaaccag ctccagctcc agaaactcca gccccagaag caccagctga acaaccaaaa 1020
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aaagcaagcc aatggttcaa agtatcagat aaatggtact atgtcaatgg tttaggtgcc 1800
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<212> Type : DNA
<211> Length : 1860
SequenceName : SEQ ID 612
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pneumoniae R6
<400> PreSequenceString :
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gggagccagg agattgatca gtggcgcatg tattctcgtc agtgtacttc ttttgtagcc 240
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tggggacatc gtgctcgtcg ggaaggttat cgtgtagata atacaccgac gattggttcc 360
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gatcagattg agattgagga atataactat ggttatacag aatcctataa taaacgagtt 480
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attaaaactg aacccctagt tagtgcaact gtgattgatt actattatcc tggggagaag 660
gttcattatg atcagatact tgaaaaagac ggctataagt ggttgagtta tactgcctat 720
aatggaagct atcgttatgt tcaattggag gctgtgaata aaaatcctct aggtaattct 780
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cagatacttg aaaaagacgg ctataagtgg ttgagttata cggcttataa cggaagtcgt 960
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tggtattatt cttactcttc aggcgcctta gctattaata cgacggtgga tggctacaga 1320
gtaaacagtg atggagaacg agtatag 1347

<212> Type : DNA
<211> Length : 1347
SequenceName : SEQ ID 613
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pneumoniae R6
<400> PreSequenceString :
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gtagctagtg tagctgttgc cagtcttgtt atgggaagtg tggttcatgc gacagagaac 120
gagggaagta cccaagcagc cacttcttct aatatggcaa agacagaaca taggaaagct 180
gctaaacaag tcgtcgatga atatatagaa aaaatgttga gggagattca actagataga 240
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gcaaagttag acgcagcttt tgagaagttt aaaaaagata cattgaaacc aggagaaaag 420
gtagcagaag ctaagaagaa ggttgaagaa gctaagaaaa aagccgagga tcaaaaagaa 480
gaagatcgtc gtaactaccc aaccaatact tacaaaacgc ttgaacttga aattgctgag 540

ttcgatgtga aagttaaaga agcggagctt gaactagtaa aagaggaagc taaagaatct 600
cgaaacgagg gcacaattaa gcaagcaaaa gagaaagttg agagtaaaaa agctgaggct 660
acaaggttag aaaacatcaa gacagatcgt aaaaaagcag aagaagaagc taaacgaaaa 720
gcagatgcta agttgaagga agctaatgta gcgacttcag atcaaggtaa accaaagggg 780
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atgaaagcaa gccaatggtt caaagtatca gataaatggt actatgtcaa tggctcaggt 2040
gcccttgcag tcaacacaac tgtagatggc tatggagtca atgccaatgg tgaatgggta 2100
aactaa 2106

<212> Type : DNA
<211> Length : 2106
SequenceName : SEQ ID 614
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pneumoniae R6
<400> PreSequenceString :

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cctaatgaac caatcctagc agcatatgtc cctaatgaac caatcctagc agatactcct 120
agttcggaag taatcaaaga gactaaagtt ggaagtatta ttcaacaaaa taatatcaaa 180
tataaggttc taactgtaga aggtaacata ggaactgttc aagtgggtaa tggagttact 240
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aaaatacaaa aaaaaggctt ccatggaagt aaagctaaaa ctattatttt tgacaaaggc 480
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tggtattact taaacgaatc aggttcaatg gctactggtt gggttaaaga caaaggctta 1860

tggtattact taaacgaatc aggttcaatg gctactggtt gggttaaaga caaaggctta 1920
tggtattact taaatgaatc aggttcaatg gctactggtt gggttaaagt ttctggtaaa 1980
tggtactata cctataattc aggagattta ttagtaaaca cgactacacc cgatggctat 2040
cgagtcaatg ctaacggtga gtgggtagga tag 2073

<212> Type : DNA
<211> Length : 2073
SequenceName : SEQ ID 615
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pneumoniae R6
<400> PreSequenceString :
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aggcaagtac acgcacactc aactgggaat ccgcattcaa ccgtacagaa tgaagcggat 120
tatcactggc ggaaagaccc agaattaggt tttttctcgc acattgttgg gaacggttgc 180
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tgggtcaagt acaaggacac ttggtactac ttagacgcta aagaaggcgc catggtatca 840
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ctggcagaca ggccagaatt cacagtagag ccagatggct tgattacagt aaaataa 957

<212> Type : DNA
<211> Length : 957
SequenceName : SEQ ID 616
SequenceDescription :

Sequence

<213> OrganismName : Neisseria meningitidis serogroup A strain Z2491
<400> PreSequenceString :
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tatgccaaaa aagcgggcgg attccggttt aaagacaacc acaatccgcg cgattttctg 120
gcgcgcacgc aaggcacagc cgcccgtgcc cacgccgcgc agcaaaacgg ttttgaagcc 180
tttgcaccgt ttgcagccgc cgttttgacg gcacacgcaa ccggcaatgc cggacaagca 240
accgtcaaca cgcttgccgg cctgttcatc ctgttccgcc tcgctttat ctggtgctac 300
atcgcagaca aagcagcatt acgctcgctg atgtgggtgg gcggatttgt ctgcaccgtc 360
gggctgtttg tcgtggctgc ttga 384

<212> Type : DNA
<211> Length : 384
SequenceName : SEQ ID 617
SequenceDescription :

Sequence

<213> OrganismName : Neisseria meningitidis serogroup A strain Z2491
<400> PreSequenceString :
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gagctcacac gcaaccacac caaacgcgcc tccgcaaccg tgaagaccgc cgtattggcg 120
acactgttgt ttgcaacggt tcaggcgaat gctaccgatg aagatgaaga agaagagtta 180
gaatccgtac aacgctctgt cgtagggagc attcaagcca gtatggaagg cagcggcgaa 240
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attaaagaaa aagacggtaa gttggttact ggtaaaggca aaggcgagaa tggttcttct 900
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atgatggcga tcggcggcgg cacttatcgc ggcgaagccg gttacgccat cggctactcc 1680
agtatttccg acggcggaaa ttggattatc aaaggcacgg cttccggcaa ttcgcgcggc 1740
catttcggtg cttccgcatc tgtcggttat cagtggtaa 1779
<212> Type : DNA
<211> Length : 1779
SequenceName : SEQ ID 618
SequenceDescription :

Sequence

<213> OrganismName : Neisseria meningitidis serogroup A strain Z2491
<400> PreSequenceString :
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tggcccagca acaacagtga tgccggcgtg gcatccaccg ccaccgacat caaaggaaaa 120
tatgttaaag aagttaaagt cgaaaaaggc gtcattaccg ccacaatgct ttcaagcggc 180
gtaaacaacg aaatcaaagg caaaaaactc tccctgtggg ccaagcgtca agccggttcg 240
gtaaaatggt tctgcggaca gccggttgag cgcgccgcca acaacgccgc caacgacgcc 300
gtcaccgccg ccaccgccaa cggcaacggc aagatcgaca ccaaacacct gccgtcaacc 360
tgccgcgacg cagcatctgc cgtttgcata gaaacaccac ctacggcttt ctataaaaat 420
acctaa 426
<212> Type : DNA
<211> Length : 426
SequenceName : SEQ ID 619
SequenceDescription :

Sequence

<213> OrganismName : Neisseria meningitidis serogroup A strain Z2491
<400> PreSequenceString :
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gctcaggatt tcggcaaaac ccgcagtgcg gaatggggcg taaacgccga aatcaaaggt 4260
ttcacgctgt ccctccacgc tgccgccgcc aaaggccccc aactggaagc gcaacacagc 4320
gcgggcatca aattaggcta ccgctggtaa 4350

<212> Type : DNA
<211> Length : 4350
SequenceName : SEQ ID 620
SequenceDescription :

Sequence

<213> OrganismName : Neisseria meningitidis serogroup A strain Z2491
<400> PreSequenceString :
atgaacaccc ttcaaaaagg ttttaccctt atcgagctga tgattgtgat tgccatcgtc 60
ggcattttgg cggcagtcgc ccttcctgct tatcaagact acacagcccg cgcacaagtt 120
tccgaagcca ttcttttagc cgaaggtcaa aaatcagccg tcaccgagta ttacctgaat 180
cacggcgaat ggcccagcaa caacacttct gccggcgtgg catcctccac cgacattaaa 240
ggcaaatatg ttcaaagcgt tgaagtcaaa aacggcgtcg ttaccgccac aatggcttca 300
agcaacgtaa acaacgaaat caaaggcaaa aaactctccc tgtgggccaa gcgtcaagac 360
ggttcggtaa aatggttctg cggacagccg gttaagcgca acgacaccgc caccaccaac 420
gacgacgtca aagccgacac cgccgccaac ggcaagcaga tcgacaccaa gcacctgccg 480

tcaacctgcc gcgacgcagc atctgccgga taa 513
<212> Type : DNA
<211> Length : 513
SequenceName : SEQ ID 621
SequenceDescription :

Sequence

<213> OrganismName : Neisseria meningitidis serogroup A strain Z2491
<400> PreSequenceString :
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acactgacag gtattccatc gcatggcgga ggtaaacgct ttgcggtcga acaagaactt 120
gtggccgctt ctgccagagc tgccgttaaa gacatggatt tacaggcatt acacggacga 180
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cgctactcca ttgatgcact gattcgtggc gaatacataa acagccctgc cgtccgtacc 300
gattacacct atccacgtta cgaaaccacc gctgaaacaa catcaggcgg tttgacaggt 360
ttaaccactt ctttatctac acttaatgcc cctgcactct cgcgcaccca atcagacggt 420
agcggaagta aaagcagtct gggcttaaat attggcggga tgggggatta tcgaaatgaa 480
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ttcctgcgcg gcatagacgt tgtttctcct gccaatgccg atacggatgt gtttattaac 600
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atcaaaccaa aaaccaatgc gtttgaagct gcctataaag aaaattacgc attgtggatg 780
ggaccgtata aagtaagcaa aggaattaaa ccgacagaag gattaatggt cgatttctcc 840
gatatccaac catacggcaa tcatatgggt aactctgccc catccgtaga ggctgataac 900
agtcatgagg ggtatggata cagcgatgaa gcagtgcgac gacatagaca agggcaacct 960
tga 963
<212> Type : DNA
<211> Length : 963
SequenceName : SEQ ID 622
SequenceDescription :

Sequence

<213> OrganismName : Neisseria meningitidis serogroup A strain Z2491
<400> PreSequenceString :
atgcgcccaa tcttcctatc tttcgtttta ttccctattt tgataaccgc ctgcagcaca 60
ccggacaagt ctgcccgatg ggaaaatatc ggcacaatct caaacggcaa tattcataca 120
tatatcaata aagacagcgt gagaaaaaac ggaaatctga tgattttcca agataaaaaa 180
gttgttacca atctaaaaca agaacgtttt gccaacaccc ccgatacaa gactgccatt 240
gccgagtggg aaatccactg caacaacaaa acataccgct taagttcgct acaattgttt 300
gatacaaaaa acacggaaat ttccacacaa aactacacag cctcttccct ccgcccgatg 360
agcatcctgt ccgggacatt aaccgaaaaa caatatgaaa ccgtatgcgg aaaaaaactc 420
tga 423
<212> Type : DNA
<211> Length : 423
SequenceName : SEQ ID 623
SequenceDescription :

Sequence

<213> OrganismName : Neisseria meningitidis serogroup A strain Z2491
<400> PreSequenceString :
atgaacaaac ttttcattac cgccctgtcc gccctcgcct tgtccgcctg cgccggcact 60
tgggagggcg cgaaacaaga caccgcccgc aaccttgaca aaacacaggc cgccgccgaa 120
cgcgccgccg aacaaacagg caacgccgtc gaaaaaggct gggacaaaac caaagaagcc 180
gtcaaaaaag gcggcaatgc cgtcggacgc ggcatttccc atctcggcgg aaaaatcgaa 240
aacgccaccg aataa 255
<212> Type : DNA
<211> Length : 255
SequenceName : SEQ ID 624
SequenceDescription :

Sequence

<213> OrganismName : Neisseria meningitidis serogroup A strain Z2491
<400> PreSequenceString :

atgaaactcc tcttcatccc cctagtcctc ttcgtcgccg tcgaacattt ctacatcgcc 60
tggcttgaaa tgacgcagat tcccagcgaa aaagcggcgg aaacgttcaa gctgccttat 120
gaatttatgg aacaaaatcg cgtgcagacc ctgttcggca accaagggct gtataacggc 180
tttctcggca tcgggctggt gtggtcgcgg tttgccgctc cggataacgc ggtgtacggc 240
gcaacggtac tgtttctcgg cttcgtcctg attgccgccg cgtggggcgc gttctcttcc 300
ggcaacaaag gcatactcgt caaacaaggt ttgcccgcat ttttggcagc ggcggcggtg 360
ttggcggtat ga 372
<212> Type : DNA
<211> Length : 372
SequenceName : SEQ ID 625
SequenceDescription :

Sequence

<213> OrganismName : Neisseria meningitidis serogroup A strain Z2491
<400> PreSequenceString :
atggcttcaa gcaacgtaaa caacgaaatc aaagacaaaa aactctccct gtgggccaag 60
cgtcaagacg gttcggtaaa atggttctgc ggacagccgg ttaagcgcga cgccgccacc 120
gacgccgacg tcaccgccga cagcggcaac gaaatcgaca ccaagcacct gccgtcaacc 180
tgccgcgacg cagcatctgc cgtttgcaca aaaacacccg agtattaccc gaatcacggc 240
gaatggccga aaaacttcgt cattcccgcg caggcgggaa tccaggtctg tcggcacgga 300
aacttatcgg gtaaaaaggt ttctccggtc ctgagttcta gattcccact ttcgtgggaa 360
tga 363
<212> Type : DNA
<211> Length : 363
SequenceName : SEQ ID 626
SequenceDescription :

Sequence

<213> OrganismName : Neisseria meningitidis serogroup A strain Z2491
<400> PreSequenceString :
atcctttag ccgaaggtca aaaatcagcc gtcaccgagt attacctgaa tcacggcgaa 60
tggcccagca acaacacttc tgccggcgtg gcaacctcca ccgacattaa aggcaaatat 120
gttcaaagcg ttgaagtcaa aaacggcgtc gttaccgcca caatggcttc aagcaacgta 180
aacaacgaaa tcaaaggcaa aaaactctcc ctgtgggcca agcgtcaaga cggttcggta 240
aaatggttct gcggacagcc ggttaagcgc aacgacaccg ccaccaccaa cgacgacgtc 300
aaagccgaca ccgccgccaa cggcaagcag atcgacacca agcacctgcc gtcaacagca 360
tcgacaagaa aatcgacacc aaactag 387
<212> Type : DNA
<211> Length : 387
SequenceName : SEQ ID 627
SequenceDescription :

Sequence

<213> OrganismName : Neisseria meningitidis serogroup A strain Z2491
<400> PreSequenceString :
atgcccatcc cctttaaacc cgtattggct gccgccgcca tcgcccaagc gtttcccgcc 60
tttgcggcag accccgcgcc gcagtccgcc caaacgctga acgaaatcac cgttaccggc 120
acgcacaaaa cccaaaaact cggcgaagaa aaaatccgcc gcaaaacttt agacaagctc 180
ttggtcaacg acgaacacga cctggtgcgc tacgaccccg gcatttccgt cgtcgaaggc 240
ggcagggcgg gttctaacgg ctttaccata cgcggcgtgg acaaagaccg cgtcgccatc 300
aacgttgacg ggctggcgca ggcggaaagc cgctcttccg aagccttcca agaattgttc 360
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gtcaaccgcg ttgacaacaa aacccacgcc ggcatccaac gctttacctc gccgggcagg 2400
agctacaatt tcaccatcga agcgaagttc taa 2433

<212> Type : DNA
<211> Length : 2433
SequenceName : SEQ ID 628
SequenceDescription :

Sequence

<213> OrganismName : Neisseria meningitidis serogroup A strain Z2491
<400> PreSequenceString :
atgaaaaaat ccctgattgc cctgactttg gcagcccttc ctgttgcagc aatggctgac 60
gttaccctgt acggcaccat caaaaccggc gtagaaactt cccgctctgt agaacacaat 120
ggaggtcagg tggttagcgt tgaaaccggt accggcatcg ttgatttggg ttcgaaaatc 180
ggcttcaaag gccaagaaga cctcggtaac ggcctgaaag ccatttggca ggttgagcaa 240
aaggcatcta tcgccggcac tgactccggt tggggcaacc gccaatcctt catcggcttg 300
aaaggcggct tcggtaaatt gcgcgtcggc cgtttgaaca gcgtcctgaa agacaccggc 360
gacatcaatc cttgggatag caaaagcgac tatttgggtg taaacaaaat tgccgaaccc 420
gaagcacgcc tcatttccgt acgctacgat tctcccgaat ttgccggcct cagcggcagc 480
gtacaatacg cgcttaacga caatgtaggc agacataaca gcgaatctta ccacgccggc 540
ttcaactaca aaaacggcgg cttcttcgtg caatatggcg gtgcctataa aagacatcag 600
gatgtggatg acgtgaagat tgagaaatac cagattcacc gtttggtcag cggttacgac 660
aatgatgccc tatacgcttc cgtagccgta cagcaacaag acgcgaaact ggttgaagac 720
aattcgcaca actctcaaac cgaagttgcc gctaccttgg cataccgctt cggcaacgta 780
acgcccgcg tttcttacgc ccacggcttc aaaggctcgg ttgatgatgc aaaacgcgac 840
aatacttacg accaagtggt tgtcggtgcg gaatacgact tctccaaacg cacttctgcc 900
ttggtttctg ccggttggtt gcaagaaggc aaaggcgaaa acaaattcgt agcgactgcc 960
ggcggtgtcg gtctgcgcca caaattctaa 990

<212> Type : DNA
<211> Length : 990
SequenceName : SEQ ID 629
SequenceDescription :

