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(57) Abstract: The disclosure provides, e.g., compositions, systems, and methods for targeting, editing, modifying, or manipulating a host cell's genome at one or more locations in a DNA sequence in a cell, tissue, or subject. Gene modifying systems for treating sickle cell disease (SCD) are described.

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HBB-MODULATING COMPOSITIONS AND METHODS

SEQUENCE LISTING

The instant application contains a Sequence Listing which has been submitted electronically in XML format compliant with WIPO Standard ST.26 and is hereby incorporated by reference in its entirety. Said XLM copy, created on September 1, 2022, is named V2065-7027WO_SL.XML and is 15,727,019 kb in size.

CROSS REFERENCE TO RELATED APPLICATIONS

This application claims the benefit of U.S. Provisional Application No. 63/241,994, filed September 8, 2021, U.S. Provisional Application No. 63/250,143, filed September 29, 2021, and U.S. Provisional Application No. 63/303,900, filed January 27, 2022. The contents of the aforementioned applications are hereby incorporated by reference in their entirety.

BACKGROUND

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

Sickle cell disease is an inherited blood disorder that affects red blood cells. There are several types of sickle cell disease (e.g., hemoglobin SS disease, hemoglobin SC disease; sickle beta-plus thalassemia; sickle beta-zero thalassemia). People with sickle cell disease have red blood cells that contain mostly hemoglobin S, an abnormal type of hemoglobin. Sickle-shaped cells die prematurely, which can lead to a shortage of red blood cells (anemia). Sickle-shaped cells are rigid and can block small blood vessels, causing severe pain and organ damage. Tissue that does not receive a normal blood flow eventually becomes damaged. This is what causes the complications of sickle cell disease.

The HBB gene provides instructions for making a protein, beta-globin. Beta-globin is a component (subunit) of a larger protein called hemoglobin, which is located inside red blood cells. In adults, hemoglobin normally consists of four protein subunits: two subunits of beta-globin and two subunits of another protein called alpha-globin, which is produced from another gene called HBA. Each of these protein subunits is bound to an iron-containing molecule called heme; each heme contains an iron molecule in its center that can bind to one oxygen molecule. Hemoglobin within red blood cells binds to oxygen molecules in the lungs. These cells then travel through the bloodstream and deliver oxygen to tissues throughout the body.

Sickle cell anemia, a common form of sickle cell disease, is caused by a particular mutation in the HBB gene. This mutation results in the production of an abnormal version of beta-globin called hemoglobin S or HbS. In this condition, hemoglobin S replaces both betaglobin subunits in hemoglobin. The mutation changes a single amino acid in beta-globin. Specifically, the amino acid glutamic acid is replaced with the amino acid valine at position 6 in beta-globin, written as Glu6Val or E6V. Replacing glutamic acid with valine causes the abnormal hemoglobin S subunits to stick together and form long, rigid molecules that bend red blood cells into a sickle or crescent shape. Mutations in the HBB gene can also cause other abnormalities in beta-globin, leading to other types of sickle cell disease. In these other types of sickle cell disease, just one beta-globin subunit is replaced with hemoglobin S. The other beta-globin subunit is replaced with a different abnormal variant, such as hemoglobin C or hemoglobin E.

There is currently no universal cure for sickle cell disease. The available options for treating sickle cell disease are limited to a bone marrow or stem cell transplant. Accordingly, there is a need for new and more effective treatments for sickle cell disease utilizing the HBB E6V mutation.

SUMMARY OF THE INVENTION

This disclosure relates to novel compositions, systems, and methods for altering a genome at one or more locations in a host cell, tissue, or subject, *in vivo* or *in vitro*. In particular, the invention features compositions, systems, and methods for inserting, altering, or deleting sequences of interest in a host genome. For example, the disclosure provides systems that are capable of modulating (e.g., inserting, altering, or deleting sequences of interest) the HBB gene

activity and methods of treating sickle cell disease (SCD) disease by administering one or more such systems to alter a genomic sequence at a HBB nucleotide to correct a pathogenic mutation causing SCD.

In one aspect, the disclosure relates to a system for modifying DNA to correct a human HBB gene mutation causing SCD comprising (a) a nucleic acid encoding a gene modifying polypeptide capable of target primed reverse transcription, the polypeptide comprising (i) a reverse transcriptase domain and (ii) a Cas9 nickase that binds DNA and has endonuclease activity, and (b) a template RNA comprising (i) a gRNA spacer that is complementary to a first portion of the human HBB gene, (ii) a gRNA scaffold that binds the polypeptide, (iii) a heterologous object sequence comprising a mutation region to correct the mutation, and (iv) a primer binding site (PBS) sequence comprising at least 3, 4, 5, 6, 7, or 8 bases of 100% homology to a target DNA strand at the 3′ end of the template RNA. The HBB gene may comprise an E6V mutation. The template RNA sequence may comprise a sequence described herein, e.g., in Table 1, 3, 4, A, AA, B, B1, 5A-5D, X4, or X4A.

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

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

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

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

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

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

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

In one aspect, the disclosure relates to a method of correcting a mutation in the human HBB gene in a cell, tissue or subject, the method comprising administering the system described above to the cell, tissue or subject, wherein optionally the correction of the mutant HBB gene comprises an amino acid substitution of V6E (reversing the pathogenic substitution which is E6V. The system may be introduced *in vivo*, *in vitro*, *ex vivo*, or *in situ*. The nucleic acid of (a) may be integrated into the genome of the host cell. In some embodiments, the nucleic acid of (a) is not integrated into the genome of the host cell. In some embodiments, the heterologous object sequence is inserted at only one target site in the host cell genome. The heterologous object sequence may be inserted at two or more target sites in the host cell genome, e.g., at the same corresponding site in two homologous chromosomes or at two different sites on the same or different chromosomes. The heterologous object sequence may encode a mammalian polypeptide, or a fragment or a variant thereof. The components of the system may be delivered on 1, 2, 3, 4, or more distinct nucleic acid molecules. The system may be introduced into a host cell by electroporation or by using at least one vehicle selected from a plasmid vector, a viral vector, a vesicle, and a lipid nanoparticle.

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

Enumerated Embodiments

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

(i) a gRNA spacer that is complementary to a first portion of the human HBB gene, wherein the gRNA spacer has a sequence comprising the core nucleotides of a gRNA spacer sequence of Table 1, or a sequence having 1, 2, or 3 substitutions thereto, and optionally comprises one or more consecutive nucleotides starting with the 3' end of the flanking nucleotides of the gRNA spacer (e.g., comprises one or more flanking nucleotides that are adjacent to the core nucleotides), or wherein the gRNA spacer has a sequence of a spacer chosen from Table A, Table AA, Table B, Table B1, Tables 5A-5D, Table X4, or Table X4A;

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

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

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

2. The template RNA of embodiment 1, wherein the heterologous object sequence comprises the core nucleotides of an RT template sequence from Table 3, or a sequence having 1, 2, or 3 substitutions thereto, and optionally comprises one or more consecutive nucleotides starting with the 3' end of the flanking nucleotides of the RT template sequence, or wherein the heterologous object sequence comprises a sequence of an RT template sequence from Table A, Table AA, Table B, Table B1, Tables 5A-5D, Table X4, or Table X4A.

3. The template RNA of embodiment 1, wherein the heterologous object sequence comprises the core nucleotides of the RT template sequence of Table 3 that corresponds to the

gRNA spacer sequence, or a sequence having 1, 2, or 3 substitutions thereto, and optionally comprises one or more consecutive nucleotides starting with the 3' end of the flanking nucleotides of the RT template sequence (e.g., comprises one or more flanking nucleotides that are adjacent to the core nucleotides), or wherein the heterologous object sequence comprises a sequence of an RT template sequence from Table A, Table AA, Table B, Table B1, Tables 5A-5D, Table X4, or Table X4A that corresponds to the gRNA spacer sequence.