Sequence

<213> OrganismName : Neisseria meningitidis serogroup A strain Z2491
<400> PreSequenceString :
atgaaaaccc tgctcctcct catccccctc gtcctcacag cctgcggcac actgaccggc 60
atacccgccc acggcggcgg caaacgcttt gccgtcgaac aagaactcgt cgccgcatcg 120
tcccgcgccg ccgtcaaaga aatggacttg tccgccctga aaggacgcaa agccgccctt 180
tacgtctccg ttatgggcga ccaaggttcg ggcaacataa gcggcggacg ctactctatc 240
gacgcactga tacgcggcgg ctaccacaac aaccccgaaa gtgccaccca atacagctac 300
cccgcctacg acactaccgc caccaccaaa tccgacgcgc tctccagcgt aaccacttcc 360
acatcgcttt tgaacgcccc cgccgccgcc ctgacgaaaa acagcggacg caaaggcgaa 420
cgctccgccg gactgtccgt caacggcacg ggcgactacc gcaacgaaac cctgctcgcc 480
aacccccgcg acgtttcctt cctgaccaac ctcatccaaa ccgtcttcta cctgcgcggc 540
atcgaagtcg taccgcccga atacgccgac accgacgtat tcgtaaccgt cgacgtattc 600

ggcaccgtcc gcagccgcac cgaactgcac ctctacaacg ccgaaaccct taaagcccaa 660
accaagctcg aatatttcgc cgttgaccgc gacagccgga aactgctgat tgcccctaaa 720
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gtcggcaaaa ccgtcaaagc ctcagaccgc ctgatggtcg atttctccga catcacccc 840
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gatgtcggca acgaagtcat ccgccgccgc aaaggaggat aa 942
<212> Type : DNA
<211> Length : 942
SequenceName : SEQ ID 630
SequenceDescription :

Sequence

<213> OrganismName : Neisseria meningitidis serogroup A strain Z2491
<400> PreSequenceString :
atgaataaaa ccttgtctat tttgccggtg gcaatcttac tcggcggctg cgccgccggg 60
ggcggtaaca cattcggcag cttagacggc ggcacaggta tgggcggcag catcgtcaaa 120
atggcggtag aaagccaatg ccgtgcggaa ttgaacaaac gcagcgaatg gcgtttgacc 180
gcgctggcga tgagtgccga aaaacaggcg gaatgggaaa acaagatttg cgcttgcgtc 240
gcccaagaag cacccaacca gctgacggc aacgatgtga tgcagatgct ggatccgtcc 300
acgcgcaatc aggcacttgc cgccctgacc gccaaaacgg tttccgcctg cttcaaacac 360
ctgtaccgct aa 372
<212> Type : DNA
<211> Length : 372
SequenceName : SEQ ID 631
SequenceDescription :

Sequence

<213> OrganismName : Neisseria meningitidis serogroup A strain Z2491
<400> PreSequenceString :
atgaatccac ttattcatca agcaaaggaa tcatctatgc aaacccgcat cctctccgcc 60
gtactgctgg ctttttcaac cgctgccttt gccgggggcg cattcacgct gcaattcgac 120
aacccgtccg aagacggcgg cttcacgcaa aaccagattt tgagcgcgcc ttacggcttt 180
ggctgttcgg gcggcaatgc ttcgcccgcg ctgtcgtgga aaaatccgcc cgccgggaca 240
aaaagtttcg tcctgaccgt ttacgataaa gacgcgccga ccggactggg ctggatgcac 300
tgggtggtcg ccgacattcc cgccgatgtc cgccgccgca atgcgacctc gctgcaatta 360
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cagatttgcc gcatcaggtt gacgccttcg tacacggcaa aaccgatgcc gtcatgctgc 480
aaccacgcca acacgccgca aagcgcggcc tccgccgcat tgtgcggcac ttcttcatcc 540
gtcagcaccg ccgccgcata a 561
<212> Type : DNA
<211> Length : 561
SequenceName : SEQ ID 632
SequenceDescription :

Sequence

<213> OrganismName : Neisseria meningitidis serogroup A strain Z2491
<400> PreSequenceString :
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atgttttccc ataccggcgg gggggggggg gcgatggcgc aaacccgtca atacgctatt 120
atcatgaacg agagaaacca gcccgaggta cagtggaatg ggtcatattc aataaaggac 180
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cgcgacaatt cgcccattta caaattgaag gatcatccat ggttgggcgt gtctttcaat 600
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aagtgggaca ttaaagatac cgggcagatt ccagtcaagc tcagcttgac gcaagtcaaa 960
gcaggccgct gcgtcaacaa agataacccc aataagaata ccaaaacctc ttccccgca 1020

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<212> Type : DNA
<211> Length : 3114
SequenceName : SEQ ID 633
SequenceDescription :

Sequence

<213> OrganismName : Neisseria meningitidis serogroup A strain Z2491
<400> PreSequenceString :
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cccctgccgg ttgtaaccag cttcagcatt ttaggcgacg tagccaaaca aatcggcgga 120
gagcgcgtat ccatacaaag tttggtcgga gccaaccaag atacgcacgc ctatcatatg 180
accagcggcg acattaaaaa aatccgcagt gcaaaactcg tcctgattaa cggcttagga 240
cttgaagctg ccgacatcca acgtgccgtc aaacagagca aagtatccta tgccgaagcg 300
accaaaggca tccaaccgct caaagccgaa gaagaaggcg gacaccatca cgaccacgat 360
catgaccacg accatgacca cgaaggacac caccacgacc acggcgaata tgaccccccac 420
gtctggaacg accccgtcct tatgtccgcc tatgcccaaa acgtcgccga agccctgata 480
aaggccgacc ccgaaggcaa agtttattat caacaacgct tgggcaacta ccaaatgcag 540
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aaagtcctga ccgggcacga tgccttttcc tatatgggca aacgttacca tatcgaattc 660
atcgccccac aaggtgtgag cagcgaagcc gagccttcag ccaaacaagt cgccgccatc 720
atccgacaaa tcaaacgcga aggcatcaaa gccgtattta ccgaaaatat caaagacacc 780
cgcatggttg accgcatcgc caaagaaacc ggtgtcaacg tcagcggcaa actgtattcc 840
gacgcactcg gcaacgcacc cgcagacacc tacatcggca tgtaccgcca caacatcaaa 900
gccttaacca acgcgatgaa gcaataa 927

<212> Type : DNA
<211> Length : 927
SequenceName : SEQ ID 634
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pyogenes strain MGAS8232
<400> PreSequenceString :
atgaaaaaaa gaattttatc agcagttctt gtaagtggtg ttaccctcgg agcagctaca 60
actgtaggag cggaggattt gagtactaag attgctaagc aggattctat tatctcaaat 120
ctgactacag agcaaaaagc tgcacagaat caagtttcag cgttacaggc tcaagtaagt 180
tcactacaat ctgaacaaga taaactgacc gcaagaaata cagaacttga ggcactttca 240
aagcgatttg agcaagaaat taaggctcta acaagtcaaa ttgttgctcg taatgaaaaa 300
ttaaaaaatc aagctcgtag tgcttataaa aacaatgaaa cttctggtta cattaatgca 360
cttttgaatt ctaaatcaat ttctgatgtt gtaaaccgtt tagtagcaat taatagagct 420
gtctctgcta acgctaaatt gttagaacaa caaaaagctg ataaagtttc ccttgaagaa 480
aagcaagctg ctaaccaaac agctattaat accattgccg ctaatatggc aatggctgaa 540
gaaaaccaaa atacattacg tactcaacaa gctaatttgg aagctgcaac tgcaaattta 600
gctctccaat tagcatctgc tactgaagat aaagctaatt tggtagctca aaaagaagct 660
gcagaaaaag ctgctgctga agccttagca caagaacagg ctgctaaagt taaggcacaa 720
gaacaggctg cacaacaagc agcatctgtt gaagcagcaa aatctgctat tactccagca 780
ccacaagcta ctccggcagc gcaaagtagt aatgctattg aaccagctgc actcacggct 840
ccggcagctc cttctgcaag accacaaaca tcatatgatt cttctaatac ttatccagtt 900
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gttcaaagtg cctcaagtat tcgtgtgatg gagtctaact acagtggtag acagtacatt 1140
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<212> Type : DNA
<211> Length : 1197
SequenceName : SEQ ID 635
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pyogenes strain MGAS8232
<400> PreSequenceString :
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cttagcctta ttatccttgt tattattatt ggtggtcttt tgtttacctt ctacattagc 120
agtgctccga aactgtcaga agcccagtta aaatcaacaa actctagctt ggtttatgac 180
ggtaataaca atctgattgc tgatttgggt tctgaaaagc gtgaaaatgt aacagctgat 240
agtatccctа ttaatctagt taatgctatt acctcaattg aagataaacg tttctttaac 300
catcgtggag tagatcttta tcgtattttt ggtgctgcct ttcataatct aacgagtcag 360
accactcaag gggggtcaac gcttgatcag caactcatta aactagccta ttttttctact 420
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gagcgaaaat atactaaaca agaaatcctg acttttaca tcaacaaagt atatatgggt 540
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gaagactgga ccatgccaaa tggtctttat cgcagtggtg gattcctcta cttaagcgga 1980
acctatgcga gcaacaccga ctatactaat tcggtttaca acaatcttta cagcaataac 2040

acaacaacag cttctagcca aacgacttca gatgatacta gtagtagcaa tgatacaagt 2100
aattcaacca atacagacaa caatggcagc catccatcta ccgatgataa aaagacaact 2160
cattaa 2166
<212> Type : DNA
<211> Length : 2166
SequenceName : SEQ ID 636
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pyogenes strain MGAS8232
<400> PreSequenceString :
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gtgacagcgc aggcacaaga gtggacacca cgatcggtta cagaaatcaa gtctgaactc 120
gtcctagttg ataatgtttt tacttatact gtaaaatacg gtgacacttt aagcacaatt 180
gctgaagcaa tgggaattga tgtgcatgtc ttaggagata ttaatcatat tgctaatatt 240
gacttaattt ttccagacac gatcctaaca gcaaactaca accaacacgg tcaggcaacg 300
actttgacgg ttcaagcacc tgcttctagt ccagctagcg ttagtcatgt acctagcagt 360
gagccattac cccaagcatc tgccacctct caatcgactg ttcctatggc accatctgcg 420
acaccatctg atgttccaac gacaccatta gcatctgcaa agccagatag ttttgtgaca 480
gcgtcatctg agctcacatc gtcaacgaat gatgtttcga ctgagttgtc tagcgaatca 540
caaaagcagc cagaagtatc acaagaagca gttccaactc ctaaagcagc tgaaacgact 600
gaagtcgaac ctaagacaga catctcagaa gatccaactt cagctaatag gcctgttcct 660
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gcagggcttc aaccacaaac agcagcgttc aaagaagaag tggcttctgc ctttggtatt 900
acgtcgttta gtggttaccg tccaggagat ccaggagatc atggtaaagg attagccatt 960
gactttatgg taccggttag ctctacgctt ggtgatcaag ttgctcaata tgccattgac 1020
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gcaagtattt acggaccagc ctatacatgg aaccccatgc cagatcgcgg cagtattaca 1140
gaaaaccatt atgatcatgt tcatgtctcc tttaatgctt aa 1182
<212> Type : DNA
<211> Length : 1182
SequenceName : SEQ ID 637
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pyogenes strain MGAS8232
<400> PreSequenceString :
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actcaggcaa aacaagtctt agcagagggt aaagtgaagg tggtgacaac tttctaccct 120
gtttatgaat ttacaaaagg ggttattggt aatgatggcg atgtttccat gcttatgaaa 180
gcaggaacgg aacctcatga ttttgagcct tctacaaaag acattaaaaa aatccaagat 240
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tcattgacat ctaaaaaagt gaccatcgtc aagggaactg gtaacatgct cttggtagca 360
ggagctggac atgaccatca ccatgaggat gctgacaaaa agcatgagca taataaacat 420
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attacggtcg ttgaaaatat tcgcgacagt ctttcaaaag cttacccaga aaaagcagag 540
aacttcaaag ccaatgccgc tacttatatt gaaaaattaa aagagcttga caaagactat 600
acggcagcac tttcagatgc taagcaaaag agctttgtga cacaacacgc agcttttggt 660
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gacgtggaac aaatcaaaat caatggtaag aaaaagacca tgacctttgt tcgtaatggt 1260
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aatcgcggag ttcgtttcat gtttgaagct aaagaaccaa atgctggcga attcaaatac 1380
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ggtggtgaca gccaagaaaa attacataaa gagttagaac attggccaac ttactacggt 1500
tcagacttat ctggtcgtga aattgcccaa gaaatcaatg ctcattaa 1548

<212> Type : DNA
<211> Length : 1548
SequenceName : SEQ ID 638
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pyogenes strain MGAS8232
<400> PreSequenceString :
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gtacctacta tgccatctac acttatttcg caacaggaaa atcttgttca tgcagctgtt 120
ttaggcgata actatccgag taagtggaaa aaaggcaatg gaatcgattc gtggaacatg 180
tatatccgcc aatgcacttc ttttgcagct tttcgtttaa gctctgctaa tggttttcag 240
ttacctaaag gctacggtaa tgcctgcacg tggggacata tcgcgaaaaa tcagggttat 300
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tcaaatgctg cttacgatca tgtagcatgg gtagctgata tccgtggaga cactgtcact 420
atcgaagagt ataattacaa cgctggacaa ggccctgaaa gataccataa gcgtcaaatt 480
ccaaaatctc aggtaagtgg ttatatccat tttaaagact tatcatctca gacaagtcat 540
tcctacccaa gacaactaaa acacatttct caagcttcat ttgacccctc tggaacttat 600
cactttacaa ccagattacc agtcaaagga caaaccagta tcgatagccc tgatcttgct 660
tactatgaag caggtcaatc tgtttattac gataaagtcg tgactgctgg aggttataca 720
tggcttagct acctcagttt ttctggaaac cgacgctata ttcccattaa agagcccgca 780
cagtctgtgg ttcaaaatga caatacaaaa ccttccatta aggtcggtga tactgttacc 840
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gccggaggag acccaactcc actaaactgg attgatccca caccattaga tgaaacagat 960
aaccaaggaa aagttttagg aaatcaaatt ctccgtgtgg gtgaatattt taccgtcact 1020
ggtagttata aagtattaaa aattgatcaa ccaagtaatg gtatttatgt tcaaatcgga 1080
tctcgtggaa catgggtaaa tgctgataaa gctaacaaat tatag 1125

<212> Type : DNA
<211> Length : 1125
SequenceName : SEQ ID 639
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pyogenes strain MGAS8232
<400> PreSequenceString :
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cctggaggct gctgttgctg ctgtactact tgttgcttct caattgctac tggaagtggt 120
aattctcaag gtggtagcgg aagttatacg ccaggtaaat aa 162

<212> Type : DNA
<211> Length : 162
SequenceName : SEQ ID 640
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pyogenes strain MGAS8232
<400> PreSequenceString :
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acattacaat cggcaatccg ttcaatcgaa ggcttggaaa agcgttcaac cggtttttca 120
tcggtgtctc aaaaagctag ttccatgttt aaatccatgt taggagcgaa tttagctgga 180
caagctatct cggcaatgac aaggacagtg tcatcaggcc ttggctctat gcttggcgag 240
atgaatagtt cagcgaaagc gtggaaaact tttgacgcta atttagcgga cattgggttt 300
ggaaaaaaac aaattttggc agttaaaacg gcgatgcaag actatgcaac taaaacaatc 360
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caagacttta ggataatgtt ggaacagacg cctgcaggga tggctaaagt cgctaaatct 600
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gatttttgg aagcggtaaa aaaagcaggc aatgataaga gtttccaaaa gatggcaact 720
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gccgcagtag ctggaggttt taagttattc gaaaaattaa cgggacaaag cgtcattggt 1260
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ggagttggta ttaaaactgc tttgtctgga atccccccct atcattag 1488

<212> Type : DNA
<211> Length : 1488
SequenceName : SEQ ID 641
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pyogenes strain MGAS8232
<400> PreSequenceString :
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ccaatgtatg cgatgacaaa agaagtatct ggagacctaa atgatgtgag gatgatccaa 180
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gcggatttgt ttgtttacca ttcacatacc ttagaagctt gggcaaggga tctagaccct 300
aatttaaaaa aatcaaaggt tgatgtgttt gaagcgtcaa aacctttgac actagataga 360
gtcaaagggc tagaagatat ggaagtcaca caaggcattg accctgcgac actttatgac 420
ccacatacct ggacggatcc cgttttagct ggtgaagaag ctgttaatat cgctaaagag 480
ctaggacgtt tggatcctaa acacaaagac agttacacta aaaatgctaa ggctttcaaa 540
aaagaagcag agcaactaac tgaagaatac actcaaaaat ttaaaaaggt gcgctcaaaa 600
acattcgtga cgcaacacac ggcattttct tatctggcta aacgattcgg cttgaaacaa 660
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caagactttg tcaaagaata caacgtcaag actatttttg cagaagacaa tgtcaatccc 780
aaaattgctc atgctattgc gaaatcaaca ggagctaaag taaagacatt aagtccactt 840
gaagctgctc caagcggaaa caagacatat ctagaaaatc ttagagcaaa tttggaagtg 900
ctctatcaac agttgaagta a 921

<212> Type : DNA
<211> Length : 921
SequenceName : SEQ ID 642
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pyogenes strain MGAS8232
<400> PreSequenceString :
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agtgaaccaa caatcacgaa tcacactcaa caacaagcgc aacatctcac caatacagag 180
ttgagctcag ctgaatcaaa atctcaagac acatcacaaa tcactcccaa gacaaatcgt 240
gaaaaagagc aaccacaagg tctagtctct gagccaacca caactgagct agctgacaca 300
gatgcagcac caatggctaa tacaggtcct gatgcgactc aaaaaagcgc ttctttaccg 360
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caaaaagccg ccggtattaa ttatgggagt tggataaatg ataaagttgt ttttgcacat 600
aattatgtgg aaaatagcga taatatcaaa gaaaatcaat tcgaggattt tgatgaggac 660
tgggaaaact ttgagtttga tgcagaggca gagccaaaag ccatcaaaaa acacaagatc 720
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cgaaaaaaat caaccaaaga ttga 4944

<212> Type : DNA
<211> Length : 4944
SequenceName : SEQ ID 643
SequenceDescription :

Sequence

<213> OrganismName : Treponema pallidum subsp. pallidum str. Nichols
<400> PreSequenceString :
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gtcattggga acaacgtcgc gaacgttaac actaccggtt ttaagcgtgg gcgtgttaat 120
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ggagtgaatc ccaaggaagt gggattgggc gtgctgattg caagcatcga tactgttcac 240
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tttttgtgc tgaaaagtgg ggaaaagacg tttttcaccc gcgcaggtgc ctttggggtt 360
gataatgcgg gcactctcgt gaaccctgcg aatggtatgc gcgttcaagg ttggatggcg 420
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cccattgggc aaaagataga tgcgcagcag accagcactg ttcactatgc ctgtaattta 540
gacaagcgtc tgcctgagct tgctgcagat gcgaacgaag cggacgtgcg taagtccacg 600
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ggtgtgtatt caaatggggt gagccaagac attggccagc tcgcacttgc aggatttgca 1140
aatcaaggtg gtcttgagaa ggcaggagag aacacctacg tacaatcgaa caactcaggg 1200
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gagatgagca acgtagattt aaccgatcaa tttacggata tgatcattac ccaaaaaggg 1320
tttcaggcgg gcgcaaagac gattcagaca tcagacacca tgttggatac ggtgttgagt 1380
ttgaagcgct ga 1392