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

5. The template RNA according to any one of embodiments 1-3, wherein the PBS sequence has a sequence comprising the core nucleotides of a PBS sequence of Table 3 that corresponds to the RT template sequence, or a sequence having 1, 2, or 3 substitutions thereto, the gRNA spacer sequence, or both, and optionally comprises one or more consecutive nucleotides starting with the 5' end of the flanking nucleotides of the PBS sequence, or wherein the PBS sequence has a sequence comprising a sequence of a PBS from Table A, Table AA, Table B, Table B1, Tables 5A-5D, Table X4, or Table X4A that corresponds to the RT template sequence, or a sequence having 1, 2, or 3 substitutions thereto, the gRNA spacer sequence, or both.

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

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

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

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

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

(iii) a heterologous object sequence comprising a mutation region to introduce a mutation into (e.g., to correct a mutation in) a second portion of the human HBB gene, wherein the heterologous object sequence comprises the core nucleotides of an RT template sequence of Table 3, , or a sequence having 1, 2, or 3 substitutions thereto, and optionally comprises one or more consecutive nucleotides starting with the 3' end of the flanking nucleotides of the RT template sequence, or wherein the heterologous object sequence comprises an RT template sequence of Table A, Table AA, Table B, Table B1, Tables 5A-5D, Table X4, or Table X4A; and

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

9. The template RNA of embodiment 8, wherein the gRNA spacer comprises the core nucleotides of a gRNA spacer sequence of Table 1, or a sequence having 1, 2, or 3 substitutions thereto, and optionally comprises one or more consecutive nucleotides starting with the 3' end of the flanking nucleotides of the gRNA spacer sequence, or wherein the gRNA spacer comprises a gRNA spacer sequence of Table A, Table AA, Table B, Table B1, Tables 5A-5D, Table X4, or Table X4A.

10. The template RNA of any one of embodiments 1-9, wherein the gRNA spacer comprises CATGGTGCATCTGACTCCTG (SEQ ID NO: 21668) or CATGGTGCACCTGACTCCTG (SEQ ID NO: 19249), or a sequence having 1, 2, or 3 substitutions thereto.

11. The template RNA of any one of embodiments 1-9, wherein the gRNA spacer comprises GTAACGGCAGACTTCTCCAC (SEQ ID NO: 19971), or a sequence having 1, 2, or 3 substitutions thereto.

12. The template RNA of embodiment 8, wherein the heterologous object sequence comprises the core nucleotides of the gRNA spacer sequence of Table 1 that corresponds to the RT template sequence, or a sequence having 1, 2, or 3 substitutions thereto, and optionally comprises one or more consecutive nucleotides starting with the 3' end of the flanking nucleotides of the gRNA spacer sequence, or wherein the heterologous object sequence comprises the nucleotides of the gRNA spacer sequence of Table A, Table AA, Table B, Table B1, Tables 5A-5D, Table X4, or Table X4A that corresponds to the RT template sequence, or a sequence having 1, 2, or 3 substitutions thereto.

13. The template RNA according to any one of embodiments 8-12, wherein the PBS sequence has a sequence comprising the core nucleotides of the PBS sequence from the same row of Table 3 as the RT template sequence, or a sequence having 1, 2, or 3 substitutions thereto, and optionally comprises one or more consecutive nucleotides starting with the 5' end of the flanking nucleotides of the PBS sequence.

14. The template RNA according to any one of embodiments 8-12, wherein the PBS sequence has a sequence comprising the core nucleotides of a PBS sequence of Table 3 that corresponds to the RT template sequence, or a sequence having 1, 2, or 3 substitutions thereto, the gRNA spacer sequence, or both, and optionally comprises one or more consecutive nucleotides starting with the 5' end of the flanking nucleotides of the PBS sequence, or wherein the PBS sequence has a sequence comprising the core nucleotides of a PBS sequence of Table A, Table AA, Table B, Table B1, Tables 5A-5D, Table X4, or Table X4A that corresponds to the RT template sequence, the gRNA spacer sequence, or both.

15. The template RNA according to any of embodiments 8-14, wherein the gRNA scaffold comprises a sequence of a gRNA scaffold of Table 12, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto.

16. The template RNA according to any of embodiments 8-14, wherein the gRNA scaffold comprises a sequence of a gRNA scaffold of Table 12 that corresponds to the RT template sequence, the gRNA spacer sequence, or both, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto.

17. The template RNA according to any of the preceding embodiments, wherein the gRNA spacer has a sequence of a gRNA spacer sequence of Table A, or Table B, or a sequence having 1, 2, or 3 substitutions thereto.

18. The template RNA according to embodiment 17, wherein the gRNA spacer has a sequence of SEQ ID NO: 21668.

19. The template RNA of embodiment 17 or 18, wherein the PBS sequence has a sequence of a PBS sequence from the same row as Table A or B as the gRNA spacer sequence, or a sequence having 1, 2, or 3 substitutions thereto.

20. The template RNA of any of embodiments 17-19, wherein the PBS sequence has a sequence comprising the core nucleotides of the PBS sequence of SEQ ID NO:21669, and optionally comprises one or more consecutive nucleotides starting with the 5' end of the flanking nucleotides of the PBS sequence.

21. The template RNA of any of embodiments 17-19, wherein the gRNA scaffold has a sequence of a gRNA scaffold from the same row as Table A or B as the gRNA spacer sequence, or a sequence having 1, 2, or 3 substitutions thereto.

22. The template RNA of any of embodiments 17-20, wherein the heterologous object sequence has a sequence of the RT template sequence from the same row as Table A or B as the gRNA spacer sequence, or a sequence having 1, 2, or 3 substitutions thereto, wherein optionally the bolded T shown in the RT template sequence of Table A is replaced with a G (e.g., a sequence without a PAM-kill mutation), or wherein further optionally the bolded C shown in the RT template of Table B is replaced with a T or U (e.g., a sequence without a SNP that is present in HEK293T cells but absent in the hg38 human reference genome).

23. The template RNA of any of embodiments 17-22, wherein the heterologous object sequence has a sequence comprising the core nucleotides of the RT template sequence of SEQ

ID NO:21670, and optionally comprises one or more consecutive nucleotides starting with the 3' end of the flanking nucleotides of the RT template sequence.

24. The template RNA of any of embodiments 17-23, wherein the heterologous object sequence has a sequence comprising the core nucleotides of the RT template sequence of SEQ ID NO:21671, and optionally comprises one or more consecutive nucleotides starting with the 3' end of the flanking nucleotides of the RT template sequence.

25. The template RNA of any of embodiments 17-24, wherein the template RNA has a sequence of a template RNA of Table A or Table B, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto, wherein optionally the template RNA comprises one or more (e.g., all) chemical modifications shown in the sequence of Table A or Table B.

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

(a) a first RNA comprising, from 5' to 3, (i) a guide RNA sequence that is complementary to a first portion of the human HBB gene, wherein the guide RNA sequence has a sequence comprising the core nucleotides of a spacer sequence of Table 1, or a sequence having 1, 2, or 3 substitutions thereto, and optionally comprises one or more consecutive nucleotides starting with the 3' end of the flanking nucleotides of the guide RNA sequence, or wherein the guide RNA sequence has a sequence comprising a spacer from Table A, Table AA, Table B, Table B1, Tables 5A-5D, Table X4, or Table X4A; and (ii) a sequence (e.g., a scaffold region) that binds a gene modifying polypeptide (e.g., binds the Cas domain of the gene modifying polypeptide), and

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

27. The gene modifying system of embodiment 26, wherein the heterologous object sequence comprises the core nucleotides of an RT template sequence from Table 3, or a sequence having 1, 2, or 3 substitutions thereto, and optionally comprises one or more consecutive nucleotides starting with the 3' end of the flanking nucleotides of the RT template sequence, or wherein the heterologous object sequence comprises a sequence of an RT template sequence from Table A, Table AA, Table B, Table B1, Tables 5A-5D, Table X4, or Table X4A, or a sequence having 1, 2, or 3 substitutions thereto.

28. The gene modifying system of embodiment 26, wherein the heterologous object sequence comprises the core nucleotides of the RT template sequence of Table 3 that corresponds to the gRNA spacer sequence, or a sequence having 1, 2, or 3 substitutions thereto, and optionally comprises one or more consecutive nucleotides starting with the 3' end of the flanking nucleotides of the RT template sequence, or wherein the heterologous object sequence comprises a sequence of an RT template sequence from Table A, Table AA, Table B, Table B1, Tables 5A-5D, Table X4, or Table X4A that corresponds to the gRNA spacer sequence, or a sequence having 1, 2, or 3 substitutions thereto.

29. The gene modifying system of any one of embodiments 26-28, wherein the PBS sequence has a sequence comprising the core nucleotides of the PBS sequence from the same row of Table 3 as the RT template sequence, or a sequence having 1, 2, or 3 substitutions thereto, and optionally comprises one or more consecutive nucleotides starting with the 5' end of the flanking nucleotides of the PBS sequence.

30. The gene modifying system of one of embodiments 26-28, wherein the PBS sequence has a sequence comprising the core nucleotides of a PBS sequence of Table 3 that corresponds to the RT template sequence, or a sequence having 1, 2, or 3 substitutions thereto, the gRNA spacer sequence, or both, and optionally comprises one or more consecutive nucleotides starting with the 5' end of the flanking nucleotides of the PBS sequence, or wherein the PBS sequence comprises a PBS sequence from Table A, Table AA, Table B, Table B1, Tables 5A-5D, Table

X4, or Table X4A that corresponds to the RT template sequence, or a sequence having 1, 2, or 3 substitutions thereto, the gRNA spacer sequence, or both.

31. The gene modifying system of any one of embodiments 26-30, wherein the gRNA scaffold comprises a sequence of a gRNA scaffold of Table 12, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto.

32. The gene modifying system of any one of embodiments 26-30, wherein the gRNA scaffold comprises a sequence of a gRNA scaffold of Table 12 that corresponds to the RT template sequence, the gRNA spacer sequence, or both, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto.

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

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

(b) a second RNA comprising (iii) a heterologous object sequence comprising a nucleotide substitution to introduce a mutation into a second portion of the human HBB gene, wherein the heterologous object sequence comprises the core nucleotides of an RT template sequence of Table 3, or a sequence having 1, 2, or 3 substitutions thereto, and optionally comprises one or more consecutive nucleotides starting with the 3' end of the flanking nucleotides of the RT template sequence, or wherein the heterologous object sequence comprises an RT sequence from Table A, Table AA, Table B, Table B1, Tables 5A-5D, Table X4, or Table X4A, or a sequence having 1, 2, or 3 substitutions thereto, and (iv) a primer region comprising at least 5, 6, 7, or 8 bases of 100% homology to a third portion of the human HBB gene, and (v) an RRS (RNA binding protein recognition sequence) that binds a gene modifying protein.

34. The gene modifying system of embodiment 33, wherein the gRNA spacer comprises the core nucleotides of a gRNA spacer sequence of Table 1, or a sequence having 1, 2, or 3 substitutions thereto, and optionally comprises one or more consecutive nucleotides starting with the 3' end of the flanking nucleotides of the gRNA spacer sequence, or wherein the gRNA

spacer comprises a gRNA spacer sequence of Table A, Table AA, Table B, Table B1, Tables 5A-5D, Table X4, or Table X4A.

35. The gene modifying system of embodiment 33, wherein the heterologous object sequence comprises the core nucleotides of the gRNA spacer sequence of Table 1 that corresponds to the RT template sequence, or a sequence having 1, 2, or 3 substitutions thereto, and optionally comprises one or more consecutive nucleotides starting with the 3' end of the flanking nucleotides of the gRNA spacer sequence, or wherein the gRNA spacer comprises a gRNA spacer sequence from Table A, Table AA, Table B, Table B1, Tables 5A-5D, Table X4, or Table X4A that corresponds to the RT template sequence, or a sequence having 1, 2, or 3 substitutions thereto.

36. The gene modifying system of any one of embodiments 33-35, wherein the PBS sequence has a sequence comprising the core nucleotides of the PBS sequence from the same row of Table 3 as the RT template sequence, or a sequence having 1, 2, or 3 substitutions thereto, and optionally comprises one or more consecutive nucleotides starting with the 5' end of the flanking nucleotides of the PBS sequence.

37. The gene modifying system of any one of embodiments 33-35, wherein the PBS sequence has a sequence comprising the core nucleotides of a PBS sequence of Table 3 that corresponds to the RT template sequence, the gRNA spacer sequence, or both, or a sequence having 1, 2, or 3 substitutions thereto, and optionally comprises one or more consecutive nucleotides starting with the 5' end of the flanking nucleotides of the PBS sequence, or wherein the PBS sequence comprises a PBS sequence from Table A, Table AA, Table B, Table B1, Tables 5A-5D, Table X4, or Table X4A that corresponds to the the RT template sequence, the gRNA spacer sequence, or both, or a sequence having 1, 2, or 3 substitutions thereto.

38. The gene modifying system of any one of embodiments 33-37, wherein the gRNA scaffold comprises a sequence of a gRNA scaffold of Table 12, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto.

39. The gene modifying system of any one of embodiments 33-37, wherein the gRNA scaffold comprises a sequence of a gRNA scaffold of Table 12 that corresponds to the RT template sequence, the gRNA spacer sequence, or both, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto.

40. A gRNA comprising (i) a gRNA spacer sequence that is complementary to a first portion of the human HBB gene, wherein the gRNA spacer has a sequence comprising the core nucleotides of a gRNA spacer sequence of Table 1, Table 2, or Table 4, or a sequence having 1, 2, or 3 substitutions thereto and optionally comprises one or more consecutive nucleotides starting with the 3' end of the flanking nucleotides of the gRNA spacer sequence; and (ii) a gRNA scaffold, or wherein the gRNA spacer has a sequence of a gRNA spacer sequence from Table A, Table AA, Table B, Table B1, Tables 5A-5D, Table X4, or Table X4A, or a sequence having 1, 2, or 3 substitutions thereto.

41. The gRNA of embodiment 40, wherein the gRNA scaffold comprises a sequence of a gRNA scaffold of Table 12, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto.

42. The gRNA of embodiment 40, wherein the gRNA scaffold comprises a sequence of a gRNA scaffold of Table 12 that corresponds to the gRNA spacer sequence, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto.

43. A template RNA comprising: (iii) a heterologous object sequence comprising a mutation region to introduce a mutation into a second portion of the human HBB gene, wherein the heterologous object sequence comprises the core nucleotides of an RT template sequence of Table 3, or a sequence having 1, 2, or 3 substitutions thereto, and optionally comprises one or more consecutive nucleotides starting with the 3' end of the flanking nucleotides of the RT template sequence, or wherein the heterologous object sequence comprises an RT sequence from Table A, Table AA, Table B, Table B1, Tables 5A-5D, Table X4, or Table X4A , or a sequence having 1, 2, or 3 substitutions thereto, and (iv) a PBS sequence comprising at least 5, 6, 7, or 8 bases of 100% homology to a third portion of the human HBB gene.

44. The template RNA according to embodiment 43, wherein the PBS sequence has a sequence comprising the core nucleotides of the PBS sequence from the same row of Table 3 as the RT template sequence, or a sequence having 1, 2, or 3 substitutions thereto, and optionally comprises one or more consecutive nucleotides starting with the 5' end of the flanking nucleotides of the PBS sequence.

45. The template RNA according to embodiment 43, wherein the PBS sequence has a sequence comprising the core nucleotides of a PBS sequence of Table 3 that corresponds to the RT template sequence, or a sequence having 1, 2, or 3 substitutions thereto, and optionally comprises one or more consecutive nucleotides starting with the 5' end of the flanking nucleotides of the PBS sequence, or wherein the PBS sequence has a sequence comprising a PBS sequence from Table A, Table AA, Table B, Table B1, Tables 5A-5D, Table X4, or Table X4A , or a sequence having 1, 2, or 3 substitutions thereto.

46. The template RNA according to any one of embodiments 1-16 or 43-45, the gene modifying system of any one of embodiments 26-39, or the gRNA of any one of embodiments 31-33, wherein the mutation introduced by the system is a V6E mutation (e.g., to correct a pathogenic E6V mutation) of the HBB gene.

47. The template RNA according to any one of embodiments 1-16 or 43-46 or the gene modifying system of any one of embodiments 36-39 or 46, wherein the pre-edit sequence comprises between about 1 nucleotide to about 35 nucleotides (e.g., comprises about 1-5, 5-10, 10-15, 15-20, 20-25, 25-30, or 30-35 nucleotides) in length.