<212> Type : DNA
<211> Length : 1392
SequenceName : SEQ ID 644
SequenceDescription :

Sequence

<213> OrganismName : Treponema pallidum subsp. pallidum str. Nichols
<400> PreSequenceString :

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ggagtgctcg gacaggagtt ttccccgaag ctaactggct ctgccacact tgagtggggc 120
atcagctatg gcaaggggct aggcagtcat ggccaggccc ctggtgcagt tatgggcacc 180
ggtccctaca atctgaagca cgggtttcgt actaccaaca cggtgggagt atcctttccc 240
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<212> Type : DNA
<211> Length : 2277
SequenceName : SEQ ID 645
SequenceDescription :

Sequence

<213> OrganismName : Treponema pallidum subsp. pallidum str. Nichols
<400> PreSequenceString :
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tatgcaggcg tactcactcc gcaggtcagt ggcacagccc agctccagtg gggcattgcg 120
ttccagaaga atccacgcac tggcccgggc aagcacaccc atgggtttcg cactaccaat 180
agtctgacta tttccctgcc gttggtgtca aagcacaccc acacccgccg aggggaggca 240
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<212> Type : DNA
<211> Length : 1797
SequenceName : SEQ ID 646
SequenceDescription :

Sequence

<213> OrganismName : Treponema pallidum subsp. pallidum str. Nichols
<400> PreSequenceString :
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tatgcaggcg tactcactcc gcaggtcagt ggcacagccc agctccagtg gggcattgcg 120
ttccagaaga atccacgcac tggcccgggc aagcacaccc atgggtttcg cactaccaat 180
agtctgacta tttccctgcc gttggtgtca aagcacaccc acacccgccg aggggaggca 240
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<212> Type : DNA
<211> Length : 1797
SequenceName : SEQ ID 647
SequenceDescription :

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<213> OrganismName : SARS coronavirus Frankfurt 1
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<212> Type : DNA
<211> Length : 3768
SequenceName : SEQ ID 648
SequenceDescription :

Sequence

<213> OrganismName : SARS coronavirus HSR 1
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<212> Type : DNA
<211> Length : 3768
SequenceName : SEQ ID 649
SequenceDescription :

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<213> OrganismName : SARS coronavirus ZJ01
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<212> Type : DNA
<211> Length : 3768
SequenceName : SEQ ID 650
SequenceDescription :

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<213> OrganismName : SARS coronavirus TW1
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<212> Type : DNA
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SequenceDescription :

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<213> OrganismName : SARS coronavirus CUHK-Su10
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<212> Type : DNA
<211> Length : 3768
SequenceName : SEQ ID 652
SequenceDescription :

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<213> OrganismName : SARS coronavirus Urbani
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<212> Type : DNA
<211> Length : 3768
SequenceName : SEQ ID 653
SequenceDescription :

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<213> OrganismName : SARS coronavirus
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<213> OrganismName : SARS coronavirus GD01
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<213> OrganismName : SARS coronavirus CUHK-W1

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<213> OrganismName : SARS coronavirus BJ01
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<212> Type : DNA
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SequenceDescription :

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<213> OrganismName : Escherichia coli O157:H7
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<212> Type : DNA
<211> Length : 4038
SequenceName : SEQ ID 661
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
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<212> Type : DNA
<211> Length : 4386
SequenceName : SEQ ID 662
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :

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<212> Type : DNA
<211> Length : 4032
SequenceName : SEQ ID 663
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
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<212> Type : DNA
<211> Length : 1644
SequenceName : SEQ ID 664
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
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<211> Length : 705
SequenceName : SEQ ID 665
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
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<212> Type : DNA
<211> Length : 588
SequenceName : SEQ ID 666
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
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agcggaaatg gtcagttcgc cgcagtggct gaagtcaccg ttactgaagc gggcgctgca 600
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<212> Type : DNA
<211> Length : 606
SequenceName : SEQ ID 667
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
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tctgtagcgg aagaacgcag caaaattacg ccggtcagtg cgattaaggt gacgccgaca 360
tccggtacgg tggcaaaagg gaaaacaacc accctgacgg tttcttttga gccggaaagt 420
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aaagatatga caattacggt aaacggcgtg gcgacaggta aggtgcagat ccctgtggtg 540
agcggaaatg gtcagttcgc cgcagtggct gaagtcaccg ttactgaagc gggcgctgca 600
gggtaa 606
<212> Type : DNA
<211> Length : 606
SequenceName : SEQ ID 668
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
atgttatata atataccttg tcgaatttat atcctttcca ctctgtcatt atgcatttct 60
gggatagttt ctactgcaac cgcaacttct tcagaaacaa aaatcagcaa cgaagagacg 120
ctcgtcgtga ccacgaatcg ttcggcaagc aacctttggg aaagcccggc gactatacag 180
gttattgacc aacaaacatt gcagaactcc accaatgcct ccatagccga taatttgcag 240
gacatccccg gagtagagat aacagacaac tccttggcag gccgtaaaca aatccgcatt 300

cgtggcgaag catcctcccg tgttttaatt ctcattgatg gtcaggaggt aacttatcag 360
cgcgccggag ataattatgg tgtgggactg ttgatagatg agtctgcgct ggagcgtgtt 420
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aattccgcaa cagcaggctg ggaagaatca atcgcggtcc aggggagcat cggtggattt 600
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cgtcggcaat atgaaacttc aacattaaaa acaactaata caggtgaacc agcgataaac 1860
ggacgtatag ggctgaaaca tactcttgtg atgggtcagg ccaacataat ctctgatgtt 1920
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cctgcagcag gttttaatgc agctataggt tttgtatgga atttctga 2148

<212> Type : DNA
<211> Length : 2148
SequenceName : SEQ ID 669
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
atgacaaaaa tgagtcgcta cgccttgatt accgcgctgg cgatgtttct cgccgggtgt 60
gtggggcaac gtgaacctgc accggtagaa gaagtgaaac cagcgccgga acaaccagcc 120
gagccacaac agcctgtccc cacagtgccc tcggtgccga cgatcccgca gcagccaggc 180
ccaattgagc acgaagatca aactgcaccg cctgcgccgc atattcgcca ttatgactgg 240
aatggcgcaa tgcagccgat ggtcagtaag atgcttgggg ctgacggggt gactgcgggt 300
agcgtcctgc tggttgatag cgttaacaac cgtactaacg gttcgctgaa tgccgcagaa 360
gcgaccgaaa cgctgcgaaa tgcgctggct aataacggga aatttaccct ggtttccgcc 420
cagcagctgt cgatggctaa gcaacagtta ggtttgtcgc cgcaggatag tttaggcacc 480
cgtagtaaag ccataggcat tgcccgcaat gtcggcgctc attacgtgct gtactccagc 540
gcctctggca acgttaacgc tccgacccta caaatgcagc tgatgctggt gcagacgggc 600
gaaattatct ggtcaggtaa aggtgccgtt tcgcagcaat aa 642

<212> Type : DNA
<211> Length : 642
SequenceName : SEQ ID 670
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
atgaaaagca aagtactggc acttttaatt cctgccctgc tcggcgcagg tgctgcacat 60
gcagccgaag tttataataa agacggcaac aaattagatc tgtatggcaa agttgatggc 120
ctgcattatt tttctgataa ttcagcgaaa gatggcgacc agagctatgc gcgtctgggt 180
tttaaaggcg aaacccaaat taacgatcaa cttactggct acggtcaatg ggaatacaat 240
attcaggcaa acaacactga atcttcaaaa aaccagtcat ggacccgtct ggcatttgcc 300
ggactgaaat tttcagatta cggttctttc gattacggac gtaattatgg gctggaccga 360
tatgctgcct ga 372

<212> Type : DNA
<211> Length : 372
SequenceName : SEQ ID 671
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli 0157:H7
<400> PreSequenceString :
atggcaacac caaatcccct tgagccggta aaaggtgccg gtaccactct gtgggtttac 60
aacggcaagg gtgatgctta tgcaaacccg ttgtcagacg atgactggca gcgactggct 120
aaggtgaagg atctgacgcc gggcgagatg acggcagaac cctacgatga taactacctg 180
gatgatgaag acgcggactg gaccgcgacc gggcaggggc agaagtctgc aggagatacc 240
agttttacgc tggcctggaa accgggagaa gaaggtcaga aagggcttat aggctggttt 300
gaaagcgggg atgtgcgggc ctataaaatc cgtttcccaa atggcacggt ggatgtgttc 360
cgtggctggg tcagcagtat cggtaaggcc gtgacggcga aagaagtgat cacccgcacg 420
gtgaaagtca ctaacgtggg caaaccttcc gtggcggaag aacgcagcga aattacgccg 480
gccactgcaa ttaaggtgac accgacatcc ggtacggtgg caaaagggaa aacaaccacc 540
ctgactgttt cttttgagcc ggaaagtgca accgacaaga cgttcagagc ggtttccgcc 600
gatccgtcga aagccaccat tagtgtgaaa gatatgacaa ttacggtaaa cggcgtggcg 660
acaggtaagg tgcagatccc tgtggtgagc ggaaatggtc agttcgccgc agtggctgaa 720
gtcaccgtta ctgaagcggg cgctgcaggg taa 753
<212> Type : DNA
<211> Length : 753
SequenceName : SEQ ID 672
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli 0157:H7
<400> PreSequenceString :
atggcaacac caaatcccct tgagccggta aaaggtgccg gtaccactct gtgggtttac 60
aacggcaagg gtgatgctta tgcaaacccg ttgtcagacg atgactggca gcgactggct 120
aaggtgaagg atctgacgcc gggcgagatg acggcagaac cctacgatga taactacctg 180
gatgatgaag acgcggactg gaccgcgacc gggcaggggc agaagtctgc aggagatacc 240
agttttacgc tggcctggaa accgggagaa gaaggtcaga aagggcttat aggctggttt 300
gaaagcgggg atgtgcgggc ctataaaatc cgtttcccaa atggcacggt ggatgtgttc 360
cgtggctggg tcagcagtat cggtaaggcc gtgacggcga aagaagtgat cacccgcacg 420
gtgaaagtca ctaacgtggg caaaccttcc gtggcggaag aacgcagcga aattacgccg 480
gccactgcaa ttaaggtgac accgacatcc ggtacggtgg caaaagggaa aacaaccacc 540
ctgacggttt cttttgagcc ggaaagtgca accgacaaga cgttcagagc ggtttccgcc 600
gatccgtcga aagccaccat tagtgtgaaa gatatgacaa ttacggtaaa cggcgtggcg 660
acaggtaagg tgcagatccc tgtggtgagc ggaaatggtc agttcgccgc agtggctgaa 720
gtcaccgtta ctgaagcggg cgctgcaggg taa 753
<212> Type : DNA
<211> Length : 753
SequenceName : SEQ ID 673
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli 0157:H7
<400> PreSequenceString :
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tttatgactg gtcgtgccaa tggcgtcgcg acttatcgta atactgattt cttcggtctg 120
gtaaatggtc tgaacttcgc ggtgcagtat caaggtaaca acgaaggtgc cagtaatggt 180
caggaaggca ccaacaacgg acgtgatgtt cgccatgaaa acggtgacgg ctggggtctt 240
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cgcaccaatg accaggttaa ccatactgcg gcgggtggtg ataaagcaga cgcgtggact 360
gctgggctaa aatacgatgc taacaatatt tacctggcaa ccatgtattc agaaacgcgt 420
aatatgaccc cgtttggcga cagcgattat gctgttgcaa acaaaaccca gaactttgaa 480
gtcactgcac agtaccagtt tgattttggt ctgcgtccgg cagtcttctt cctgatgtct 540
aaaggccgtg acctgcacgc tgccggtggt gcagacaacc cggcaggtgt tgatgataaa 600
gatctggtta aatacgccga tgttggcgcg acttactatt tcaataaaaa catgtccact 660
tatgttgact ataaaatcaa cctgttggat gaagatgaca gtttctacgc tgccaacggc 720
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<212> Type : DNA

<211> Length : 768
SequenceName : SEQ ID 674
SequenceDescription :

Sequence

<213> OrganismName : Haemophilus influenzae Rd
<400> PreSequenceString :
atggggttta ttatgaaact aactaaaaca gcattatgta ctgcactttt tgccaccttt 60
acttttttcag cgaacgcaca aacttatcct gatttgccag tggggatcaa aggaggaaca 120
ggcgcattaa ttggcgacac agtttatgtg ggattaggtt ctggtggcga taaattctat 180
accttagacc taaaagatcc ttcagcacaa tggaaagaaa ttgctacatt tccgggtggc 240
gaacgcaatc aacctgttgc agccgcagtg gatggaaaac tttatgtatt cggtggttta 300
caaaaaaatg aaaaaggcga acttcaactc gttaatgacg cttatcgcta taaccccaagc 360
gataatactt ggatgaaact tcctactcgt tctccccgtg gtttagtagg atcaagtggt 420
gcatctcacg gagataaagt ttatatttta ggcggctcta atctctctat atttaatggc 480
ttcttccaag acactgtggc agcaggtgaa gataaagcga aaaaagatga aatcgcagca 540
gcttatttcg atcaacgtcc agaagattat ttctttacaa cagaattatt gagctatgaa 600
ccatcaacca ataaatggcg caatgaaggt cgtattccat tctctggtcg tgctggtgca 660
gcctttacaa ttcaaggtaa tgagctagtg gttgtcaatg gcgaaattaa acctggactt 720
cgcaccgctg aaacccatca aggtaaattc actgctaaag gtgtgcaatg gaaaaactta 780
cctgacttac ctgctccaaa aggcaaatca caagatggtt tagctggtgc gctttcaggc 840
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ggtttttctg tatcttacaa caataaagtt ttactgattg gcggtgaaac tgatggaggt 1080
aaggctttaa ctagcgtcaa agcaataagc tatgacggta aaaaattaac catcgaataa 1140

<212> Type : DNA
<211> Length : 1140
SequenceName : SEQ ID 675
SequenceDescription :

Sequence

<213> OrganismName : Haemophilus influenzae Rd
<400> PreSequenceString :
atgggagaac aatatatgct tacgacgata ctcagcttcc tcattgtaac cactgtggtt 60
gcgtatgttt cttggttaaa aacaaaaggg gatgatttaa aatcttcaaa agggtatttt 120
ttggcagggc gtgggttaag cggtttagta attggctgct caatggtgct gacatcgctt 180
tcaactgaac aacttatcgg tgtcaatgcg gtgtcctata aaggtaattt ttccgtgatt 240
gcttggacag ttccaacggt tattccgctt tgtttcttgg ctctttatat aattggctgg 300
ctataa 306

<212> Type : DNA
<211> Length : 306
SequenceName : SEQ ID 676
SequenceDescription :

Sequence

<213> OrganismName : [Helicobacter pylori, strain J99
<400> PreSequenceString :
atgaaaaatc aacacaaaaa tcccctaaca aaagctttaa tgaaaactta tccatataac 60
catttttat ttttctgctt tattctagga gcgtttttat taggtttgct cagtccagct 120
tatgctttaa gtattatcac cactaaagaa attgacgcta atttgcttaa tggagcgata 180
gaaagcaggg tggtgttagg caagagggtg tttaaagtag aagctcatgg gttttatttt 240
agaaacaatg cgactaacag catagatata gaaatcacca gtcttttaag agacaatcaa 300
tcgtttcctt tgactagcag tgctaaaacc agtttaaaaa tacctcctaa cgccaagatt 360
aaaaaatcca ctatccttgt tttgaaaggc gagaacgctg aagaagtggc taagatttta 420
ggcgttagca aagaagaata ccaaaagcta gaaaacatcg ctcaaaccaa agcggctaat 480
gaccctatgt atgctaacac gccttttagt aatggttctg atagttcctt ttacgataac 540
aatcctaata gccctagcaa taacgctatc aatggcaaag atggcgcaaa tgggagtaac 600
ggctatgggg caaatggcaa tgatggggta aatgggatca gtgggagtaa tggtgcaaat 660
gggagtcatt caaataataa tgcaataggc agtggtattg atacagatgg cgtgttaggg 720
gtggatgggg tgaatggctc tagttcttca agtggcggct ctgtaggggg ttatgagaat 780
aatttcacta atcatggctc tactaacaat aacacaggag ggtatgacaa ttttaataat 840
ggcagctcaa gtggtgggag tttagggaat ggggggcttt tccctattcc ttttggtaat 900

ggagacacaa acaattccaa taattccact aacaccacta gcccaactaa tggcagtagt 960
tctaataacg ccactaatcc tagttcgcaa gaaaacaatt actccagcca gtattgtaaa 1020
gtgccagagt taagccccaa caacacgatg aaactagatg ttatcgctaa agatggctct 1080
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gccggtaaag ccatcaagca aacgcaatac tactatgtag atagggaaaa taaaacgcaa 1200
aatatcggtg gttgtgtgga tttacaaggc gctcaatacg ccatgcaact ttacaaagat 1260
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gagattttaa atcgtgggat tgccacccaa ttaagctcgc aatatcaaga atttgcatgc 1560
ggtcaatggg aatacaatga cgctaaatta gaagccaaaa gacctacaat gctaaaaagc 1620
tataacaagc ttaatggaga atgggtagaa gttacgccct gtaattttga agcagggatt 1680
aaaagcggtg cggttgttag ccattatgtg atgggcgtgc ctagttctaa agtcttaagc 1740
gatattacta caagccatta ttttaggata gaaaggaaaa attatggtga gagagaacaa 1800
tgccaaaaac tttatggagt caatcgttgc caaccgcaat attccatact gatcctagta 1860
tcacgattg gagcgccact tacaaaacca ctaccaccca aaccactcaa ccttatttac 1920
gcccagccca agataatgaa aaacacccca caacctataa tcttatcacc actcaaacca 1980
ccatcaacag gactcaaagc gttttga 2007

<212> Type : DNA
<211> Length : 2007
SequenceName : SEQ ID 677
SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori, strain J99
<400> PreSequenceString :
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gcaaaagaaa agaaagtttt taagaatgtg ggaatatcta taatggggat tgcttttttgg 120
gaagcgataa aagactcgat aaaaaaacaa attaaaaaaa gcgattggat atgcgggaat 180
gttaagactg cggatgatta tttaaaaacg catcctaact catggtttaa ttcagcaata 240
ggtgtaacag cgataacagc catgcttatg aatgtgtgtt ttgctgatga ccaatccaaa 300
aaagaagtgg ctcaagctca aaaggaagct gaaaacgcta gggatagagc gaacaagagt 360
gggatagaac tggaacaaga agagcaaaag acagaacaag aaaaacaaaa gacagaacaa 420
gaaaaacaaa agacagaaca agaaaaacaa aagacagaac aagaaaaaca aaagacagaa 480
caagaaaaac aaaagacaag caatatagag actaacaatc aaataaaagt agaacaagaa 540
caacaaaaga cagaacagga aaaacaaaag acaaacaata cgcaaaaaga tttggttaac 600
aaagcagaac aaaattgcca agaaaatcat aatcaattct ttattaaaaa attaggaatt 660
aaggctggca ttgctataga aatagaagct gaatgcaaaa cccctaaacc cacaaaaacc 720
aatcaaaccc ctatccagcc aaaacacctc ccaaactcca aacaacccca ttctcaaaga 780
ggatcaaaag cgcaagagct tatcgcttat ttgcaaaaag agctagaatc tctgccctat 840
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caccttttcaa cctctcaaag cctttttgctc gttcaaaaaa tatttgctga tgttagtaaa 1080
gaaataaaag tagttgctaa taccgagaaa aaagtagaaa aagcgggtta tggttatagt 1140
aaaaggatgt ag 1152