48. The template RNA according to any one of embodiments 1-16 or 43-47 or the gene modifying system of any one of embodiments 36-39, 46, or 47, wherein the mutation region comprises a single nucleotide.

49. The template RNA according to any one of embodiments 1-16 or 43-47 or the gene modifying system of any one of embodiments 26-39, 46, or 47, wherein the mutation region is at least two nucleotides in length.

50. The template RNA according to any one of embodiments 1-14, 41-45, or 47 or the gene modifying system of any one of embodiments 24-37, 44-45 or 47, wherein the mutation region is up to 32 (e.g., up to 5, 10, 15, 20, 25, 30, or 32) nucleotides in length and comprises one, two, or three sequence differences relative to a second portion of the human HBB gene.

51. The template RNA according to any one of embodiments 1-16, 43-47, 49, or 50 or the gene modifying system of any one of embodiments 26-39, 46, 47, 49, or 50, wherein the mutation region comprises two sequences differences relative to a second portion of the human HBB gene.

52. The template RNA according to any one of embodiments 1-16, 43-47, or 49-51 or the gene modifying system of any one of embodiments 26-39, 46, 47, or 49-51, wherein the mutation region comprises a first region (e.g., a first nucleotide) designed to correct a pathogenic mutation in the HBB gene and a second region (e.g., a second nucleotide) designed to inactivate a PAM sequence (e.g., a "PAM-kill" mutation exemplified in Table A, AA, B, or B1).

53. The template RNA according to any one of embodiments 1-16, 43-51 or the gene modifying system of any one of embodiments 26-39 or 46-51, wherein the mutation region comprises less than 80%, 70%, 60%, 50%, 40%, or 30% identity to corresponding portion of the human HBB gene.

54. The template RNA of any one of the preceding embodiments, wherein the template RNA comprises one or more silent mutations (e.g., silent substitutions), e.g., as exemplified in Table 7A, X4, or X4A.

55. The template RNA of embodiment 54, wherein the one or more silent mutaitons comprises a silent substitution at the codon encoding the 6th amino acid, counting the initial methionine, of the HBB gene (proline), e.g., to CCC or CCG.

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

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

58. A gene modifying system comprising:

a template RNA of any of embodiments 1-16, 43-57, or a system of any of embodiments 26-39 or 46-57, and

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

59. The gene modifying system of embodiment 58, wherein the gene modifying polypeptide comprises:

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

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

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

60. The gene modifying system of embodiment 59, wherein:

(a) the RT domain comprises:

(i) an RT domain of Table 6, or

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

(b) the gene modifying polypeptide comprises an amino acid sequence according to Table C, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto.

61. The gene modifying system of embodiment 59 or 60, wherein the Cas domain comprises a Cas domain of Table 7 or Table 8.

62. The gene modifying system of any one of embodiments 59-61, wherein the Cas domain:

(a) is a Cas9 domain;

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

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

63. The gene modifying system of embodiment 62, wherein the Cas9 domain binds a PAM sequence listed in Table 7 or Table 12.

64. The gene modifying system of embodiment 63, wherein a second portion of the human HBB gene overlaps with a PAM recognized by the Cas domain, e.g., wherein the second portion

of the human HBB gene is within the PAM or wherein the PAM is within the second portion of the human HBB gene).

65. The gene modifying system any one of embodiments 58-64, wherein the gRNA spacer is a gRNA spacer according to Table 1, and the Cas domain comprises a Cas domain listed in the same row of Table 1, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto.

66. The gene modifying system of any one of embodiments 58-64, wherein the template RNA comprises a sequence of a template RNA sequence of Table 3, Table A, Table AA, Table B, Table B1, Tables 5A-5D, Table X4, or Table X4A or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto.

67. The gene modifying system of any one of embodiments 58-66, wherein:

(a) the template RNA comprises a sequence of a template RNA sequence of Table 3, Table A, Table AA, Table B, Table B1, Tables 5A-5D, Table X4, or Table X4A;

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

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

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

68. The gene modifying system of any of embodiments 58-67, which produces a first nick in a first strand of the human HBB gene.

69. The gene modifying system of embodiment 68, which further comprises a second strand-targeting gRNA that directs a second nick to the second strand of the human HBB gene.

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

(i) a sequence comprising the core nucleotides of a left gRNA spacer sequence or a right gRNA spacer sequence from Table 2, and optionally comprises one or more consecutive nucleotides starting with the 3' end of the flanking nucleotides of the left gRNA spacer sequence or right gRNA spacer sequence; or

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

71. The gene modifying system of embodiment 69, wherein the second strand-targeting gRNA comprises a sequence comprising the core nucleotides of a left gRNA spacer sequence or a right gRNA spacer sequence from Table 2 that corresponds to the gRNA spacer sequence of (i), and optionally comprises one or more consecutive nucleotides starting with the 3' end of the flanking nucleotides of the left gRNA spacer sequence or right gRNA spacer sequence.

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

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

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

73. The gene modifying system of embodiment 69, wherein the second strand-targeting gRNA comprises a sequence comprising the core nucleotides of the second nick gRNA sequence from Table 4 that corresponds to the gRNA spacer sequence of (i), or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto, and optionally comprises one or more consecutive nucleotides starting with the 3' end of the flanking nucleotides of the second nick gRNA sequence.

74. The gene modifying system of any one of embodiments 58-73, wherein the second strand-targeting gRNA has a "PAM-in orientation" with the template RNA of the gene modifying system, e.g., as exemplified in Table 4, 6A, X4, or X4A.

75. The gene modifying system of any one of embodiments 58-63, the second strand-targeting gRNA targets a sequence overlapping the target mutation of the template RNA.

76. The gene modifying system of embodiment 75, wherein second strand-targeting gRNA comprises:

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

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

(iii) a sequence (e.g., a spacer sequence) complementary to the Makassar sequence at the sickle cell locus;

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

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

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

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

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

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

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

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

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

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

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

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

87. The gene modifying system of embodiment 86, wherein the linker comprises a sequence of a linker of Table 10 (e.g., of any of SEQ ID NOs: 5217, 5106, 5190, and 5218).

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

89. The gene modifying system of embodiment 88, wherein the gene modifying polypeptide comprises a first NLS and a second NLS.

90. The gene modifying system of embodiment 88 or 89, wherein the NLS comprises a sequence of a NLS of Table 11 (e.g., of any of SEQ ID NOs: 5245, 5290, 5323, 5330, 5349, 5350, 5351, and 4001).

91. A template RNA comprising a sequence of a template RNA of Table A, Table AA, Table B, Table B1, Tables 5A-5D, Table X4, or Table X4A, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto.

92. A template RNA comprising a sequence of a template RNA of Table A, Table AA, Table B, Table B1, Tables 5A-5D, Table X4, or Table X4A.

93. A gene modifying system comprising:

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

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

94. A gene modifying system comprising:

(i) a template RNA comprising a sequence of a template RNA of Table 4; and

(ii) a second-nick gRNA sequence from the same row of Table 4 as (i).

95. A DNA encoding the template RNA of any one of embodiments 1-16, 43-53, 77-85, 91, or 92, or the gRNA of any one of embodiments 40-42.

96. A pharmaceutical composition, comprising the system of any one of embodiments 58-90, 93, or 94, or one or more nucleic acids encoding the same, and a pharmaceutically acceptable excipient or carrier.

97. The pharmaceutical composition of embodiment 96, wherein the pharmaceutically acceptable excipient or carrier is selected from the group consisting of a plasmid vector, a viral vector, a vesicle, and a lipid nanoparticle.

98. The pharmaceutical composition of embodiment 97, wherein the viral vector is an adeno-associated virus.

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

100. A method of making the template RNA of any one of embodiments 1-16, 43-53, 77-85, 91, or 92, the method comprising synthesizing the template RNA by *in vitro* transcription (e.g., solid state synthesis) or by introducing a DNA encoding the template RNA into a host cell under conditions that allow for production of the template RNA.

101. A method for modifying a target site in the human HBB gene in a cell, the method comprising contacting the cell with the gene modifying system of any one of embodiments 58-90, 93, or 94, or DNA encoding the same, thereby modifying the target site in the human HBB gene in a cell.

102. A method for modifying a target site in the human HBB gene in a cell, the method comprising contacting the cell with: (i) the template RNA of any one of embodiments 58-90, 93, or 94, or DNA encoding the same; and (ii) a gene modifying polypeptide or a nucleic acid encoding a gene modifying polypeptide, thereby modifying the target site in the human HBB gene in a cell.

103. A method for treating a subject having a disease or condition associated with a mutation in the human HBB gene, the method comprising administering to the subject the gene modifying system of any one of embodiments 58-90, 93, or 94, or DNA encoding the same, thereby treating the subject having a disease or condition associated with a mutation in the human HBB gene.

104. A method for treating a subject having a disease or condition associated with a mutation in the human HBB gene, the method comprising administering to the subject the template RNA of any one of embodiments 58-90, 93, or 94, or DNA encoding the same; and (ii) a gene modifying polypeptide or a nucleic acid encoding a gene modifying polypeptide, thereby treating the subject having a disease or condition associated with a mutation in the human HBB gene.

105. The method of embodiment 103 or 104, wherein the disease or condition is sickle cell disease (SCD) (e.g., sickle cell anemia).

106. The method of any one of embodiments 103-105, wherein the subject has a pathogenic EV6 mutation.

107. A method for treating a subject having SCD the method comprising administering to the subject the gene modifying system of any one of embodiments 58-90, 93, or 94, or DNA encoding the same, thereby treating the subject having SCD.

108. A method for treating a subject having SCD the method comprising administering to the subject (i) the template RNA of any one of embodiments 58-90, 93, or 94, or DNA encoding the same, and (ii) a gene modifying polypeptide or a nucleic acid encoding a gene modifying polypeptide, thereby treating the subject having SCD.

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

110. The gene modifying system or method of any one of the preceding embodiments, wherein the pathogenic mutation is a E6V mutation, and wherein the correction comprises an amino acid substitution of V6E.

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

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

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

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

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

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

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

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

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

120. The method of any of the preceding embodiments, wherein the gRNA spacer is perfectly complementary at all nucleotide positions to the first portion of the human HBB gene in the cell, wherein the first portion is situated on the second strand of the HBB gene.

121. The method of any of the preceding embodiments, wherein the heterologous object sequence is perfectly complementary to the second portion of the human HBB gene in the cell, at all nucleotide positions except the mutation region, wherein the second portion is situated on the first strand of the HBB gene.

122. The method any of the preceding embodiments, wherein the PBS sequence is perfectly complementary to the third portion of the human HBB gene, wherein the third portion is situated on the first strand of the HBB gene.

Further Enumerated Embodiments

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

(i) a gRNA spacer that is complementary to a first portion of the human HBB gene, wherein the gRNA spacer has a nucleotide sequence comprising CATGGTGCATCTGACTCCTG (SEQ ID NO: 21668), or a nucleotide sequence having 1 substitution thereto;

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

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

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

A2. The template RNA of embodiment A1, wherein the gRNA spacer has a nucleotide sequence comprising CATGGTGCATCTGACTCCTG (SEQ ID NO: 21668) or CATGGTGCACCTGACTCCTG (SEQ ID NO: 19249).

A3. The template RNA of embodiment A1 or A2, wherein the gRNA spacer has a nucleotide sequence consisting of CATGGTGCATCTGACTCCTG (SEQ ID NO: 21668) or CATGGTGCACCTGACTCCTG (SEQ ID NO: 19249).

A4. The template RNA of any of the preceding embodiments, wherein the gRNA spacer has a length of 20 nucleotides.

A5. The template RNA of embodiment A1, wherein the gRNA scaffold has a sequence according to GTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTT GAAAAAGTGGCACCGAGTCGGTGC (SEQ ID NO: 11,012), or a sequence having at least 90% identity thereto.

A6. The template RNA of embodiment A1, wherein the gRNA scaffold has a sequence according to GTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTT GAAAAAGTGGCACCGAGTCGGTGC (SEQ ID NO: 11,012).

A7. The template RNA of embodiment A1, wherein the heterologous object sequence comprises a sequence of at least 8 nucleotides from the 3' end of a sequence according to AGTAACGGCAGACTTCTCTTCAG (SEQ ID NO: 20954), or a sequence having 1, 2, or 3 substitutions thereto.

A8. The template RNA of embodiment A1, wherein the heterologous object sequence comprises a sequence of 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, or 23 nucleotides from the 3' end of a sequence according to AGTAACGGCAGACTTCTCTTCAG (SEQ ID NO: 20954), or a sequence having 1, 2, or 3 substitutions thereto.

A9. The template RNA of embodiment A1, wherein the heterologous object sequence comprises a sequence of at least 8 nucleotides from the 3' end of a sequence according to AGTAACGGCAGACTTCTCTTCAG (SEQ ID NO: 20954).

A10. The template RNA of embodiment A1, wherein the heterologous object sequence comprises a sequence of at least 8 nucleotides from the 3' end of a sequence according to AGTAACGGCAGACTTCTCTGCAG (SEQ ID NO: 20955).

A11. The template RNA of embodiment A1, wherein the PBS sequence comprises a sequence of at least 8 nucleotides from the 5' end of a sequence according to GAGTCAGGTGCACCATG (SEQ ID NO: 19431), or a sequence having 1 substitution thereto.

A12. The template RNA of embodiment A1, wherein the PBS sequence comprises a sequence of at least 8 nucleotides from the 5' end of a sequence according to GAGTCAGGTGCACCATG (SEQ ID NO: 19431).

A13. The template RNA of embodiment A1, wherein the PBS sequence comprises a sequence of 9, 10, 11, 12, 13, 14, 15, 16, or 17 nucleotides from the 5' end of a sequence according to GAGTCAGGTGCACCATG (SEQ ID NO: 19431), or a sequence having 1 substitution thereto.

A14. The template RNA of embodiment A1, wherein:
the gRNA scaffold has a sequence according to
GTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCA

ACTTGAAAAAGTGGCACCGAGTCGGTGC (SEQ ID NO: 11,012), or a sequence having at least 90% identity thereto;

the heterologous object sequence comprises a sequence of at least 8 nucleotides from the 3' end of a sequence according to AGTAACGGCAGACTTCTCTTCAG (SEQ ID NO: 20954), or a sequence having 1, 2, or 3 substitutions thereto; and

the PBS sequence comprises a sequence of at least 8 nucleotides from the 5' end of a sequence according to GAGTCAGGTGCACCATG (SEQ ID NO: 19431), or a sequence having 1 substitution thereto.

A15. The template RNA of embodiment A1, wherein:

the gRNA scaffold has a sequence according to GTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCA ACTTGAAAAAGTGGCACCGAGTCGGTGC (SEQ ID NO: 11,012).

wherein the heterologous object sequence comprises a sequence of at least 8 nucleotides from the 3' end of a sequence according to AGTAACGGCAGACTTCTCTTCAG (SEQ ID NO: 20954); and

the PBS sequence comprises a sequence of at least 8 nucleotides from the 5' end of a sequence according to GAGTCAGGTGCACCATG (SEQ ID NO: 19431).

A16. The template RNA of any of the preceding embodiments, which does not comprise a sequence according to GCATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATA AGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGACTTC TCCACAGGAGTCAGGTGCAC (SEQ ID NO: XXX).

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

(i) a gRNA spacer that is complementary to a first portion of the human HBB gene, wherein the gRNA spacer has a nucleotide sequence comprising GTAACGGCAGACTTCTCCAC (SEQ ID NO: 19971), or a nucleotide sequence having 1 substitution thereto;

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

(iii) a heterologous object sequence comprising a mutation region to introduce a mutation into a second portion of the human HBB gene, and

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

A18. The template RNA of embodiment A17, wherein the gRNA spacer has a nucleotide sequence comprising GTAACGGCAGACTTCTCCAC (SEQ ID NO: 19971).

A19. The template RNA of embodiment A17 or A18, wherein the gRNA scaffold has a sequence according to GTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC (SEQ ID NO: 11,012), or a sequence having at least 90% identity thereto.