<212> Type : DNA
<211> Length : 1152
SequenceName : SEQ ID 678
SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori, strain J99
<400> PreSequenceString :
atgaactacc ctaatctacc taacagcgct ttagagataa gcgaacagcc agaagtgaaa 60
gaaatcacta acgagctttt aaagcaatta caaaacgctt taaggagcaa cgcgcatttt 120
agcgagcaag tggaattaag ccttaaatgc atcgttagga ttttagaagt gcttttgagt 180
ttggattttt ttaagaatgc gaatgagatt gatagcagtt taagaaattc cattgagtgg 240
ctgactaacg ccggcgagag cttgaaatta aaaatgaaag aatacgagcg ctttttttagc 300
gagtttaata cgagcatgca tgccaacgag caggaagtaa ccaatacctt aaacgctaac 360
gccgagaaca ttaaaagcga aattaaaaag ctagaaaatc aattgataga aaccacgaca 420
agacttttaa cgagctatca aatcttttta aaccaagcca gagataacgc taacaaccaa 480
atcacaaaaa acaaaaccca aagccttgaa gcgattacac aagctaaaaa caacgctaat 540
aatgaaataa gcaacaatca aacgcaagcg ataactaata tcaccgaagc gaaaacgaac 600

gctaataatg aaataagcaa caatcaaacg caagcgataa ctaacattaa cgaagccaaa 660
gaaagcgcta caacgcaaat aaacgccaat aagcaagaag caataaataa catcacgcaa 720
gaaaaaaccc aagccacaag cgagatcacc gaagcgaaaa agaccgatca ttatcaaaac 780
attgattttt ttgagtttga ataa 804

<212> Type : DNA
<211> Length : 804
SequenceName : SEQ ID 679
SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori, strain J99
<400> PreSequenceString :
gtgaaatttt tttcaaagga tttgtttaaa aaagtaactc ctttatttct aagcgtttat 50
tttttaagcc ccaccttac gcaagccaaa agccgttttt atgtggcttc tcaataccag 120
gtggggaaaa tgatcatgaa aaaatacaac gatctcaaac gcacgattga aggggcgagc 180
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tttatggatt acgggaatgt cattctcaat aaaagaacgg gcgctcaagc gaacatgttc 300
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tctcttttt atggcatgca agttgctgaa aacacatgga cgatttccaa acacagcgcg 420
aatttcatca ttgacgactg gcgcagcatt caagggtttt cgctcaaaac ttcaaatttc 480
aggatgttgg gtttagtggg gtttaaattc caaaccgtgc tattccacca tgacgctagt 540
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ttttctgtct ttatttcgca cactttctac ctttaa 636

<212> Type : DNA
<211> Length : 636
SequenceName : SEQ ID 680
SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori, strain J99
<400> PreSequenceString :
atgaaaaaat ttaccctatc gctatttttg tgttgcacct tacttaacgc tgaagaggat 60
atttttagga acaacacaaa tgaaactgat cttacaaatt cttttgaaca tggcaaagaa 120
aacaacaatc ttatcccagc aaaatccgat agtttagaaa gtttcaaaga acaagaaaac 180
aaagaaaaag ccaaacagct tatggattta aaggccttac agagcgtgta tttttctaaa 240
aatagaaaat tgcaagacaa taatttcaat gtcttgtatg tggcaggcaa caccaacaaa 300
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ttgtctaaca tgctagtgat taagccgtta cttatagggg tggatacgaa cctaaccgta 480
gtcggagcga gcggcacaat ttatacctta ttatttgttt ag 522

<212> Type : DNA
<211> Length : 522
SequenceName : SEQ ID 681
SequenceDescription :

Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
gtgttggatt atgtgccctg gattgggaat gggtacaggt atgggaataa ccaccgggag 60
agcaacagta gtacgagtgg ggtaacgacc cagggacaat cccaaaatgc atccagtaac 120
gaacccgcac cgacgttttc gaatgtcggc gttggtctca aagccaatgt caacggcacc 180
ttaagtggtt cgcgaactac gcctaatcag caaggcactc cctggttaac cctcgaccaa 240
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gaaaactaca ccaatttcgc gagtgctaag ggcagtacga accagcaggg ttcaacaacg 360
ggtggatcag cgggcaaccc cgactcgtta aagcaggata aggctgataa aagtggtgat 420
tcggtaacgg ttgcagaagc cacatcgggc gacaacttga cgaattacac caacctcccc 480
ccaacatcac ccccacatcc gactgaccga acgcgctgtc attcaccaac aagaacaacg 540
cccagcgggt gcagctgttc ctgcgcggcc tgttgggcag catcccggtg ttggtcaata 600
agagtgggca agatgataac agtaagttta attccaccga ccaaaaatgg tcttacaccg 660
aattaa 666

<212> Type : DNA
<211> Length : 666
SequenceName : SEQ ID 682
SequenceDescription :

Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
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aatgtccagg gcaccctcgg gggcagacag acgacgacta cggggaacaa tattcccaaa 180
tgagccaccc tcgaccaagc caacctccag ctctgaacgg gggcggggtg aaggaatgat 240
aagactacaa gtggttcaac cggcaatgcc aatgacacca agttcacgag tgctacgggc 300
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tcaggggaca acttgacgaa ttacaccaac ctccccccg ccaacctcac ccccaccgct 480
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aaactgaacc tccccgctta cggcgaggtg aatgggttgt tgaatccggc gttggtggaa 720
acctattttg ggaacacgcg agcgagtggt tcggggtcca acacgaccag ttcacccggt 780
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cgcaccaagc tgcgccaaag ctttggtaca gaccattcca cccagcccca gccccaatcg 1440
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ggtgggggtg ctggaggggg ttcttcaggc tcaggtcaat ctggcgtgga tctctccccc 1560
gttgaacggg tgagtggtca ctaa 1584
<212> Type : DNA
<211> Length : 1584
SequenceName : SEQ ID 683
SequenceDescription :

Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
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ttcaacctcg cggggtcggt gctcgaccag gtgttggatt atgtgccctg gattgggaat 120
gggcacaggt atgggaataa ccaccggggc gtggatgata taaccgcgcc taaaaccggc 180
gcggggtcgt ccagcggaac tagtacgaac acaagtggtt cgcgttcctt tctcccgacg 240
ttctcgaatg tcggcgttgg cctcaaagcg aatgtccagg gcaccctggg tggcagtcag 300
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ctctgaacgg gggcggggtg aaggaatgat aaggcttcaa acaaacaaag tgacgaaaac 420
cacaccacct ttaaaagcgc tacgggcagt ggccagcagg gtggttctac aacgggtggt 480
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cacctccccc ccaacctcac ccccacatcc gattgaccga acgcgctgtc attcaccaac 660
aagaacaacg cgcagcgcgc ccagctcttc ctccgcggct tgttgggcag catcccggtg 720
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tcttacaccg acttaaagtc ggaccaaacc aagctcaacc tccccgctta tggtgaagtg 840
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caagctcagg cggccgcgca agcagctacc accgccgccg caacagggga cgccttaccg 1320
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ccaaccaggt tcgcaccaag ctgcgccaaa gctttggtac agaccattcc acccaagcca 1560

aaccccaatc cctcaaaaca accacaccgg tgtttgggac gaatagtggt aacattggca 1620
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ttctttttaa attgttcccc cactttattc atatgaacca ccgcctcccc cgcgacggga 1860
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tacacccgcc ctgacgaggt cgcgctgcgc cacaccaatg ccatcaaccc gcgcttaacc 1980
ccgtgaacgt atcgtaacac gagcttttcg tccctccccc tcacgggtga aaaccccggg 2040
gcgtgggcct tagtgcgcga caacaccgcc aagggcatca ctgccggcag tggcagtcaa 2100
caaaccacgt atgatcccac ccgaaccgaa gcggctttga ccaccgccac caccttgtg 2160
ttacgccgat acgacctcgc cgggcgttgt acgacctcga cttttcgaag ttaa 2214

<212> Type : DNA
<211> Length : 2214
SequenceName : SEQ ID 684
SequenceDescription :

Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
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agcaacagta gtacgagtgg ggtaacaacc cagggacaac aatcgcaaaa tgcatccgga 120
accgaacccg catccacttt ttcgaatgtc ggcgttggcc tcaaagcgaa tgtccagggc 180
accctgggtg gcagtcagac gacgactacg gggaaagata ttcctaaatg acccaccctc 240
gaccaagcca acctccagct ctgaacgggg gcggggtggc ggaatgataa ggcttcaagt 300
ggacaaagtg acgaaaacca caccaagttc acgagcgcta cgggcagtgg gcagcagggc 360
agttcttcag gtacaactaa ttccgcgggc aatcccgact cgttaaagca ggataaggtt 420
gataaaagtg gtgattcggt aacggttgca gaaaccactt caggggacaa cttgacgaat 480
tacaccaacc tccctcccaa cctcacccgc accgctgatt gaccgaacgc gctgtcattc 540
accaacaaga acaacgcgca gcgcgcccag ctcttcctcc gcgccctgtt gggcagcatc 600
ccggtgttgg tgaataagag tggccaagat gattccaaca agttccaagc caccgaccaa 660
aaatggtctt acaccgaatt aaagtcggat caaaccaagc tcaacctccc cgcttacggg 720
gaggtgaatg ggttgttgaa tccggcgttg gtggaggtgt acggtctgag ttccactcaa 780
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caccaatgct ttggcctttc aggtgagtta taccgaccag gattcgtaca aggcttccac 1320
tcaaagctcc ggccaaaacc aaaacacctc cccctacctg cacttggtgc aggggaaaaa 1380
agtaggttcc tctgataa 1398
<212> Type : DNA
<211> Length : 1398
SequenceName : SEQ ID 685
SequenceDescription :

Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
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gccaccgacc aaaaatggtc ctacaccgac ttacagtcgg accaaaccaa actgaacctc 120
tccgcttacg gtgaggtgaa tgggttgttg aatccggctt tggtagaaac ctattttggg 180
acgacgcgta cgtctagcac tgcgaaccaa aacagtacaa ccgtccccgg tatcggtttt 240
aaaattcccg aacaaaataa tgattccaaa gccaccctga tcaccccccgg gttggcttga 300
acgccccagg acgtcggtaa cctcgttgtc agtggcacca cggtgagctt ccagctcggc 360
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ttaagtggcc tgaatgccag tgacagcgac caaagggagt taatttgggc cccccggccc 480
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accaccaccg caacaggggc taccttaccg gagcacccga atgctttggc gtaccaaatt 660
agctataccg acaaggattc gtacaaggct tccactcaag gttcgggtca aaccaattcc 720
caaaacaatt cgctctacct ccatttgatt aaacctaaga aagtcgaaag cacgacccaa 780

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gtgtttggag ccatgagtgg taacctcggc agtgtgctta gtggtggggg tgctggagga 960
gcaggcagca ccaattcggt ggacctctcc cccgttgaac gggtgagtgg gtcactaacc 1020
attaatagga atttttctta ttaa 1044

<212> Type : DNA
<211> Length : 1044
SequenceName : SEQ ID 686
SequenceDescription :

Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
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aagattagta agagtgggga tagtttaacc acgcaggacg gcaatgcgac cggtcaacaa 120
gaggccacta actacaccaa cctccccccc aacctcaccc ccaccgctga ttgaccgaac 180
gcgctgtcat tcaccaacaa gaacaacgcg catcgcgccc agctcttcct tcgcggcttg 240
ttgggcagca tcccggtgtt ggtgaatcga agtgggtccg attccaacaa attccaagcc 300
accgaccaaa aatggtccta caccgactta cagtcggatc aaaccaagct gaacctcccc 360
gcttacggtg aggtgaatgg gttgttgaat ccggcgttgg tggaaaccta ttttgggaac 420
acgcgagcgg gtggttcggg gtccaacacg accagttcac cggtatcgg ttttaaaatt 480
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caggacgtcg gtaacctcgt tgtcagtggc accagcttga gcttccagct cggcgggtgg 600
ctggtcagct tcacggactt tatcaaaccc cgcgcgggtt atttgggcct ccagttaagt 660
ggcctggatg ccagtgacag cgaccaaagg gagttaattt gggccaagcg gccctgagcg 720
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gcttacagct cttcaacctc aagttcgggt tccgggtcaa gttcaaacac ctccccctac 960
ctccatttga ttaaacctaa gaaagtcgaa agcacgaccc aactcgacca gggcttaaaa 1020
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tccacccagc cccaatcgct caaaacaacg acaccggtat ttgggacgag tagtggtaac 1140
attggcagtg tgcttagtgg tgggggtgct ggagggggtt cttcaggctc aggtcaatct 1200
ggtgtggacc tctccccgt tgaacgggtg agtggtcact aa 1242

<212> Type : DNA
<211> Length : 1242
SequenceName : SEQ ID 687
SequenceDescription :

Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
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gccaagcggc cctgagcggc atttcgtggc agttgggtca accggttggg acgggtcgag 120
agtgtgtggg atttgaaggg ggtgtgggcg gatcaagctc acagcgcggt gtccgagtcg 180
caagcagcta caagtagtac caccaccacc gcaacagggg acaccttacc ggagcacccg 240
aatgccctcg cgtaccaaat tagctccacc gacaaggatt cgtacaaggc ttccactcaa 300
ggctccggtc aaaccaattc ccaaaacacc tccccctacc tgcatttgat taaacctaaa 360
aaagttactg cttccgacaa gttagacgac gatcttaaaa acctgttgga ccccaacgag 420
gttcgggtga agctgcgcca aagctttggt acagaccatt ccacccaacc ccaaccccaa 480
cccctcaaaa caacgacacc ggtgtttggg acgaatagtg gtaacctcgg tagtgtgctt 540
agtggtgggg gtaccacgca ggactcaagc accaccaatc aactgtcacc cgttcaacgg 600
gtgagtgggt ggcttgtggg gcagttacca agcacgagtg acggaaacac ctcctccacc 660
aacaacctcg cgcctaatac taatacgggg aatgaggtgg tgggggtggg agatttgtct 720
aagcgagctt ccattgaatc aagtcgtttg tgaatagcat taaaaccttа g 771

<212> Type : DNA
<211> Length : 771
SequenceName : SEQ ID 688
SequenceDescription :

Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :

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gatcctgcgc gaaccgaggc caccttgacc accaccacct ttgcgctgcg ccggtatgac 120
ctcgccgggc gcgccttata cgacctcgac tttcgaagt taaacccaca aacgccaacg 180
cgtgatgcca actgccagat caccttaac ccctttggcg gctttggttt gagtggcagt 240
gcaccccaac agtgaaacga ggtcaaaaac aaggtccccg tcgaggtggc ccaagacccc 300
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accaccattg gcgcgtatgg gctgaaggtg aagaacgccg aggcggacac cgcaaagagc 480
aatgaaaaac tccagggcga tgaatccaag tcttccaatg gatcttcaag cacttccacc 540
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accgcgcctt tgagtatttg gctttatata tatttagtaa aggcagtcac ttttaggttg 1260
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<212> Type : DNA
<211> Length : 1317
SequenceName : SEQ ID 689
SequenceDescription :

Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
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gacctcgccg ggcgcgcctt atacgacctc gatttttcga agttaaaccc acaaacgccc 180
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ccctccaatc cttatcggtt tgccgtttta ctcgtgccgc gtagcgtggt gtactatgag 360
cagttgcagc gggggttagc gctccctaac caagggagtt cgtcaggctc cggtcaacaa 420
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tttcaaaagg aagctgactc cgacaagtcg gccccgatcg ccctcccgtt tgaagcgtac 1200
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ttgtcttaa 1269
<212> Type : DNA
<211> Length : 1269
SequenceName : SEQ ID 690
SequenceDescription :

Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
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ccggccaaac ccaatccact aacagttccc cctacctgca cttggtgaag cctaagaaag 120
ttacccaatc cgacaaagtt agacgacgat cttaaaaacc tgttggaccc caacgaggtt 180
cgcgccagaa tgctcaaatc atttggtaca gaaaatttca cccaacccca accccaaccc 240

caagccctca aaacaacgac accggtattt gggacgagta gtggtaacct cggtagtgtg 300
cttagtggtg gggggtacca cgcagggctc aagcaccacc aatcaactgt cacccgttca 360
acgggtgagt gggtggaccg ctaa 384
<212> Type : DNA
<211> Length : 384
SequenceName : SEQ ID 691
SequenceDescription :

Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
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gacctcgccg ggcgcgcctt atacgacctc gactttagta ggttaaaccc acagacacca 180
acgcgcgacc aaaccgggca gatcaccttt aaccccttg gcggctttgg tttgagtggg 240
gctgcacccc aacagtgaaa cgaggtcaaa aacaaggtcc ccgtcgaggt ggcccaagac 300
ccctccaatc cttatcggtt tgccgtttta ctcgtgccgc gtagcgtggt gtactatgag 360
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aacaccacca ttggcgcgta tgggctgaag gtgaagaacg ccgaggcgga caccgcgaag 480
agcaatgaaa aactccaggg cgatgaatcc aagtcttcca atggatcttc aagcacttcc 540
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gtgaaaaaga aatccgggag tcagggcaac tccggtgaac aaggcaccga acaggtggaa 660
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cgtaccgcca ttgatcgcgt tgatcacttg gatcccaagg tgatgaccgc gaactatccg 960
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gttttgctcc aaaccaccgg gttcttcaac tcgcggcgcc accccgagtg gtttgaccag 1080
ggccaagcgg tcgcggataa tacccaaacc gggtttgata cagatgacac cgataataaa 1140
aaaacaaggc tttcaaaagg aagctgactc cgacaagccg gccccgatcg ccctcccgtt 1200
tgaagcgtac ttcgccaaca ttggcaacct cacctggttc gggcaagcgc ttttggtgtt 1260
tgggatttgt ttgtcttaat taactaa 1287
<212> Type : DNA
<211> Length : 1287
SequenceName : SEQ ID 692
SequenceDescription :

Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
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gggggttcgt caggggacac caaagtcaag gcgttgcagg tggcggtgaa aaagaaatcc 180
gggagtcagg gcaactccgg tgaccaaggc accgaacagg tggaacttga atctaatgat 240
ttagccaacg ccccgattaa acggggctcc aatccagcaa gtccaactca aggcagccga 300
cttcggcacc accccatcca gttcggaatc tggtcaatca ggcaccccca ccccctgaag 360
gccgtggctt gcgaccgagc aaattcacaa ggacctcccc aaatgatccg cctcgatcct 420
cattctgtac gatgcgcctt atgcctttaa 450
<212> Type : DNA
<211> Length : 450
SequenceName : SEQ ID 693
SequenceDescription :

Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
atgtttggct tgaaggtgaa ggatgcaacc gtggatagtt cgaagcaatc aacggaaagc 60
ttaaagggcg aagaatcgag ttccagttcc accacatctt ccacctccac cacccaacgt 120
gggggttcgt caggggacac caaagtcaag gcgttgcagg tggcggtgaa aaagaaatcg 180
gactcggagg acaatggtca gatcgaactt gaaaccaaca acctcgccaa cgccccgatt 240
aaacggggct ccaataacaa ccagcaagtc caactcaagg cggacgattt tggtacttcc 300
ccttccagtt cggaatctgg tcaatcaggc acccccaccc cctgaacgcc gtggcttgcg 360
accgagcaaa ttcacaagga cctccccaaa tgatccgcct cgatcctgat tctgtacgat 420

gcgccttatg cgcgcaatcg taccgccatt gatcgcgttg atcacttgga tcccaaggtg 480
atgaccgcga actatccgcc cagttgaaga acgcccaagt gaaaccacca cgggttgtgg 540
gactgaaagg cgcgcgatgt cctggtccaa accaccgggt tcttcaaccc gcgccgccac 600
cccgattggt ttgaccaggg ccaagcggtc gcggagaata cccaaaccgg gtttgataca 660
gatgacaccg ataataaaaa gcagggcttt cgcaaacaag gcgaacaatc ccctgccccc 720
atcgccctcc cgtttgaagc gtacttcgcc aacattggca acctcacctg gttcgggcaa 780
gcgcttttgg tgtttgggat ttgtttgtct taa 813

<212> Type : DNA
<211> Length : 813
SequenceName : SEQ ID 694
SequenceDescription :

Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
atgggcagtc aaaaccaggg ttctacaaca actacctcag cgggcaatcc cgattcttta 60
gttactgata aagttgatca aaaaggtcag gtgcaaacaa gtggtcaaaa tttaagtgat 120
accaactaca ccaacctctc ccccaacttc acccccacat ccgactgacc gaacgcgctc 180
agcttcacca acaagaacaa cgcgcagcgc gcccagctgt tcctgcacgg cttgttgggc 240
agcatcccgg tgttggttaa taagagtggc gaaaataacg aaaaattcca agccaccgac 300
caaaaatggt cctacaccga attaaagtcg gatcaaacca agctcaacct ccccgcttat 360
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gaacaaaata atgattcaaa ggctgtgctg atcacccccg ggttggcttg aacgccccag 540
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gtcagcttca cggactttgt caaaccccgc gcgggttacc tcggactcca gttaacgggc 660
ttggatgcaa gtgatgcgac gcagcgcgcc ctcatttggg ccccccggc cctgagcggc 720
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ggtgtgggcg gatcaagctc agtccgactc gcaaggatct accaccaccg caacaggggc 840
taccttaccg gagcacccga atgctttggc ctttcaggtg agtgtggtgg aagcgagtgc 900
ttacaagcca aacacgagct ccggccaaac ccaatccact aa 942

<212> Type : DNA
<211> Length : 942
SequenceName : SEQ ID 695
SequenceDescription :

Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
atgagttttg gtttagtggg cactgttaat aataacggtt ggaaatcgcc gtttcgacat 60
gaaacaaaat accgagcagg gtatgataag ttcaagtatt acaaaaccca ctaccggggt 120
gcaaaaaaag ctggaaccaa tgatgatcga tggagatgaa ctgcttggtt tgaccttgac 180
tttgcccacc aaaagatagt gctcattgaa aggggtgaac ttcaccgtca agcagattta 240
aaaaaatctg accccgcaac aaacgaaact tccaaaaccg tttggggtag cattaaagaa 300
aagctgttac aaaacgtcaa caacctccac tcagagaaag gagtattctt atggttccgt 360
caatctggtt ttacaactac tagaaactag 390

<212> Type : DNA
<211> Length : 390
SequenceName : SEQ ID 696
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
atggctgaac cgttggccgt cgatcccacc ggcttgagcg cagcggccgc gaaattggcc 60
ggcctcgttt ttccgcagcc tccggcgccg atcgcggtca gcggaacgga ttcggtggta 120
gcagcaatca acgagaccat gccaagcatc gaatcgctgg tcagtgacgg gctgcccggc 180
gtgaaagccg ccctgactcg aacagcatcc aacatgaacg cggcggcgga cgtctatgcg 240
aagaccgatc agtcactggg aaccagtttg agccagtatg cattcggctc gtcgggcgaa 300
ggcctggctg gcgtcgcctc ggtcggtggt cagccaagtc aggctaccca gctgctgagc 360
acacccgtgt cacaggtcac gacccagctc ggcgagacgg ccgctgagct ggcaccccgt 420
gttgttgcga cggtgccgca actcgttcag ctggctccgc acgccgttca gatgtcgcaa 480
aacgcatccc ccatcgctca gacgatcagt caaaccgccc aacaggccgc ccagagcgcg 540
cagggcggca gcggcccaat gcccgcacag cttgccagcg ctgaaaaacc ggccaccgag 600

caagcggagc cggtccacga agtgacaaac gacgatcagg gcgaccaggg cgacgtgcag 660
ccggccgagg tcgttgccgc ggcacgtgac gaaggcgccg gcgcatcacc gggccagcag 720
cccggcgggg gcgttcccgc gcaagccatg gataccggag ccggtgcccg cccagcggcg 780
agtccgctgg cggcccccgt cgatccgtcg actccggcac cctcaacaac cacaacgttg 840
tag 843
<212> Type : DNA
<211> Length : 843
SequenceName : SEQ ID 697
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
atgcgttatc tgatagcgac cgcagtgctc gttgctgtgg tcctggtggg ctgggccggcg 60
gctggtgcgc cgccgtcatg cgccggcctg ggcggcactg tgcaggccgg ccagatctgc 120
catgtgcacg cctcgggccc taagtacatg ctggatatga catttcctgt cgactatccc 180
gaccagcagg cgctgaccga ctacatcacg caaaaccgcg acgggttcgt caacgtcgcg 240
caggggtccc cgctgcgaga ccagccctac caaatggacg ccaccagcga acagcacagc 300
tccggccagc cgccgcaggc cacccgcagc gtagtgctca aattcttcca ggacctcggt 360
ggggcacatc cgtccacctg gtacaaggcc ttcaactaca acctcgcgac ctccgcagccc 420
atcaccttcg acacgttgtt cgtgcccggc accacgccac tggacagcat ctacccccatc 480
gttcagcgcg agctggcacg tcagaccggt ttcggtgccg cgatattgcc ttccgaccggc 540
ctcgacccgg ctcactacca gaactttgct atcaccgacg acagtctgat ttttctacttc 600
gcccagggtg agctgctgcc gtcgtttgtc ggcgcttgcc aagcccaggt gccgcgcagc 660
gccattccgc cgctggcaat ctaa 684
<212> Type : DNA
<211> Length : 684
SequenceName : SEQ ID 698
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
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gcggccggtg tgacttcgat catggctggc ggcccggtcg tataccagat gccagccggtc 120
gtcttcggcg cgccactgcc gttggacccg gcatccgccc ctgacgtccc gaccgccgcc 180
cagttgacca gcctgctcaa cagcctcgcc gatcccaacg tgtcgtttgc gaacaagggc 240
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aaggccgccg agcacgggga tctgccgctg tcgttcagcg tgacgaacat ccagccggcg 360
gccgccggtt cggccaccgc cgacgtttcc gtctcgggtc cgaagctctc gtcgccggtc 420
acgcagaacg tcacgttcgt gaatcaaggc ggctggatgc tgtcacgcgc atcggcgatg 480
gagttgctgc aggccgcagg gaactga 507
<212> Type : DNA
<211> Length : 507
SequenceName : SEQ ID 699
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
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ggcgtcacac cctcgttcgc ccacgccgat gagggtgcga gcaagctacc gatgtacctg 120
aacatcgcgg tggcagtgct cggcctggct gcgtacttcg ccagcttcgg ccccaatgttc 180
accctcagta ccgaactcgg cggaggtgat ggcgcagtgt ccggtgacac tgtggctgccg 240
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ggcggctatt cgtccagtcc gagccaatcg ggcagtggat acactgctca gccccccggcc 720
cagccgccgg cgcagtccgg gtcgcaacaa tcgcaccagg gcccatccac gccacctacc 780
ggctttccga gcttcagccc gccgccaccg gtcagtgccg ggacggggtc gcaggctggt 840

tcggctccag tcaactattc aaaccccagc gggggcgagc agtcgtcgtc ccccgggggg 900
gcgccggtct aa 912
<212> Type : DNA
<211> Length : 912
SequenceName : SEQ ID 700
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
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accaaactgc tcgtcgggge catcgcgggc ggaatgctag cttgcgcagc tatattgggc 180
gacggaatcg cttcggccga tactgcgttg atagtacccg gtaccgcacc gtccccgtac 240
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tactacaacc ccaccgctac ccgccacgtc gtttcatatc caggcagctt ttggcctgtc 360
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gccagtgccg ccaccagcac cgctgccgcc acggcagcag caacaaatgc gctccgcggg 1140
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gggaagaagc actag 1215
<212> Type : DNA
<211> Length : 1215
SequenceName : SEQ ID 701
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
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cccatcgagg atcttgacgt tctcgtagcc gcagctgtag ccgtcgcggc tggcagtttg 120
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gatctccctg aggtcggagg acgggtcacc agcccgccac agccgccggt cgccgcgctc 300
accggctact ccgctaacat cggcggactc tccgtgccgc acagctggaa tcttccgcca 360
gcggtgcgcc aagttgcggc gatgttcccc ggcgcgactc cgatgtatat gacggggagt 420
tcggacggct cctacgccgg cctggcagcg gcgggtttgg ccggcaccgg tctggccggt 480
cttgccgccc gcggtggctc cgcgccgacc ccggctgcag ccgccccggc cggagccggc 540
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gccgccgggt cagccatacc tggcctaccg cccggtttgc cgcccggcgt ggttgccaac 660
cttgcggcga ccctggcggc gatccccgga gcgaccatca tcgtggtacc gccgtccccg 720
aacgccaatc aatag 735
<212> Type : DNA
<211> Length : 735
SequenceName : SEQ ID 702
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
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gaggtgttaa ccgagaccgt ggtgggcacg gatcggtcat tggccggcga aaaccaccgg 180
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ccgacgcagc agcccacgca acaaccaacc caacagatgc caacccagca gcagaccgtg 1560
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gggggcgact tattcggcgg gttctga 1647

<212> Type : DNA
<211> Length : 1647
SequenceName : SEQ ID 703
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
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tcaccagccg gtatcgccaa tgccgacgac gcgggcttgg acccaaacgc cgcagccggc 120
ccggatgccg tgggctttga cccgaacctg ccgccggccc cggacgctgc acccgtcgat 180
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gcggccaacg cgagccggga ggagcagatc cgggtggctg agaacgtgct gcgttcgcag 480
ggtatccgcg cctggccggt ctgcggccgc cgcggctga 519

<212> Type : DNA
<211> Length : 519
SequenceName : SEQ ID 704
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
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<212> Type : DNA
<211> Length : 531
SequenceName : SEQ ID 705
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
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atcgtatgca cggtgttcat cgaaaccgcc gttgtcgcga ccatgtttgt cgcgttgttg 120
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caacagatcg aggtcgcaga caacattatg aaaacccaag gcccgggtgc gtggccgaaa 360
tgtagttctt gtagtcaggg agacgcaccg ctgggctcgc tcacccacat cctgacgttc 420
ctcgcggccg agactggagg ttgttcgggg agcagggacg attga 465
<212> Type : DNA
<211> Length : 465
SequenceName : SEQ ID 706
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
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atgggcccac tcacgcagct tccccagcag gccatgcaag cggggcaggg agcaatgcag 120
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gccgagtgtt ccggtgaaat ctgccgacga caagccggtg gtcaccaagt cgacgcgacg 600
gatccttgtt gtgccgaacg acgacaaggt taa 633
<212> Type : DNA
<211> Length : 633
SequenceName : SEQ ID 707
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
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caggcggccg cgcagtctcc ggatgggttg ccgatgctgt gtctgggagc ccgtggatgg 360
cagccgggat ggtttaccgg ggccgggttc ttccctccgg agccataa 408
<212> Type : DNA
<211> Length : 408
SequenceName : SEQ ID 708
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
atgaaaacca caggcacaac tatcaaactc ggcatcgtct ggttggtgct gtcggtgttc 60
accgtgatga tcatcgtggt gttcgggcag gtgcggttcc atcacaccac cgggtactcc 120
gcggtgttca cccatgtcag cgggctgcgg gccgggcaat ttgtccgcgc tgcgggcgta 180
gaggtcggca aggtcgccaa ggtaacgctg atcgacgggg acaagcaagt attggtggac 240
ttcaccgtgg atcgctcgct gtcactggat caggcgacga ccgcctcgat ccgctacctc 300
aacctgatcg gcgaccggta ccttgagctc ggccgcggtc acagcggtca gcggctggcg 360
ccgggtgcca cgatcccgct cgagcacacc catccggcct tggatctcga cgctctgctc 420
ggcgggtttc gcccactctt ccaaacgttg gacccagaca aggtcaacag catcgcctcc 480
tcgatcatca ccgtgttcca agggcaaggc gccaccatca acgacatcct cgaccagacc 540
gcctcgctga cggcaacgct ggccgaccgg gaccatgcga taggtgaggt cgtcaacaac 600
ttgaacaccg tgctggccac caccgtcaag catcaaacgg aattcgaccg cacggtcgac 660

aagctagagg tgctgatcac tggactgaag aacagggcgg acccgctggc cgcggcggcg 720
gcacacatca gcagcgccgc gggaacccta gccgacctgc tggggcggat cgtccattgc 780
tgcacagcag cttcgggcac ctcgagggca tccagcagcc gctcatag 828
<212> Type : DNA
<211> Length : 828
SequenceName : SEQ ID 709
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
atgactccac gcagccttgt tcgcatcgtt ggtgtcgtgg ttgcgacgac cttggcgctg 60
gtgagcgcac ccgccggcgg tcgtgccgcg catgcggatc cgtgttcgga catcgcggtc 120
gttttcgctc gcggcacgca tcaggcttct ggtcttggcg acgtcggtga ggcgttcgtc 180
gactcgctta cctcgcaagt tggcgggcgg tcgattgggg tctacgcggt gaactaccca 240
gcaagcgacg actacccgcc gagcgcgtca aacggttccg atgatgcgag cgcccacatc 300
cagcgcaccg tcgccagctg cccgaacacc aggattgtgc ttggtggcta ttcgcagggt 360
gcgacggtca tcgatttgtc cacctcggcg atgccgcccg cggtggcaga tcatgtcgcc 420
gctgtcgccc ttttcggcga gccatccagt ggtttctcca gcatgttgtg gggcggcggg 480
tcgttgccga caatcggtcc gctgtatagc tctaagacca taaacttgtg tgctcccgac 540
gatccaatat gcaccggagg cggcaatatt atggcgcatg tttcgtatgt tcagtcgggg 600
atgacaagcc aggcggcgac attcgcggcg aacaggctcg atcacgccgg atga 654

<212> Type : DNA
<211> Length : 654
SequenceName : SEQ ID 710
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
gtgataagca ccacaagaat tgatttccta tggatattgt cggtagcgtt cgcgtccatg 60
attgctcttg caacgctgtt gacgcttatc aatcaagtcg tcggcactcc gtatattccc 120
ggtggcgatt ctcccgccgg gaccgactgc tcggagctgg cttcgtgggt atcgaatgcg 180
gcgacggcca ggccggtttt cggagatagg ttcaacaccg gcaacgagga agccgccttg 240
gcggctcggg gctttcaaca gggaaccgcc cccaatgcct tggtgatcgg ttggaatggc 300
caccacacgg cggtgacgct gcccgatggc acgcccgtat ccagtggtga aggcggtggc 360
gtgcgggtcg gtggcggtgg cgcctaccag cccaaattca cccaccacat gtatctgccg 420
atggatgtgg acgcgggaga agaccagccg ccggcgccag atgagccggt caccgcggtc 480
gacgacgtgg aaccggaaat gcctgcaccg tgcccgaccc agcgcccgcc ggtgacccca 540
agacataacc tgtgcaacaa actccggact atgccagggg cgctctcggc cgcgctggcc 600
gcggcggcgc cggtctggcc ggcccctata agcggctgcc gcgggttcag cacgtccctc 660
ttagcaaaaa gaaatcaccc agtaatcgtc gggaaatag 699
<212> Type : DNA
<211> Length : 699
SequenceName : SEQ ID 711
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
atgacgacga tgattactct tcggcgacgg ttcgcggtgg ccgtcgccgg cgtcgccact 60
gccgccgcga cgaccgtcac cctggctccc gcaccagcaa atgccgccga tgtctatggc 120
gcaattgcct actccggcaa cggctcgtgg ggccgatcgt gggactaccc aacccgggcg 180
gctgccgaag ccaccgccgt caagtcgtgt ggctactccg actgcaaggt gctcaccagt 240
ttcaccgcct gcggcgccgt cgccgccaac gatagggcat accagggagg agttggaccc 300
accttggccg ccgccatgaa ggacgccctg accaagctcg gcggcggcta catcgacacc 360
tgggcctgca actaa 375
<212> Type : DNA
<211> Length : 375
SequenceName : SEQ ID 712
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
atggccggac tgaacattta cgtgaggcgc tggcggacag cgcttcacgc aaccgtgtcg 60
gcattgatag ttgccatcct cggactcgcc atcaccccgg tcgctagtgc ggcgacggcc 120
agggcgacgt tgtcggtgac atcgacgtgg cagaccggtt tcatcgcccg cttcaccatc 180
acaaactcga gcacggcgcc gctaaccgat tggaagcttg aattcgactt gccggcagga 240
gaatccgtct tgcacacatg gaatagcacc gttgcacgat ctggcacgca ctacgttctc 300
agcccagcga attggaatcg catcattgcc cccggtggtt cagccacggg cggcctaaga 360
ggcgggctga ccggttctta ctcgccgccg tcgagttgtc tgctcaacgg gcaatatcct 420
tgcacctag 429
<212> Type : DNA
<211> Length : 429
SequenceName : SEQ ID 713
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
atgctgactc gcgctatcaa gacccagctg gtgttgttga cggtgttggc ggtcatcgcg 60
gtggtggtcc ttggttggta tttcctgcgg atacccagcc tggtcggcat cggtcgatac 120
acgctttatg ccgaattgcc tcggtccggg ggtctatacc gaacagccaa cgtcacatat 180
cggggcatca ccataggaa ggtcaccggc gtcgaaccaa ccgagcgggg cgcgcgagca 240
accatgagca tcgacaatgg ctaccagatc cccaccgacg cctcggccaa tgtgcactca 300
gtgtcggcgg tcggcgagca gttcgttgac ctggtgtcga cccgcaccag cggtccgtat 360
ctgcggcatg ggcagacgat caccacgact acggtcccca gccagattgg cccggcgctg 420
gacgccgcca accgtggatt ggcagtgctg cccaaagacc gggtcgcgtc ggtgctgcac 480
gaggcgtcgg aggccgtggg cgggctggga tcctcactga atcgcctcat cgaagccacc 540
caggcaatcg cccacgatgt cagcggcagc ctcgaggaca tcgacgacat catcgagcgt 600
tcggcgccta tcatcgatag ccaggtcaat tccggcaacg agatcgcccg ctgggccgcc 660
aacctcaaca cgctggccgc tcagaccgcg cagaccgatc cggcggtgcg aagcattctg 720
gccaacgcgg caccgactgc cgatcaggtc aacgccacgt tcagcgacgt gcgggagtcg 780
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acagagttcc ccggccaggc cggactgggt gtcggcggcc tggcgctcaa ccaaccaccg 960
ccgtgcctga ccggcttcct gccggcgtcg gagtggcggt cacctgctga caccagcacc 1020
gcaccgctac ccaagggcac ctactgcagg attccgatgg acgcgagcaa tgtggttcgt 1080
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tgccgcagca atgaagctta tgtgcccggg ggcaccaatc cctggtatgg ggaccccaac 1200
cagatgctca gctgtcccgc gccggccgcg cgttgtgacc agccggtgaa gccaggccag 1260
gtgatcccgg cgccgtcagt taacaatggc atcaacccgc tgcccgccga tcagctgcca 1320
ggcacacctc caccggtcaa cgatcctttg cagcgacctg ggtcaggcac cgtccagtgc 1380
aatgggcaac aacccaaccc gtgcgtctac accccgagca catttcctac aaccatttac 1440
gacgtgcaga gcggcaaagt cgtagcaccc gacggtgtgg tgtattccgt tgaggcttcg 1500
actcatgccg gagccgacgg atggaaggtg atgctggcac caaccggctg a 1551