A20. The template RNA of any of embodiments A17-19, wherein the gRNA scaffold has a sequence according to GTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC (SEQ ID NO: 11,012).

A21. The template RNA of any of embodiments A17-20, wherein the heterologous object sequence comprises a sequence of at least 8 nucleotides from the 3' end of a sequence according to CCATGGTGCACCTGACTCCTGAG (SEQ ID NO: 20956) or CCATGGTGCACCTGACTCCTGCG (SEQ ID NO: 21906), or a sequence having 1, 2, or 3 substitutions thereto.

A22. The template RNA of any of embodiments A17-21, wherein the heterologous object sequence comprises a sequence of 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, or 23 nucleotides from the 3' end of a sequence according to CCATGGTGCACCTGACTCCTGAG (SEQ ID NO: 20956) or CCATGGTGCACCTGACTCCTGCG (SEQ ID NO: 21906), or a sequence having 1, 2, or 3 substitutions thereto.

A23. The template RNA of any of embodiments A17-22, wherein the heterologous object sequence comprises a sequence of at least 8 nucleotides from the 3' end of a sequence according to CCATGGTGCACCTGACTCCTGAG (SEQ ID NO: 20956) or CCATGGTGCACCTGACTCCTGCG (SEQ ID NO: 21906).

A24. The template RNA of any of embodiments A17-23, wherein the heterologous object sequence comprises a sequence of 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, or 23 nucleotides from the 3' end of a sequence according to CCATGGTGCACCTGACTCCTGAG (SEQ ID NO: 20956) or CCATGGTGCACCTGACTCCTGCG (SEQ ID NO: 21906).

A25. The template RNA of any of embodiments A17-24, wherein the PBS sequence comprises a sequence of at least 8 nucleotides from the 5' end of a sequence according to GAGAAGTCTGCCGTTAC (SEQ ID NO: 20957), or a sequence having 1 substitution thereto.

A26. The template RNA of any of embodiments A17-25, wherein the PBS sequence comprises a sequence of at least 8 nucleotides from the 5' end of a sequence according to GAGAAGTCTGCCGTTAC (SEQ ID NO: 20957).

A27. The template RNA of any of embodiments A17-26, wherein the PBS sequence comprises a sequence of 9, 10, 11, 12, 13, 14, 15, 16, or 17 nucleotides from the 5' end of a sequence according to GAGAAGTCTGCCGTTAC (SEQ ID NO: 20957), or a sequence having 1 substitution thereto.

A28. The template RNA of any of embodiments A17-27, wherein the PBS sequence comprises a sequence of 9, 10, 11, 12, 13, 14, 15, 16, or 17 nucleotides from the 5' end of a sequence according to GAGAAGTCTGCCGTTAC (SEQ ID NO: 20957).

A29. The template RNA of any of embodiments A17-28, which does not comprise a sequence according to

GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGGACCGAGTCGGTCCGACTCCTGa GGAGAAGTCTGCC (SEQ ID NO: YYY).

A30. The template RNA of any of the preceding embodiments, wherein the mutation region comprises a single nucleotide.

A31. The template RNA of any of the preceding embodiments, wherein the mutation region is at least two nucleotides in length.

A32. The template RNA of any of the preceding embodiments, wherein the mutation region is up to 20 nucleotides in length and comprises one, two, or three sequence differences relative to the second portion of the human HBB gene.

A33. The template RNA of any of the preceding embodiments, wherein the mutation region comprises a first region designed to correct a pathogenic mutation in the HBB gene and a second region designed to inactivate a PAM sequence.

A34. The template RNA of any of the preceding embodiments, wherein the mutation region comprises a first region designed to correct a pathogenic mutation in the HBB gene and a second region designed to introduce a silent substitution.

A35. The template RNA of any of the preceding embodiments, which is configured to edit an E6V mutation in the human HBB gene.

A36. The template RNA of embodiment A35, which is configured to convert an E6V mutation to glutamine or alanine.

A37. The template RNA of any of the preceding embodiments, which comprises one or more chemically modified nucleotides.

A38. A gene modifying system comprising:
a template RNA of any of the preceding embodiments, and
a gene modifying polypeptide, or a nucleic acid encoding the gene modifying polypeptide.

A39. The gene modifying system of embodiment A38, wherein the gene modifying polypeptide comprises an RT domain having a sequence according to SEQ ID NO: 8,003, or a sequence having at least 70%, 80%, 85%, 90%, 95%, 98%, or 99% identity thereto.

A40. The gene modifying system of embodiment A38, wherein the gene modifying polypeptide comprises an RT domain having a sequence according to SEQ ID NO: 8,020, or a sequence having at least 70%, 80%, 85%, 90%, 95%, 98%, or 99% identity thereto.

A41. The gene modifying system of embodiment A38, wherein the gene modifying polypeptide comprises an RT domain having a sequence according to SEQ ID NO: 8,074, or a sequence having at least 70%, 80%, 85%, 90%, 95%, 98%, or 99% identity thereto.

A42. The gene modifying system of embodiment A38, wherein the gene modifying polypeptide comprises an RT domain having a sequence according to SEQ ID NO: 8,113, or a sequence having at least 70%, 80%, 85%, 90%, 95%, 98%, or 99% identity thereto.

A43. The gene modifying system of embodiment A38, wherein the gene modifying polypeptide comprises DNA binding domain having a sequence of a Cas9 nickase comprising an N863A mutation, e.g., a sequence according to SEQ ID NO: 11,096, or a sequence having at least 70%, 80%, 85%, 90%, 95%, 98%, or 99% identity thereto.

A44. The gene modifying system of embodiment A38, which produces a first nick in a first strand of the human HBB gene.

A45. The gene modifying system of embodiment A44, which further comprises a second strand-targeting gRNA that directs a second nick to the second strand of the human HBB gene.

A46. The gene modifying system of embodiment A45, wherein the first nick and the second nick are 80-120 nucleotides apart.

A47. The gene modifying system of embodiment A45, wherein the template RNA and the second strand-targeting gRNA are configured to produce an outward nick orientation.

A48. The gene modifying system of embodiment A45, wherein the second strand-targeting gRNA comprises a spacer sequence that is complementary to a human HBB gene having a sickle cell disease mutation, a wild-type sequence, or a Makassar variant.

A49. A method for modifying a target site in the human HBB gene in a cell, the method comprising contacting the cell with the gene modifying system of embodiment 38, thereby modifying the target site in the human HBB gene in a cell.

A50. The method of embodiment A49, wherein correction of the mutation occurs in at least 30% of target nucleic acids.

A51. A method for treating a subject having a disease or condition associated with a mutation in the human HBB gene, wherein the disease or condition is sickle cell disease (SCD), the method comprising administering to the subject the gene modifying system of embodiment 38, thereby treating the subject having a disease or condition associated with a mutation in the human HBB gene.

A52. A template RNA comprising, from 5' to 3':

(i) a gRNA spacer that is complementary to a first portion of the human HBB gene, wherein the gRNA spacer has a nucleotide sequence comprising the core nucleotides of a gRNA spacer sequence of Table 1, and optionally comprises one or more consecutive nucleotides starting with the 3' end of the flanking nucleotides of the gRNA spacer, or a nucleotide sequence having 1, 2, or 3 substitutions thereto;

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

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

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

BRIEF DESCRIPTION OF THE DRAWINGS

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

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

FIG. 2 is a pair of graphs showing rewrite levels in 293T cells (left panel) and CD34+ primary human HSCs following transfection of gene modifying systems comprising a gene modifying polypeptides various template RNAs.

FIG. 3 is a pair of graphs showing rewrite levels in 293T cells (left panel) and CD34+ primary human HSCs following transfection of gene modifying systems comprising a gene modifying polypeptides various template RNAs.

FIG. 4 is a graph showing the percent editing in primary human fibroblasts following electroporation with a gene modifying system comprising tgRNA14 with or without a second nick.

FIG. 5 is a graph showing percent editing in wild type human primary fibroblasts (to install the Makassar mutation) and sickle human primary fibroblasts (to install the wild-type sequence) following electroporation with a gene modifying system comprising tgRNA14 with or without a second nick.

FIG. 6 is a graph showing the percent rewriting achieved using the RNAV209-013 or RNAV214-040 gene modifying polypeptides with the indicated template RNAs.

FIG. 7 is a graph showing the amount of *Fah* mRNA relative to wild type when template RNAs are used with the RNAV209-013 or RNAV214-040 gene modifying polypeptides.

FIG. 8 is a graph showing the percentage of Cas9-positive hepatocytes 6 hours following dosing with LNPs containing various gene modifying polypeptides and template RNAs.

FIG. 9 is a graph showing the rewrite levels in liver samples 6 days following dosing with LNPs containing various gene modifying polypeptides and template RNAs.

FIG. 10 is a graph showing wild type *Fah* mRNA restoration compared to littermate heterozygous mice in liver samples following dosing with LNPs containing various gene modifying polypeptides and template RNAs.

FIG. 11 is a graph showing Fah protein distribution in liver samples following dosing with LNPs containing various gene modifying polypeptides and template RNAs.

FIG. 12 is a series of western blots showing Cas9-RT Expression 6 hours after infusion of Cas9-RT mRNA + TTR guide LNP. Each lane represents an individual animal where 20 µg of tissue homogenate was added per lane. Positive control was from an *in vitro* cell experiment where Cas9-RT was expressed (described previously). GAPDH was used as a loading control for each sample. n=4 per group, vehicle or treated.

FIG. 13 is a graph showing gene editing of TTR locus after treatment with Cas9-RT mRNA + TTR guide LNP. Level of indels detected at the TTR locus measured by TIDE analysis of Sanger sequencing of the TTR locus where the protospacer targets.

FIG. 14 is a graph showing that TTR Serum levels decrease after treatment with Cas9-RT mRNA + TTR guide LNP. Measurement of circulating TTR levels 5 days after mice were treated with LNPs encapsulating Cas9-RT + TTR guide RNA.

FIG. 15 is a graph showing Cas9-RT Expression after infusion of Cas9-RT mRNA + TTR guide LNP. Relative expression quantified by ProteinSimple Jess capillary electrophoresis Western blot. Numbers in the symbols are animal number in group. Vehicle n=2, Cas9-RT + TTR guide n=3.

FIG. 16 is a graph showing gene editing of TTR locus after infusion of Cas9-RT mRNA + TTR guide LNP. Level of indels detected at the TTR locus were measured by amplicon sequencing of the TTR locus where the protospacer targets. Each animal had 8 different biopsies taken across the liver where amplicon sequencing measured the percentage of reads showing an indel.

FIG. 17 is a graph showing average perfect rewrite levels in primary human HSCs following transfection with various gene modifying polypeptides and template RNAs.

FIGs. 18A and 18B are graphs showing average perfect rewrite levels in primary human HSCs following transfection with various gene modifying polypeptides and template RNAs comprising an HBB5 spacer (FIG. 18A) or an HBB8 spacer (FIG. 18B).

FIGs. 19A and 19B are a heatmap (FIG. 19A) and graph (FIG. 19B) showing average perfect rewrite levels in primary human HSCs following transfection with various gene modifying polypeptides and template RNAs comprising an HBB5 spacer (FIG. 19A) or an HBB8 spacer (FIG. 19B).

FIGs. 20A-20C are graphs showing average perfect rewrite levels in primary human HSCs following transfection with various gene modifying polypeptides and template RNAs comprising an HBB5 spacer (FIGs. 20A and 20C) or an HBB8 spacer (FIG. 20B).

FIGs. 21A and 21B are a pair of graphs showing perfect rewrite levels in primary human HSCs (FIG. 21A) and HSC subpopulation percentages (FIG. 21B) following transfection with various gene modifying polypeptides and template RNAs.

FIGs. 22A and 22B are graphs showing perfect rewrite levels in primary human HSCs subpopulations following transfection with various gene modifying polypeptides and template RNAs.

FIGs. 23A-23C are graphs showing total colony number (FIG. 23A), colony number (FIG. 23B), and percent enucleated CD235+ cells (FIG. 23C) following transfection with various gene modifying polypeptides and template RNAs.

DETAILED DESCRIPTION

Definitions

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

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

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

A "gene modifying polypeptide", as used herein, refers to a polypeptide comprising a retroviral reverse transcriptase, or a polypeptide comprising an amino acid sequence having at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% amino acid sequence identity to a retroviral reverse transcriptase, which is capable of integrating a nucleic acid sequence (e.g., a sequence provided on a template nucleic acid) into a target DNA molecule (e.g., in a mammalian host cell, such as a genomic DNA molecule in the host cell). In some embodiments, the gene modifying polypeptide is capable of integrating the sequence substantially without relying on host machinery. In some embodiments, the gene modifying polypeptide integrates a sequence into a random position in a genome, and in some embodiments, the gene modifying polypeptide integrates a sequence into a specific target site. In some embodiments, a gene modifying polypeptide includes one or more domains that, collectively, facilitate 1) binding the template nucleic acid, 2) binding the target DNA molecule, and 3) facilitate integration of the at least a

portion of the template nucleic acid into the target DNA. Gene modifying polypeptides include both naturally occurring polypeptides as well as engineered variants of the foregoing, e.g., having one or more amino acid substitutions to the naturally occurring sequence. Gene modifying polypeptides also include heterologous constructs, e.g., where one or more of the domains recited above are heterologous to each other, whether through a heterologous fusion (or other conjugate) of otherwise wild-type domains, as well as fusions of modified domains, e.g., by way of replacement or fusion of a heterologous sub-domain or other substituted domain. Exemplary gene modifying polypeptides, and systems comprising them and methods of using them, that can be used in the methods provided herein are described, e.g., in PCT/US2021/020948, which is incorporated herein by reference with respect to gene modifying polypeptides that comprise a retroviral reverse transcriptase domain. In some embodiments, a gene modifying polypeptide integrates a sequence into a gene. In some embodiments, a gene modifying polypeptide integrates a sequence into a sequence outside of a gene. A "gene modifying system," as used herein, refers to a system comprising a gene modifying polypeptide and a template nucleic acid.

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

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

As used herein, "first strand" and "second strand", as used to describe the individual DNA strands of target DNA, distinguish the two DNA strands based upon which strand the reverse transcriptase domain initiates polymerization, e.g., based upon where target primed

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

The term "heterologous," as used herein to describe a first element in reference to a second element means that the first element and second element do not exist in nature disposed as described. For example, a heterologous polypeptide, nucleic acid molecule, construct or sequence refers to (a) a polypeptide, nucleic acid molecule or portion of a polypeptide or nucleic acid molecule sequence that is not native to a cell in which it is expressed, (b) a polypeptide or nucleic acid molecule or portion of a polypeptide or nucleic acid molecule that has been altered or mutated relative to its native state, or (c) a polypeptide or nucleic acid molecule with an altered expression as compared to the native expression levels under similar conditions. For example, a heterologous regulatory sequence (e.g., promoter, enhancer) may be used to regulate expression of a gene or a nucleic acid molecule in a way that is different than the gene or a nucleic acid molecule is normally expressed in nature. In another example, a heterologous domain of a polypeptide or nucleic acid sequence (e.g., a DNA binding domain of a polypeptide or nucleic acid encoding a DNA binding domain of a polypeptide) may be disposed relative to other domains or may be a different sequence or from a different source, relative to other domains or portions of a polypeptide or its encoding nucleic acid. In certain embodiments, a heterologous nucleic acid molecule may exist in a native host cell genome, but may have an altered expression level or have a different sequence or both. In other embodiments, heterologous nucleic acid molecules may not be endogenous to a host cell or host genome but instead may have been introduced into a host cell by transformation (e.g., transfection, electroporation), wherein the added molecule may integrate into the host genome or can exist as extra-chromosomal genetic material either transiently (e.g., mRNA) or semi-stably for more than one generation (e.g., episomal viral vector, plasmid or other self-replicating vector).

As used herein, "insertion" of a sequence into a target site refers to the net addition of DNA sequence at the target site, e.g., where there are new nucleotides in the heterologous object sequence with no cognate positions in the unedited target site. In some embodiments, a

nucleotide alignment of the PBS sequence and heterologous object sequence to the target nucleic acid sequence would result in an alignment gap in the target nucleic acid sequence.