<212> Type : DNA
<211> Length : 1551
SequenceName : SEQ ID 714
SequenceDescription :

Sequence

<213> OrganismName : Rickettsia prowazekii strain Madrid E
<400> PreSequenceString :
atgttaaata atacacaatt tttaaatttg atgaaatcct atatgaaacc agaattttat 60
atgagttcta taaaaaatac cactaatcta gatctttcat ctatcaccaa tacaattcaa 120
aaagccatga atatttttt taccactaac aaaatttcca cagaaagtat gcaatctttg 180
tttaagaaaa attccgagat tatacaaaat aatattaata ctattttaaa tagtactaaa 240
gaagtaataa attctaaaga ttttaaacaa gctactgaat atcatcaaaa atgtgtaaaa 300
tctatttatg aaacatctat ggacaatgct aaggaattag caaatattgc ttatgaagct 360
tcaaataaaa tatttgaagc cgcaaataaa catattacca agaatattca taatgcttct 420
aataatatac ataatactgc agaacaagta caaaaaaact ttaataacaa atctgcttaa 480

<212> Type : DNA
<211> Length : 480

SequenceName : SEQ ID 715
SequenceDescription :

Sequence

<213> OrganismName : Rickettsia prowazekii strain Madrid E
<400> PreSequenceString :
atgaatatta aattagttac atatttttta atattagtaa gctcattaaa agtaaatgct 60
gatttaaatc atattcaaga tagttttaaa tatcaagaag cagagcagtt aacaatagaa 120
ttaccttgga atgactgtac tgcaattcat aaattcttag aagaaaagtt atttttttca 180
gaacaacaaa taaaaaaaga aaataaaatt catgagaaat ataagcaatt ttatttacaa 240
cataataata agctttctga tttttctatg caatttctag aaaaaaaatc tgaaattaat 300
agtgtcgaaa ctttaatatc aggcttttta aaattttgtg aagataattt tcaaacaagt 360
aaaagtaaat cgcattcttt aaatttttta caaaaacaac aagaccaatg gttacataat 420
ataagaaatg agaattataa aacatattat aagaagaaat atgaagacaa taccttaga 480
aatattaatt aa 492
<212> Type : DNA
<211> Length : 492
SequenceName : SEQ ID 716
SequenceDescription :

Sequence

<213> OrganismName : Rickettsia prowazekii strain Madrid E
<400> PreSequenceString :
atgaaaaagt tacttttaat tgctactgca agtgcaacaa ttttatcttc tagtgtatcg 60
tttgcagagt gcattgataa tgaatggtat ttaagagcag atgcaggtgt agcaatgttt 120
aataaagaac aagataaggc aacaggtgtt aaattaaaat ctaataaggc tattccaatt 180
gatttgggta ttggttatta tatttctgaa aatgtacgtg ctgatttaac tttaggaact 240
acaataggtg gaaaactcaa gaaatacgga gcagcaacta atacacattt tactggtact 300
aacgtttcag tgagccataa gcctactgtt acacgtttgc ttattaacgg ttatgtagac 360
ttaacaagtt ttgatatgtt tgatgttttc gttggtggtg gtgtcggtcc tgcattagtg 420
aaagagaaaa ttagtggggt aagcggtctt gcatctaaca ctaaaaataa aaccaatgta 480
tcatataagc tgattttcgg tacttctgcg caaattgcag atggtgttaa agtagagcta 540
gcatatagct ggataaatga tggtaaaaca aaaactcata atgtaatgta caaaggggca 600
agtgtgcaaa ccggtggtat gcgttatcaa agtcataacc tgacagtagg tgtaagattt 660
ggtatataa 669
<212> Type : DNA
<211> Length : 669
SequenceName : SEQ ID 717
SequenceDescription :

Sequence

<213> OrganismName : Rickettsia prowazekii strain Madrid E
<400> PreSequenceString :
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ttattaagca gttgctccga atctacgcgt gatgaaaatg gattacttac agatagtcaa 120
agtactataa ttcgagatta tataatatcg caaaattcta aaaatcttaa agtgaacctt 180
aaagaaaagt ttggttccaa tttaaaagga gtaaaattaa taggaataaa gttaacaaat 240
gaagatttat cgggaataga tttcacttca tgcgaaatat tacggactga cttcatgggt 300
agcaacttag aaaaagcaat acttacaaat tcggtaattc aagaaagtaa ttttgcggat 360
tcagtaataa aaaatatttc aggctataat gctgattttc aaggttcaat ttttaataat 420
ataacattac aaaatacaaa ttttgttcaa tcaaatttca gtgatactgc ttttaataaa 480
agtactataa tcaatgtcaa ttttgaaaat tctaaattta gtaatgtatt atggtgtcac 540
agtaatattg acagtagtaa ttttcaaaaa actcatctaa aaaataatag ctttaaaaat 600
actaatgtaa tgaattcaat attttatggt gcagatttag gcaaaagtgt aataaataat 660
acaaatttta ctaataatta ttttgaatct agtgacctaa gtaacactaa attcacatca 720
gtaatcatta aagattctaa cttcacacaa agtatttta attcagtaaa tttcaataat 780
atacaaagta ataactcttt tttttcatat acttcctttg aagattcaac attacacaat 840
attcacctta ctaaatgtga tttacaaaac agcacaatta atagttcagt tttcaataat 900
tttaaaatcg acaatgctat attaacaaat atgagtctca acgataatac atttaataat 960
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attactttac tcaatactaa ctatagtaat gctatttta gcaataatga tttaaaagaa 1080
tttaaagtca ttaatactga tttaaacaac agtgaaataa taaactcaaa tttcactaat 1140
ggacaattta ataatgtaaa tttttctcaa tctttaatac aaaacgtaaa ttttacagac 1200
gtgaaaatta ctttaggcaa tttaaatcaa gtagctctaa taaattccaa tctaataaac 1260

actaatatta ttaactcagt cctttctaat tcacaaataa ataatattaa ctaccaagca 1320
tattatagtt ttatcaatac taatgtttct aataatattg ttataaatga taattcgaat 1380
caaattccac caaataatat agtaatcaat tctgaaaaag atttacaaaa catatctaat 1440
ttagcaaata tgaatttaac aaattttaac ttaagtaatt tagtgtttaa tggagtagat 1500
ttttcaaaaa gcatctttaa aaaagctaat ttaacaaata cagtaataaa aaattctatt 1560
ttaaaagatg ctaatttttc tgcagcaata cttactaaaa cagatttctc aaaatcgata 1620
ttaacaggta gtatatttaa gtttgctcaa attgatcaga catgttttag taattccgac 1680
ttaacaaata ctgattttac tgaagcaaca attaaaaata ctgcatttga taatgctaat 1740
acacacggta taaaaggatt agaataa 1767

<212> Type : DNA
<211> Length : 1767
SequenceName : SEQ ID 718
SequenceDescription :

Sequence

<213> OrganismName : Porphyromonas gingivalis W83
<400> PreSequenceString :

gtgatacaaa aatttactaa tgtaaaacta aatgatatgc gaaaaatttt gagctttttg 60
atgatgtgct ctctgcattt aggtctacaa tctcagactt ggcatggaga tccggactca 120
gtggcagccc taccttctat cggtattcaa gagtcaagtt gtacccgaat cacgttcgag 180
gttgttttcc ccggatttta tagtgtggaa aaacgagaag gcaaccaagt ctttcagcgc 240
atttccatgc cgggttgtgg ctcgtttggg aatctgggcg aagctgaatt gcctgttttg 300
aaaaagatga tagccgttcc ggaattttca acagctaacg ttgctgtaaa aatcaaagag 360
acggagacat tcgacaatta taatatctat cctaatccta cctatgtcgt agaggagttg 420
cctgaggggg ggacttatct ggtagaggct ttcgcgataa acaatgacta ttatagccaa 480
aatgtaagcc tcccttctac tcactatgtc tattctcaag acgggtattt tcgctcacaa 540
agatttatcg aagttaccct gtatcctttt cgatacaacc ctgtccgaca agaaattcta 600
tttgcaaaaa aaatcgaggt tacaataact ttcgataatc ctcagccacc tttacaaaaa 660
aacaccggca tatttaacaa agtagcctcc tctgcattta ttaattatga agctgatggc 720
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cctattgcac acaaaaatat tctttacgca gaagggaaag gctgcgatgc tccaatctta 1380
cgtttattct taaaagaaat cgcctctggt tacacagtca actctatctt aaaatctaat 1440
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tcggctgtag cagattcaac tattagatcg cttggagaag tcctgaccac atacgcacct 1680
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atttacaacc gaaataagat cagtaacaat catataggag tacgtctcct caacaacagt 2760
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aataggactt ggcagctcta ttcatcaaac ggtacattcc ctctcaactt ccattacaac 2880
agcttgcagg ggggagatac agatacatgg atttacaacg acacgtatac gaatcgctat 2940

attgacgttt caaataatca ctggggcaac aatgatttgt ttgatccgaa tcaggttttc 3000
aatacgccag acttgttcat ttggatacct ttttgggatg gattgccaaa tgggagatcg 3060
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gtcattgacc ttggtgacat ttattggaat atgcagttag actcactcag agggactggt 3480
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aaaaattatt tgttgtcaac tcttcccgaa tcaacaggta ctctcctgcc tccattagaa 3600
tgcaacaaat caagccttga taaatccaag ataatctcta tttcgcccaa tccggcgaaa 3660
gctgttgtaa caataatcta ctataccgat aacccttcct gttctgtaat aaaaatatat 3720
ggaataaatg gagcctcggc tgatataacc gggttgccca aacatctatc cgaaggttat 3780
tacagcatac agttcaatac atccaacttt gatcccggtt tctacctggt aacgctaaat 3840
gttgatcaga aaattataga tacggaaaaa ttacgaatca aataa 3885

<212> Type : DNA
<211> Length : 3885
SequenceName : SEQ ID 719
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
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acgagtggaa acctgaatac tgacaccata ataagagtca actctgacgg ttcggttacc 120
ccctcttttt ctgacggaga tgatacattt attgttactg cgggtaatca cgcagtcggc 180
gttcttgcgt gtgcatctcc cggaagcgcg tgtgcgtgtg tatcttctct tgatgaagaa 240
agtactgccg atacaggaag taatgaaaat aatgccatag caaaactgga tatggcaaaa 300
ggggagatca caacccacgg aacagaaagt tatgccgcgt acgctaatgg cactgtcgtc 360
aaggctggtg acacgcttga ttataccaat gccagcgtta cattaaccga tgttgatatc 420
accacgcatg gggacaatgc tcatgccatc gctgcccgcc aggggacagt ttcatttaac 480
cagggagaaa tttatacaac gggtcctgac gccgcgattg ctaaaattta taatggcggc 540
acggtgacgc tgaaaaatac atctgcagtc gcgcatcagg ggtctggaat tgtgctggag 600
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ctgaatccag cggccagcgt ctgggggaat gtgggcgtgc agctgggtga taatggctac 2280
aatgacaccg cagtgatggt gggcctgaaa tataagttct ga 2322

<212> Type : DNA
<211> Length : 2322
SequenceName : SEQ ID 720

SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
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gattacgata ccgatgttta cccagtaccg gtaatcaact atgaaggcga taacttctgg 180
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<212> Type : DNA
<211> Length : 747
SequenceName : SEQ ID 721
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
atgaaaaaaa ttgcgctagc aggtctggcc ggaatgctgt tggtttctgc atcggtcaat 60
gcaatgagca tcagcggcca ggcgggtaaa gaatacacca atattggtgt cggttttggg 120
actgaatcga cgggcctggc tttaagcggt aactggacac ataacgacga cgacggtgac 180
gtcgcgggcg tggggctggg gttgaatctg cctctcgggc cgttaatggc gaccgttggc 240
ggaaaaggcg tgtacaccaa cccgaattac ggcgatgaag gttatgccgc agcggtagga 300
ggtggtttgc agtggaaaat tggcaacagc ttccgtttgt ttggcgagta ttactactct 360
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accattatgc gtccagtcag tattgaggcg ggttatcgct acctgaatct gtcgggtaaa 480
gacggtaacc gcgacaacgc tgtggctgac ggcctgtatg ttggggttaa cgccagtttc 540
tga 543
<212> Type : DNA
<211> Length : 543
SequenceName : SEQ ID 722
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
atgactacct tgaccgccag ggtgtttaca acggcagaga taatttatcg gaaaacagtt 60
atcgcattgg tgtgtcattt aaactgtagt agacaggaga cagtcacaat gaataaaact 120
ataatggcgc ttgctatcat gatggcttca tttgccgcaa acgcgtctgt attaccggaa 180
actcctgtgc catttaaaag tggtaccgga gcaattgata acgacactgt ctacattggt 240
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aatgacgtac acaaatacaa ccccaaaacc aatagctggg ttaaattgat gtcgcacgcg 480
ccgatgggca tggcgggtca tgtgactttt gtacacaacg gcaaggctta tgttactggc 540
ggtgttaacc agaatatctt caatggctat tttgaagatc tcaacgaggc tggaaaagat 600
tcaaccgcta tagataaaat caacgcccac tattttgaca aaaaagcaga agattatttc 660
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ggtcgggcct acggagtatc attgccctgg aataatagtt tattaattat tggcggtgaa 1140
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acagtacaaa actaa 1215
<212> Type : DNA
<211> Length : 1215
SequenceName : SEQ ID 723
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
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gccggaggtg caagtgcact ccaagcggct tttcagaaag catcagcgag tatggaaacc 120
ggcggtgaca tgtccagcat ggggtcagtt gtcagcagtg gcggaaacgg tggtggtgaa 180
gcgggtactg ctggcagtag cccattcgcc caagcggctg gctttggtga cagcggcagt 240
agctcaagcg gtggcggctt tgccaaggcc gcgaagctgg ccacaggcac ggcctccgag 300
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acaggcggaa aactggctgc ttcgatacgc gaaagcatgg agccgaaaga agcaagccaa 420
tctggccagt tcgagggcaa tagcttgggc gccgattctg gcccagatag taacgaagtc 480
aggagttag 489
<212> Type : DNA
<211> Length : 489
SequenceName : SEQ ID 724
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
atgaagcgag ttcttattcc tggcgtcatt ttatgtggcg ctgatgtggc gcaggccgtc 60
gatgacaaaa acatgtacat gtatttttt gaagagatga cggtctatgc tcctgtccct 120
gtacccgtaa acggcaacac gcattacacc agtgaaagca tcgagcgttt accgaccggg 180
aatggcaata tcagcgatct gctgagaacc aaccctgcgg tacgcatgga ttcaacgcaa 240
agtacctcgt tgaaccaggg agatattcgc cctgagaaaa tctctattca cggtgcgtcg 300
ccctaccaga atgcctattt gattgacggt attagtgcaa ctaataacct gaacccagcg 360
aatgagtccg atgccagtag tgcaaccaat attagcggga tgtcacaggg gtattatctt 420
gatgtcagct tactggacaa tgtgacgctt tatgacagtt ttgtgccggt tgaatttggt 480
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gttattgcac gcgcaagtga agcgcatgat caaatcagca aaagcagtcg taccgacagc 1740
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agcaataccg gtgataacca ggtggtttat aacggtaatc tggtctctta cgatagcgtt 1980
ccagtggcag attttaataa cccattaaag atctccttaa acatggattt cacgcatcaa 2040
ccgagcgggt tagtgtgggc gaatacgctg gcctggcaag aagcgcgtaa agctcgcatt 2100
atccttggta agacaaatgc gcaatacatc agcgaatatt cagattacaa gcagtatgtt 2160
gacgaaaaac tggatagcag cctgacctgg gacacccgct tgtcctggac gccacaattt 2220
ctgaaacaac aaaacctgac gatcagtgcc gatattctca atgtactgga tagcaaaacc 2280
gctgttgata caacgaacac cggtgtgggg acctacgcca gtggccgtac tttctggctt 2340

gatgtcagca tgaaatttta a 2361
<212> Type : DNA
<211> Length : 2361
SequenceName : SEQ ID 725
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
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actttagtaa gccagggtac tgaagcgtca gctaatctta ctttgaccaa gcctatcgtt 120
gttaataata ccattcaacc agtgaaaggg gtatatagcg gtacgttaac tgcatggacg 180
cctttggcaa caggtattgt tggcgcatct gatgggcaga gccacgacta tgctgtaact 240
ttcccggatg atatttatgc ggagagcagt acttcagcgg atgcagtaat ttctggtgac 300
aataacccgg accataaact gaaagtttcc ctgacaacgc ttgagcagga tcctccttca 360
gctgcctccg aagagattgg cggtaagcgt tatatgatgc tgaaaaatac tggaacaggt 420
ggtgcctatc gcgtcgtttc ccatatgaaa gaacaggttg ttgagccaga ctcttacacc 480
atccgtaccc aggcttatat ctacgcagaa taa 513
<212> Type : DNA
<211> Length : 513
SequenceName : SEQ ID 726
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
atgggtattt accactggtc ccggaagaca aaaatgaaac ggacaaaatc catacgccac 60
gcatcgttcc gcaaaaactg gagcgcacgc catctgacac cagtcgctct cgcggttgcc 120
actgttttta tgctggctgg ctgtgaaaag agtgatgaaa cagtgtctct ctatcaaaat 180
gctgacgact gttcagctgc aaacccaggc aaaagcgccg aatgtaccac cgcgtacaac 240
aatgcgctga aagaagccga acgtactgcg ccgaaatacg ccacccgtga agactgtgtt 300
gctgaatttg gtgaaggtca gtgtcagcaa gcaccagccc aggctggcat ggcaccagaa 360
aaccaggcgc aggctcagca atccagcggg agtttctgga tgccgctgat ggccggttac 420
atgatggggc gtctgatggg cggcggcgcg ggatttgcac agcagccgct gttctcctcg 480
aaaaacccgg ccagtccggc ttacggtaaa tataccgacg cgacgggtaa aaactatggc 540
gcagcccagc caggccgcac catgaccgta ccgaagacgg caatggcacc aaaaccggcg 600
accaccacta ccgttacccg tggcggtttt ggtgaatctg ttgccaaaca aagcactatg 660
cagcgtagcg caaccggcac ctcttctcgt tcaatgggtg gctga 705
<212> Type : DNA
<211> Length : 705
SequenceName : SEQ ID 727
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
atgacaaaaa tgagtcgcta cgccttgatt accgcgctgg cgatgtttct cgccgggtgt 60
gtggggcaac gtgaacctgc accggtagaa gaagtgaaac cagcgccgga acaaccagcc 120
gagccacaac agcctgtccc cacagtgccc tcggtgccga cgatcccgca gcagccaggc 180
ccaattgagc acgaagatcg aacggcaccg cctgcgccgc atattcgcca ttatgactgg 240
aatggcgcaa tgcagccgat ggtcagtaag atgcttgggg ctgacggggt gactgcgggt 300
agcgtcctgc tggttgatag cgttaacaac cgtactaacg gttcgctgaa tgccgcagaa 360
gcgaccgaaa cgctgcgaaa tgcgctggct aataacggga aatttaccct ggtttccgcc 420
cagcaactgt cgatggctaa gcaacagtta ggtttgtcgc cgcaggacag tttaggcacc 480
cgtagtaaag ccataggcat tgcccgcaat gtcggcgctc attacgtgct gtactcctgc 540
gcctctggca acgttaacgc tccgacccta caaatgcagc tgatgctggt gcagacgggc 600
gaaattatct ggtcaggtaa aggtgccgtt tcgcagcaat aa 642
<212> Type : DNA
<211> Length : 642
SequenceName : SEQ ID 728
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
atgacgaaac ttatgcaatt tgttcagagg tgctattata tgactaataa gaaaatgtat 60
tttatattaa tacttgtttt cacattgcta caggtgtgtt tttttgctct ctggaaggct 120
cgtgatggta gcacaacgtc tcttgaatgt acgtcgacgt taacaagaaa tgctaaaaca 180
gatcattctt tatactactc tgctaacctt tcagtcattt taaaaaaaga tggtagcggt 240
agttttacga ttgttggctt aactgatgaa gatacaccga ggaaattttc ccattcgtat 300
ttttttacct acaaaataga tagtaacgga cggatctcag gtaatgctaa ggccaaagtt 360
tcgggactgg aaaatcagat aaaggatgag aacttcagac tcaattttct cgatgcatct 420
ttaacaggta aaggcaatgc gaggctaagc aagtttaata atgtctatat ttttagtatc 480
ccgggggttga tcattaacac atgtgctcca atataa 516
<212> Type : DNA
<211> Length : 516
SequenceName : SEQ ID 729
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
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gtcatcgcca ccagtgcaat ggcgcaggat gatttaacca ttagcagcct tgcaaagggc 120
gaaaccacca aagctgcgtt taatcagatg gtgcaagggc ataagctacc tgcatgggtg 180
atgaaaggcg gtacttatac tcccgcacaa accgtaacgt tgggagatga gacgtatcag 240
gtgatgagcg cgtgcaaacc gcatgactgt ggctcgcaac gtatcgctgt gatgtggtcc 300
gagaaatcta atcagatgac ggggctgttc tcggctattg atgagaaaac gtcgcaagag 360
aaactcacct ggctgaatgt gaacgatgcg ctttcgattg atggtaaaac ggtgctgttc 420
gcggcgttga ccggcagcct ggaaaaccat ccggatggct ttaattttaa ataa 474

<212> Type : DNA
<211> Length : 474
SequenceName : SEQ ID 730
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
atgaaaaaac aatttttgga aaaagctgtg tttactgttg cggctacggc agcaacagtt 60
gttttaggaa ataaaatggc tgatgcagac acttatactc ttcaagaagg agattctttt 120
ttcagtgttg ctcaacgata tcatatggat gcttatgagt tagcttctat gaatggaaaa 180
gatattacca gtctgatttt gccgggtcag actttaactg ttaatggttc ggcagcaccg 240
gataatcagg cggcagcgcc aactgacact acgcaagcaa ccactgaaac gaatgatgcg 300
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gcaggcgact ggtggggcaa tggcggtgat tgggcctcta gtgcttctgc acaaggttac 420
actgtcggta acactccggc agtagggtct attatgtgtt ggacagatgg tggttatgga 480
catgttgcct atgtcacagc tgttggtgaa gatggtaaag ttcaagtact ggaatccaat 540
tataaagatc aacaatgggt tgataactat cgtggttggt ttgatccaaa taatagtgga 600
acaccaggca gtgtcagtta tatttatcct aactaa 636
<212> Type : DNA
<211> Length : 636
SequenceName : SEQ ID 731
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
atgtctatta aaaatatttt agaaaacaaa acaacaacaa ttaaagttag ttttgcagga 60
attgcaacag cagctagttt aattttacct atggcagtac aggcagaaac tacttatact 120
gtgaaatcag gagatacttt atcagagatt gcttcaacac acggaacaac tgttgataaa 180
cttgctaagt taaataaaat taataatatc catcttatcc atgctggtca aattttagaa 240
ttagatgcag caacagaaga tactgatgca acgccagtac aagaaagtca gataaatgaa 300
gcagaaacct cagcatctgc caaaactagt caaacgagcg aagtgacgac aacagcaccg 360
gtacaagaaa gccaaacaag tgaagttata acttcagcac cagctgaaac cagtcagaca 420
agcgaagtgc caactgaagc caaccaaaca aatgaagtaa gttcagcagt atcggttgaa 480
accagtcaaa cgagtgaggc gacgacttca gctccagtgg aaactagtca gacaagcgaa 540

gcaacgacag cggaaccaac tgagaccaag accagccaaa caaatgaagt agcagcttca 600
gctgaagaaa accaaacaac atctaatact agcggtttga gcacatctga tgcagctgca 660
aaagaattca tcgctcaaaa agaatcaggt ggtaattata atgctaaaaa tggtcaatat 720
tatggacgtt atcaattgag tgattcttac ttgaatggtg atttgtcaga agaaaatcaa 780
gaacgtgtag cagatgctta tgtatcaagt cgttatggtt catggactgc tgctcaagct 840
ttctggaatg ctaatggttg gtattaa 867

<212> Type : DNA
<211> Length : 867
SequenceName : SEQ ID 732
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
atgaaatgtc aagcgtttga agattttaaa gctacaagtt tgaataagct gtcttatacg 60
acaggtggag ctactgatgg tgaaattata gctaatcgga tgttacaagg taaagctact 120
aagggcgaaa ttactatgta tacttggaac attattcaaa atggctgggt gaattcactc 180
gtgtcttggg gtattggtgg ttataatagt tctataggat actcagctca aggtaataga 240
ggatttagta attatccata cgatgtttct atggattcag ataatagcag tagttcaagt 300
aatacgacag gtggttatgt taattataac cagagtttta attctggatg gtaa 354

<212> Type : DNA
<211> Length : 354
SequenceName : SEQ ID 733
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
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actacctcaa ccttacctag tataagtatt ctagctgagg acagtactgg agcacctgct 120
aggccagatg gacaagctcc tgctggaggt ggtgctaaca ccacaactta tgattacagc 180
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aaactaaaag ctagtagctc tggcagtaat gggatttttg caactgataa ggcaaccatc 480
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tacaatggca atattattgc taataagatg gccatttcta caaaaggtgc tcacagcgct 600
gctattgcaa ctgaccgtgg tggcggcaat atttccacca ctaattccag tttaaatact 660
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gtatcaacca acagtaccaa tatatcccca agcacgtctc ctattaccat gaatatttct 1260
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ggtgctaaaa ttgttgataa agacggaaaa accgtcagcg tcatctcttc aagcggacaa 1380
aaacttgtta aaggtaaaag caaatatagc ctaacagtca caggaactta cagtcaaaag 1440
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aattatttta aaacaacaac agcctttgta aataatacca aaaatacaag taattaa 1557

<212> Type : DNA
<211> Length : 1557
SequenceName : SEQ ID 734
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :

atgaacaaga taggtgatac tctacgtgat gctcgtattg aaaaaaaatt gagttttgat 60
gatgttgtag ataaaactgg aattgctcct cactatatac tggcaatgga gttagatcaa 120
cttaaattat taccagaagg caaaacaaat gagtatttag aaaaatatgc tcatgctgtt 180
ggcttagatc cggtttctat tattcatggt tatcgcaatc aggaaatgag cgatgaactt 240
atcctacctt cttctgcaga attggctgct tcttcagata gcaatataga aaagaaaaat 300
gaaggaaaat caattgaaga acctcaagag ttagctattg atagtttgga tgttactcaa 360
aatattacag aagagactcc ccaaatagaa gattttaagg ttgaatcaga ggaggcaagt 420
aaaaaaatag aaaaaatacc atctcgactt agtaaatatg attatgatga agaaccgaaa 480
aagaaatttc catgggcttt aattctgcta attttacttg ctttaactat tatcagttat 540
gttggatatg tggtttataa tcagctgcaa actgattcaa ataagactga attaagtacc 600
tctacgaaaa aatctaagga tactaaaaat gatgccaatt caacgacaca aagtcagacc 660
agcataacaa cagactttgc tgatggtgga aataatatca ccttaagtaa tactaatgga 720
aaagtagagg ttacctttac tttgacaggg gatgaggaaa gttgggtttc agcaactaac 780
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ttagcagaag gttcaacaac atctatgctg acagtcggat cacctagcgg tgttgaaatt 900
acgatcaatg gtcaaaaggt ggatactaca aaccttgtta atgctggttt gactaatatt 960
aatttgacag tccaataa 978

<212> Type : DNA
<211> Length : 978
SequenceName : SEQ ID 735
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
atgaagagca gaaaacgtca gcgaaaaggg ctggttcgaa aaaatgaaat cattatttta 60
actcttttg tcgcatcagc cgtttcactc ttagcattta ccaattcttt tggggtactt 120
gctaagagtc ttcatcttga aaaaatcaat aaatcgataa ctatttcgct tccttttggt 180
aaaaaaaaga tggaacaaac agcacgttac tattcaggtg aacaggttca gatcagttcc 240
tcagctaaaa aagacagtct tggaaaaggg ctgtctcatt accaaaattg gattgggaca 300
gttaaaaaga taaaatcaca aaaagacagt cgtcaaaagc atcattatag ttatgaagtt 360
acatttgata atggcaaagc tttgaaatat gttcaggaaa aagacttagt taaaacaaaa 420
agatctaaat acagcaaagg tcaaattgtc aaattaaaat cctctgcgac agctgattta 480
gatggcagca gtttaacgga ttatcgtgca tcagctggta aaatcgatca tatttcttat 540
aatcatagca ataccacagg tggctataag tatgatatca cctttgatga aggcggcaag 600
gtgactaata ttcaagaaaa agatttggat aaggtttatg aagttcagct aaaatcagaa 660
aatactgcag ctcaaaataa tgagattctt aaacaagctt ttgcatatgc taaacaacat 720
tctggtacta tcttaagttt gccaaacggt gaatttaaga ttggcagtca gacaccagac 780
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catggtaaaa taatagcata cagcggaact atcggacagc actcttctga tgtcggcctt 1380
gtcaaaattt atgataatgt ttttagtaac tctttggtca gccgtttcaa tcaaaatggc 1440
aaaagcgagg cgtggatttt taaagctatt cacctaaaat caaattataa taatgctgtt 1500
tatgccaatt ctatcagtta a 1521

<212> Type : DNA
<211> Length : 1521
SequenceName : SEQ ID 736
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
atgagaaaac ttaaagtggc acttttgca agcagtattt taggaatgct ggctgttagt 60
tcttatacgg cagcagatac agaggataat caggtaacga ttagccatta taatgaacag 120
gctggaactt ttgatgtcaa cgctgtacag gcagccaacg gaaaaactat tcaatcgata 180
gatgttgcga tttggtctga agaaaatggg caggatgatt tgaaatggta tcatgccagt 240
aatgatggca gcaatcaatt gacagttcat tttaatgctg agaatcatgg cagtaaggta 300
ggttcttata ttgcgcatgc ttatattacc tatacagatg gtaatcgagt cggggttaat 360

ttgggaaaac gaaaattatc cttatctgca ccgcaattat ccttaaaaca aggtggcctt 420
caactatttt ctaagctgaa acctagtgca gcggatcaac ttttttcagc agtttggtcg 480
gatgagaatg gtcaagatga tcttcattgg tacacggcag atgctgacgg gaatactttg 540
gctggctatg ctaatcataa aggttatgga acttaccatg ttcatactta ccttaagcaa 600
aatggtaaga tgataccaat tagtgctcaa gatattgata ttcctaaacc gaaagtcaag 660
attcagattg ataaaataaa tgataccagt tatgatgttg ttgttaataa tgtccccctt 720
tatattagtt cagtagccat tcctgtgtgg agtgaacaaa atggccaaga cgatttgaaa 780
tggtatcagg caacaaaagt ggctgatggt atatttaaaa caactgttta tttaaagaca 840
catcgttttg aattaggcaa ctatcaagct catatttatg gcgatagcca attaagcaag 900
aaactggatg gtttaggaga aactcatttt aatgttccgt ctattattaa ctatgaagat 960
cctcaggtaa ctattgatca ttataatatt aacaaaggaa cgtttgatgt gactgtagct 1020
gaaacagata attcaaaagc gatacaatca atcagtgctg ctgtttggtc tgatgctaac 1080
caagctaatc tttattggta tgaagctaaa cagctagcaa atggaaaggc tgcaattact 1140
gtcgatgttc aaaagcatgg caatcaaaca ggaagctaca atgtccatgt ttatgttcat 1200
tataatgatg gcacgactag cggacatgtt ttggctaatc agcagctcaa tcaaattgtc 1260
cattatcaac cttctgcagt aagaataaca gcctatatga atgaaaaaaa tacttatcca 1320
gttggtcagt gtacttgggg agtgaaagaa ttagctcctt ggatacctaa ttggcttggc 1380
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aaagttggtg ctattgcttg ttggagtgat ggtggttatg gccatgttgc ttacgttacc 1500
cacgttgaga gtaataaccg tattcaagtg aaagaagcta attataagaa tcaacaatat 1560
atttccaatt ttcgcggatg gtttgatccc acgacttcct atttgggaag attaacttat 1620
atttatcctg actaa 1635

<212> Type : DNA
<211> Length : 1635
SequenceName : SEQ ID 737
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
atggcaaata actattctcg tcgtcaacaa cccactaaaa aaacaaaggg gacaagtcgg 60
aaacgtccga ctgaacatat caaaacaggt ttttcagcac tgcaaaagag tgttgctatt 120
atcgctggta ttttagggat tattaccgct ttgattacta ttaataatta tcgcaatagt 180
tcacacaatg ataaaaaaga ttccacatct aaaaccacta tcatcaaaga aaaagaagtg 240
gatgactcaa atagtaacaa caatgctgct aattctcaag ctgaaaatga cagcaataac 300
aataataatt ctgcagaatc aaatcaaaac caaactgcaa caacagcaaa tgacagtaac 360
agcaattcgg ctaatcaaaa tcaagccaat agccaatcac aagcaaataa tcagcaaaat 420
caaaacaatg ctaatgctgg tcaataa 447

<212> Type : DNA
<211> Length : 447
SequenceName : SEQ ID 738
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
ttgaaaatat ttagttttgg aaccattcga aacaacacag ctctaaaacc taactatgat 60
gacacaacag cttttagcgg ttttggaacc attcgaaaca acacagctct aaaacagagc 120
actaactgcg ctagctggtt caatcgtttt ggaaccattc gaaacaacac agctctaaaa 180
ctcaccatat taattaatgg cgtttccttt tgttttggaa ccattcgaaa caacacagct 240
ctaaaacctc gtggaccaat ttttgtctcg acatttcgta atcgcgccat tcatctcagc 300
cagatttcag cttcaaaatg a 321

<212> Type : DNA
<211> Length : 321
SequenceName : SEQ ID 739
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
atgaaaagaa aacgaaatct ttacttttctt attggtttat ttttgacagt ctttcttttg 60
ataggatgct caatgcagaa aaaaaccaaa tcagaaagca gctcgacttc tcaaaagact 120
actttacaaa caaaacagtc aagtgaaaaa tcaactgatg ctaagcaaac gacagaagct 180
cattcagaaa gcagtcagtc ttcttctcat tctaataacg aggaaaccct tgctcccatt 240

gatacaggcg ctgttttaaa ggctgattac agtagtatgg caggaacttg gaaaaatgaa 300
gaaggacaaa cgttgacatt tgatcagcga ggtctgacaa cccctggaat gacagtcagt 360
ctgttgaaca ttgatcaaga cggaaatctt ttgttaaatg ttgagactgg aacaaaaaag 420
aatctaactc tttatattgt gccagccaat aaaaccttat ctaatcaata ttttttctaat 480
ggtcaaagcg atgaatccga taaaacaaaa gatcgtattg tttcttctga gagtttaaat 540
agtggcaaat ttacaaaccg agtttattat catgtttcaa ctcattaa 588

<212> Type : DNA
<211> Length : 588
SequenceName : SEQ ID 740
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
atgacaccta aaaaaatcaa aatagctcta acagctctta tctctttgat gctcgcctta 60
tttttattct tgtttaatca ccattcagta agagaaaaca gtcagcaaga aaagttaaag 120
ataagtaaag caagttctaa aaaatcacaa acaagcactt cttctgttat gacaagtagt 180
cgaaaagcta ctgaacaaac aagccaagca cagactcaaa gtcaatcaca agcagaacaa 240
agtaacccta atgtgatcct ccccattccg caagaattag tcggcaccta caaaggttcg 300
agtccacaag catctgaaat aacttttacc atttcttcaa atggtcaatt acgtgctcaa 360
gctaattttg atcctgcttc tgatataaat gacgttaccg ccactgttag tggtgttaga 420
aaagtcgggg cagataccta tatttgggag tttgtctctg gtagttcagc tgctctttta 480
ccgggtgtta caggtatagg agggcttgga aagatgcagc ctggtttcat cctaaaaggg 540
gggcaattaa cacctatcat gtttacaggt tctgtagatg gtgaaattga ttattcacat 600
cccaatccct atccagtatc attaaacaag cagtaa 636

<212> Type : DNA
<211> Length : 636
SequenceName : SEQ ID 741
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
atgaaaaaaa taattaatgt tatcgtctta tcactatccg ttttttttcct gatagcttgc 60
agcaatagca gtaccgggga aaaaacaagt caatcatctg aagagactaa ggtccgatta 120
attgttaaaa cggattctaa taaaaccgat gaaaaagtcg ctttcaaaaa aggtgctact 180
gttatggatg tcttaaaaga caactataaa gttaaagaaa gcggtggttt tatcactact 240
attgatggtg tcactcagga taaaaaagca ggtaggtact ggatgtttga tgttaatgat 300
aagctggcat caaaagctgc tgataagatt aaggtcaaaa atggggataa aattgaattt 360
tatttgaaag tttataaagg taagaactag 390

<212> Type : DNA
<211> Length : 390
SequenceName : SEQ ID 742
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
atgtcaaata aaccatggga agaaaaagta actgatgcaa ctactgataa tgaagaaatg 60
acaagaaatt caaaggatgc tagtattatc agtacaccta ttttaacaat cctattgagc 120
ctcttttttct tgattattat tggtatttta ttttttgtac tttatacttc aaatggtgga 180
agcaatgaaa aagcagccac ttcgggtttc tatagttctt ccaaaacggt caaaaaagcc 240
aaaaatgagg caaatagtca aactgatgaa cagacaacag aagcagaaac aagttcaagt 300
gaaacgacaa gttcctcttc agacagtgat ggcgagacaa ttacagttca aggaggtgaa 360
ggggctgcag caattgctgc gcgtgcgggt atttctgttg ataaactcta tgagctgaat 420
ccagaacata tgacgcatgg ctattggtat gctaaccctg gagataacat caagattaag 480
taa 483

<212> Type : DNA
<211> Length : 483
SequenceName : SEQ ID 743
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
atgccagata atcgcatgaa ctatagtatt gatagcaata tgcagtttcc cttggtagaa 60
attactttgg aaacaggaga atttgcttat attcaacgcg gtagcatggt ctatcacaca 120
cccagtgtca ctctcaatac caaagtcaat ggacgtggtt caggacttgg caagctagta 180
ggagcaattg gtcgttctgt aacgtctgga gaaagttttt tcattactca ggcagtatca 240
aatgctagcg atggtaaatt ggccttggcc ccttctatgc cgggccaagt tattgcttta 300
gaattgggag aaaaacaata tcgcctcaat gatggtgctt ttcttgcctt agatggttct 360
gctcaatatc aaatgaaagc tcagagtgtt ggacgtgccc tttttggcgg tcaaggcggt 420
ctttttgtta tgacaacaga aggtcaaggt accttgcttg ctaatagttt tggttctatc 480
aaaaaaatag aattacagaa tcaggaaatt acaattgaca atgctcatgt tgtagcttgg 540
agtagggatt tgaactatga cattcatttg gaaaatggct ttatgcaatc gatcggaacc 600
ggtgaaggcg ttgtcaatac tttccgagga acgggtgaaa tttatgtaca aagtcttaat 660
ctgcagcagt ttgctggtgt cctacagggt ttcattacca atactaatcg ttaa 714

<212> Type : DNA
<211> Length : 714
SequenceName : SEQ ID 744
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
atgaaaaaaa attatttttg gtacggtctg cttgggcttc tcgcacttta ccttattact 60
attgctttta tcccgggatt tcatattttc tttagcaaca tgttgatgtt ggccctgttc 120
tttatgttaa tagctttgag taacaggagt atcttctttt tctttctagc cttaggtttt 180
cttagtatct acttgaaaga tatctttcat tttgactatt ctaccggacc gctttttacg 240
ggtataatca ttatcggcgt tattttaaac agtttcctca aaccacacta ttcttattct 300
tataaaggaa atcattattt taatatgaaa caacatgcta actacattga taacgaaaca 360
gatgtctttt taaaaacact tttttctgaa aataccagtt atgtgacttc tcaagaatta 420
aataaaatta ttattgatac taagtttgga gaacaatctg ttgatctctc tcaagctcaa 480
tttatgacag attctcccga aattcatata gatgttagct ttggtgaaac caatctgcgt 540
attccaaaca actggaaaat catcaataaa actcactccc cctttgcttc catttcattt 600
tcaggttttc ctagcacaaa tggtgatttt attaacgtta cattgactgg aacagtggct 660
atgggatctc taaacattca atattaa 687
<212> Type : DNA
<211> Length : 687
SequenceName : SEQ ID 745
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pneumoniae R6
<400> PreSequenceString :
atgaaatcaa taactaaaaa gattaaagca actcttgcag gagtagctgc cttgtttgca 60
gtatttgctc catcatttgt atctgctcaa gaatcatcaa cttacactgt taaagaaggt 120
gatacacttt cagaaatcgc tgaaactcac aacacaacag ttgaaaaatt ggcagaaaac 180
aaccacattg ataacattca tttgatttat gttgatcaag agttggttat cgatggccct 240
gtagcgcctg ttgcaacacc agcgccagct acttatgcgg caccagccgc tcaagatgaa 300
actgtttcag ctccagtagc agaaactcca gtagtaagtg aaacagttgt ttcaactgta 360
agcggatctg aagcagaagc caaagaatgg atcgctcaaa aagaatcagg tggtagctat 420
acagctacaa atggacgtta tatcggacgt tacggttcat ggactgctgc taaaaacttc 480
tggcttaaca atggctggta ttaa 504
<212> Type : DNA
<211> Length : 504
SequenceName : SEQ ID 746
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pneumoniae R6
<400> PreSequenceString :
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cgtaagtatt actttggtgc agctagtgtc ttgctcggta ccgctttggt attaggtgca 120
gcagctagtg tccaaacagt acaagcggaa gaaaacaaac aagaaactac caatagtatt 180
tctgttggta ggggagaagc agctactaaa ccagcagagg tttctgcgtc taataaagag 240

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aaaacctatg cagctccaac tgtagctaat ccagtagaaa cgactccagt taaaactgaa   300
gaagttacta aaccagcaga aaaagttgaa gaagcaaaag acaaaaaaga ggaagtaacg   360
catcaagatg ccgttgacaa gtcaaaatta ttaacggctc tttcgcgtgc taaaaaatta   420
gaaagcaagt tatatacaga agcaagtgct gctaacttgc aaacaagtat ccaagctggt   480
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attcaatcat ttattattgg tctagaactt cgttctaact ctaataaaga aactgtatca   600
gaaacgcctg tagcgaagaa agctgatgca gttgaatcaa aagaaggggc taaaccagct   660
gcaacaactg aacgttcagc tgttgatagc gctattttgc caactagcac agctgacaaa   720
gtagaaacaa cttcagctcc agcatctatt aatgaaatct tgaaactagg tttgagcctt   780
tctgatgctc gccaaaatcc agctatccgt aaggaagatg ttaatagagg gtatagtggt   840
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<212> Type : DNA
<211> Length : 7656
SequenceName : SEQ ID 747
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pneumoniae R6
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<212> Type : DNA
<211> Length : 1143
SequenceName : SEQ ID 748
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pneumoniae R6
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<212> Type : DNA
<211> Length : 666
SequenceName : SEQ ID 749
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pneumoniae R6
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<212> Type : DNA
<211> Length : 408
SequenceName : SEQ ID 750
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pneumoniae R6
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<212> Type : DNA
<211> Length : 5304
SequenceName : SEQ ID 751
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pneumoniae R6
<400> PreSequenceString :
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<212> Type : DNA
<211> Length : 1353
SequenceName : SEQ ID 752
SequenceDescription :

Sequence

<213> OrganismName : Neisseria meningitidis serogroup A strain Z2491
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<212> Type : DNA
<211> Length : 6048
SequenceName : SEQ ID 753
SequenceDescription :

Sequence

<213> OrganismName : Neisseria meningitidis serogroup A strain Z2491
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<212> Type : DNA
<211> Length : 2283
SequenceName : SEQ ID 754
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pyogenes strain MGAS8232
<400> PreSequenceString :
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<212> Type : DNA
<211> Length : 1083
SequenceName : SEQ ID 755
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pyogenes strain MGAS8232
<400> PreSequenceString :
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<212> Type : DNA
<211> Length : 615
SequenceName : SEQ ID 756
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pyogenes strain MGAS8232
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<212> Type : DNA
<211> Length : 2274
SequenceName : SEQ ID 757
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pyogenes strain MGAS8232
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cttggcaata ccataatcaa aaagctacag gtcgaggatg acaatacaat gcacgacttt 180
gtaaagccta aagttaccac tcaacaagct tttggactag ctcagcaggt caaagagctt 240
gatttacagc taaaagaccc taagtcagat ttgtggggca aaatcaagtt caataataag 300
gcaatgctag tcgagtacgc caacaaagag atgtcaagtg ccattgcgca atcagctgag 360
cagatattgt tacaagtcaa gtctattgat gatgaacgat attccaaatt tgagcaaact 420
ctgaatggta tcaaacaaac tgtcaaaagt gagtcagttg aatccgcacg tactcagcta 480
gcatcaatgt ttgatagtcg tattagtgga cttgatggca aatacagtcg tttgagccaa 540
acaattgata gtcttagcag tcgtcttgat gatggtgttg gtaactactc aacgctatct 600
caaaaggtaa gtggcattga tttacgagtt agtaatgcag ctaatgatgt ttctcgattg 660
tctcagacag cacaaggatt gcagtcacaa atcacaaatg caaaccaaaa ttacagcagt 720
ttgtctcaga ctgtacaggg actacaaaca actgtacgtg ataatcaatc aaatgctaca 780
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<212> Type : DNA
<211> Length : 1785
SequenceName : SEQ ID 758
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pyogenes strain MGAS8232
<400> PreSequenceString :

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aaatttgcgg ttggtgcagg agtctttaaa ttagcttcgg ctgcagttga tttggttagt 180
caatctcttg gcaaggctat cacaagattt gacacgcttg aaaaatatcc aagggtcatg 240
aaagctatgg ggcatagcgc tgaggatgtt gctagatcaa ctgataagtt agcgaacgga 300
attgatggac taccaacaac tttagacgag gttgtcggaa ccgctcaacg tttgacctct 360
attactaagg atatcaataa atcaactaat ctcacactag cattaaataa tgccttttta 420
gcttcaggag cttcatcaga ggctgcaagc cgagggctgg agcaatatgc ccaaatgcta 480
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gaggcgttaa aaaacgggca aataacattt gaccaatttt ctaataagtt gattgagtta 660
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tcttttaaca acatcaagaa cgctattgca aaaggtgtgg ccaatagcat taaggctttg 780
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acaaccatta agactgtgac tgcggtacaa gcggtaagta ccacgatgac taaagcagat 1140
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gcagctcatc aaaaattagc tgacgaaatc attaagttag ccgccaaaga aaacaaaact 1560
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gttatgaggg atgaggttgg acgttttatc cctcagggta tcgctgtagg tattgatgcg 3000
gatagaaaag tcattgactc atctatgcaa aagctaaaag agtcaatgac gattaatgcg 3060
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aataactcaa ataacagttt tacccttaat gtcaaggttg atgaatccga cggtaatagc 3180
cacgagaaat atcaacgctt attcagagaa tttagctggt atattcaaca acaacaagga 3240
aggttaggtg atgttaaatg a 3261

<212> Type : DNA
<211> Length : 3261
SequenceName : SEQ ID 759
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pyogenes strain MGAS8232
<400> PreSequenceString :
atggctaaag aaccatggga agaaaaaatt gttgatgata ctatagggac acgaacacgt 60
aaatcaagaa atgctttcat tagcacgcct tggttgactg ctttattaag tgtattcttt 120
gtcatcattg ttgctatact ttttatttte ttctatacat caaatagcgg tagtaataga 180
caagctgaaa caaatggttt ttatggagca tccactcata aaaaaacaag gaaagcttct 240
aacgctaaaa aaacatcaag tagttcaaca actacagaca caacaccttc tagcgaagaa 300
acacttgctt ctagtgaagg aaccggcgaa acccttactg tattggcagg tgaggggcga 360
gcttctattg cagctcgtgc aggtatttct gtggagcagt tacaagcact taatccagag 420
cacatgactc aaggatattg gtatgccaat ccaggagatc aagtcactat taaataa 477

<212> Type : DNA
<211> Length : 477
SequenceName : SEQ ID 760
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pyogenes strain MGAS8232
<400> PreSequenceString :
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ataacgctag tattaattat aactggagta gtcttgtgga aacaacaaca aaatacgcta 120
acagctgata tcgctaaaga accttactct actgttagtg taactgaagg gagtattgct 180
tcttcgactt tactatcagg tactgtaaag gctttatcag aggaatatat ttattttgat 240
gctaataaag gaaatgatgc aactgttaca gttaaaatag gtgatcaggt aacgcagggc 300
cagcaattag ttcaatataa tacaacaaca gctcagtcag cttatgatac tgctgttagg 360
agtcttaaca agattggccg acaaattaat catcttaaaa catacggagt tcctgctgtt 420
agtacagaaa ctaataaaga tgaagctacc ggtgaagaga cgacaacaac agttcaacca 480
tcagctcagc aaaatgctaa ttataaacag cagctgcaag atttaaatga tgcttatgca 540
gatgcacaag cagaagtaaa taaagcgcag atagcgttaa atgatacagt agttatcagt 600
agtgtctctg gaactgttgt ggaagtaaat aatgatattg atccttcttc aaagaacagt 660
caaacacttg ttcacgtagc aaccgaagga cagcttcagg tgaaaggaac attgacagag 720
tatgatttag caaacgttaa ggttggtcaa tctgtaaaaa ttaagtctaa agtttattct 780
aatcaagaat ggactggaaa aatatcatat gtttcaaact atccaactga gtctaatgca 840
ggttcaacaa cgccagcagg tagcactgga gcgggaagtt ctacaggagc tgcctatgat 900
tacaagattg atattataag tcctcttaac cagcttaaac aaggtttcac tgtttctgtt 960
gaggttgtta atgaagctaa acaggcctta gttcctttaa cggctgttat taagaaagat 1020
aaaaaacact atgtttggac ttatgatgat gctactggca aagccaaaaa agtagaggtg 1080
acacttggaa acgcagatgc acaacaacaa gaaattcata aaggagtagc tgttggtgac 1140
attgttattg ccaatccaga taaaaatatc aaaccggata aaaaactaga aggggttatt 1200
tcaataggta ccaacacaaa accggaaaaa gattctcaat caaagaataa aaaatcaggg 1260
gtggataaat ag 1272

<212> Type : DNA
<211> Length : 1272
SequenceName : SEQ ID 761
SequenceDescription :

Sequence

<213> OrganismName : Treponema pallidum subsp. pallidum str. Nichols
<400> PreSequenceString :
gtgctccgct tgccaactgc gcgcgcgtgc attacaatgg gcaccatgat cagacataca 60
tttacgcata ggtgcggagc gctcctgtgc gcgctggcgt tgggaagctc cactatggct 120

gcgaccgccg ctgcaaaacc caagaaaggg caaatgcaga aattgcggca gcggccggtg 180
tgggcgccca ccggcgggcg gtatgcgtct ttggacggtg cgtttaccgc gctggcaaat 240
gatgcaagtt tctttgaggc aaatccggca ggaagtgcga acatgacgca cggggagctg 300
gctttcttcc ataccactgg ctttggctcg tttcacgccg aaacgctctc ttacgttggc 360
cagtcgggca actggggata cggcgcgtcg atgcgtatgt ttttccctga atctgggttt 420
gacttttcta ccaccacgga gcccgtgtgc acacctgctt cgaaccccat taagcagcgc 480
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ggcttgcagt gggtggggaa cgttgccaag tcctttacct ctgaagagcc caacctgtac 660
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gccaagtcgc tgtaccagaa cctggcttac agcataggcg ccatgtttga tcccttcagc 1020
ttcctgagct tgagttcgag cttccgcatc aaccacaagg ctaacatgcg agtgggagtg 1080
ggtgcagagg cgcgcattgc ccgcattaag ctgaacgcgg gataccgctg tgacgtcagc 1140
gacatcagca gtgggagtgg gtgcacaggc gcgaaggctt cgcactacct ttccttgggt 1200
ggcgcgatac tgctcggccg aaattaa 1227

<212> Type : DNA
<211> Length : 1227
SequenceName : SEQ ID 762
SequenceDescription :

Sequence

<213> OrganismName : Treponema pallidum subsp. pallidum str. Nichols
<400> PreSequenceString :
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ctgcctgcct acagctccga gggcgtgcga gaggtacccc cctcccagtc tccgcaggtg 120
gtggtggcgt acgagcccat tcgccccggg gatcagctgc tcaaaattgg cattgttgca 180
ggctgccagt tgtacatagc agggggaaat ggaaccaacg gctcttcgag ttccggcacc 240
aacggtaacg gcaacggcaa actgctcggg ggcggggggt ttcacctcgg gtacgagtat 300
ttttttacca aaaacttttc cctcggcggg caagtttcct ttgagtgtta ccgcacgacc 360
gggtcaaact attacttttc tgttcccatc acggtaaacc ccacgtacac gtttgccgta 420
gggcgctggc gcataccgct ctccctgggc gttgggctca acattcagtc ctatctcagc 480
aagaaggcgc cggggcttat tgcggaagcc agcgcggggc tctactacca gtacaccccg 540
gactggtcca tcggcggcat tgttgcctac acgcagcttg gggacattgc aagctccccc 600
gacaagtgca gagccgtggg ccttgccacc attgactttg gggtgcgcta tcacttttag 660

<212> Type : DNA
<211> Length : 660
SequenceName : SEQ ID 763
SequenceDescription :