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

The term "inverted terminal repeats" or "ITRs" as used herein refers to AAV viral cis-elements named so because of their symmetry. These elements promote efficient multiplication of an AAV genome. It is hypothesized that the minimal elements for ITR function are a Rep-binding site (RBS; 5′-GCGCGCTCGCTCGCTC-3′ for AAV2; SEQ ID NO: 4601) and a terminal resolution site (TRS; 5′-AGTTGG-3′ for AAV2; SEQ ID NO: 4602) plus a variable palindromic sequence allowing for hairpin formation. According to the present invention, an ITR comprises at least these three elements (RBS, TRS, and sequences allowing the formation of an hairpin). In addition, in the present invention, the term "ITR" refers to ITRs of known natural AAV serotypes (e.g. ITR of a serotype 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or 11 AAV), to chimeric ITRs formed by the fusion of ITR elements derived from different serotypes, and to functional variants thereof. "Functional variant" refers to a sequence presenting a sequence identity of at least 80%, 85%, 90%, preferably of at least 95% with a known ITR and allowing multiplication of the sequence that includes said ITR in the presence of Rep proteins.

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

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

"Nucleic acid molecule" refers to both RNA and DNA molecules including, without limitation, complementary DNA ("cDNA"), genomic DNA ("gDNA"), and messenger RNA ("mRNA"), and also includes synthetic nucleic acid molecules, such as those that are chemically synthesized or recombinantly produced, such as RNA templates, as described herein. The nucleic acid molecule can be double-stranded or single-stranded, circular, or linear. If single-stranded, the nucleic acid molecule can be the sense strand or the antisense strand. Unless otherwise indicated, and as an example for all sequences described herein under the general format "SEQ ID NO:," or "nucleic acid comprising SEQ ID NO:1" refers to a nucleic acid, at least a portion which has either (i) the sequence of SEQ ID NO:1, or (ii) a sequence complimentary to SEQ ID NO:1. The choice between the two is dictated by the context in which SEQ ID NO:1 is used. For instance, if the nucleic acid is used as a probe, the choice between the two is dictated by the requirement that the probe be complementary to the desired target. Nucleic acid sequences of the present disclosure may be modified chemically or biochemically or may contain non-natural or derivatized nucleotide bases, as will be readily appreciated by those of skill in the art. Such modifications include, for example, labels, methylation, substitution of one or more naturally occurring nucleotides with an analog, inter-nucleotide modifications such as uncharged linkages (for example, methyl phosphonates, phosphotriesters, phosphoramidates, carbamates, etc.), charged linkages (for example, phosphorothioates, phosphorodithioates, etc.), pendant moieties, (for example, polypeptides), intercalators (for example, acridine, psoralen, etc.), chelators, alkylators, and modified linkages (for example, alpha anomeric nucleic acids, etc.). Also included are chemically modified bases (see, for example, Table 13), backbones (see, for example, Table 14), and modified caps (see, for example, Table 15). Also included are synthetic molecules that mimic polynucleotides in their ability to bind to a designated sequence via hydrogen bonding and other chemical interactions. Such molecules are known in the art and include, for example, those in which peptide linkages substitute for phosphate linkages in the backbone of a molecule, e.g., peptide nucleic acids (PNAs). Other modifications can include, for example, analogs in which the ribose ring contains a bridging moiety or other structure such as modifications found in "locked" nucleic acids (LNAs). In various embodiments, the nucleic acids are in operative association with additional genetic elements, such as tissue-specific expression-control sequence(s) (e.g., tissue-specific promoters and tissue-specific microRNA recognition sequences), as well as additional elements,

such as inverted repeats (e.g., inverted terminal repeats, such as elements from or derived from viruses, e.g., AAV ITRs) and tandem repeats, inverted repeats/direct repeats, homology regions (segments with various degrees of homology to a target DNA), untranslated regions (UTRs) (5′, 3′, or both 5′ and 3′ UTRs), and various combinations of the foregoing. The nucleic acid elements of the systems provided by the invention can be provided in a variety of topologies, including single-stranded, double-stranded, circular, linear, linear with open ends, linear with closed ends, and particular versions of these, such as doggybone DNA (dbDNA), closed-ended DNA (ceDNA).

As used herein, a "gene expression unit" is a nucleic acid sequence comprising at least one regulatory nucleic acid sequence operably linked to at least one effector sequence. A first nucleic acid sequence is operably linked with a second nucleic acid sequence when the first nucleic acid sequence is placed in a functional relationship with the second nucleic acid sequence. For instance, a promoter or enhancer is operably linked to a coding sequence if the promoter or enhancer affects the transcription or expression of the coding sequence. Operably linked DNA sequences may be contiguous or non-contiguous. Where necessary to join two protein-coding regions, operably linked sequences may be in the same reading frame.

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

As used herein, "operative association" describes a functional relationship between two nucleic acid sequences, such as a 1) promoter and 2) a heterologous object sequence, and means,

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

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

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

As used herein, a "tissue-specific expression-control sequence" means nucleic acid elements that increase or decrease the level of a transcript comprising the heterologous object sequence in a target tissue in a tissue-specific manner, e.g., preferentially in on-target tissue(s), relative to off-target tissue(s). In some embodiments, a tissue-specific expression-control sequence preferentially drives or represses transcription, activity, or the half-life of a transcript

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

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Introduction

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

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

The disclosure provides, in part, methods for treating SCD using a gene modifying system comprising a gene modifying polypeptide component and a template nucleic acid (e.g.,

template RNA) component. In some embodiments, a gene modifying system can be used to introduce an alteration into a target site in a genome. In some embodiments, the gene modifying polypeptide component comprises a writing domain (e.g., a reverse transcriptase domain), a DNA-binding domain, and an endonuclease domain (e.g., nickase domain). In some embodiments, the template nucleic acid (e.g., template RNA) comprises a sequence (e.g., a gRNA spacer) that binds a target site in the genome (e.g., that binds to a second strand of the target site), a sequence (e.g., a gRNA scaffold) that binds the gene modifying polypeptide component, a heterologous object sequence, and a PBS sequence. Without wishing to be bound by theory, it is thought that the template nucleic acid (e.g., template RNA) binds to the second strand of a target site in the genome, and binds to the gene modifying polypeptide component (e.g., localizing the polypeptide component to the target site in the genome). It is thought that the endonuclease (e.g., nickase) of the gene modifying polypeptide component cuts the target site (e.g., the first strand of the target site), e.g., allowing the PBS sequence to bind to a sequence adjacent to the site to be altered on the first strand of the target site. It is thought that the writing domain (e.g., reverse transcriptase domain) of the polypeptide component uses the first strand of the target site that is bound to the complementary sequence comprising the PBS sequence of the template nucleic acid as a primer and the heterologous object sequence of the template nucleic acid as a template to, e.g., polymerize a sequence complementary to the heterologous object sequence. Without wishing to be bound by theory, it is thought that selection of an appropriate heterologous object sequence can result in substitution, deletion, and/or insertion of one or more nucleotides at the target site.

Gene modifying systems

In some embodiments, a gene modifying system described herein comprises: (A) a gene modifying polypeptide or a nucleic acid encoding the gene modifying polypeptide, wherein the gene modifying polypeptide comprises (i) a reverse transcriptase domain, and either (x) an endonuclease domain that contains DNA binding functionality or (y) an endonuclease domain and separate DNA binding domain; and (B) a template RNA. A gene modifying polypeptide, in some embodiments, acts as a substantially autonomous protein machine capable of integrating a template nucleic acid sequence into a target DNA molecule (e.g., in a mammalian host cell, such as a genomic DNA molecule in the host cell), substantially without relying on host machinery. For example, the gene modifying protein may comprise a DNA-binding domain, a reverse

transcriptase domain, and an endonuclease domain. In some embodiments, the DNA-binding function may involve an RNA component that directs the protein to a DNA sequence, e.g., a gRNA spacer. In other embodiments, the gene modifying polypeptide may comprise a reverse transcriptase domain and an endonuclease domain. The RNA template element of a gene modifying system is typically heterologous to the gene modifying polypeptide element and provides an object sequence to be inserted (reverse transcribed) into the host genome. In some embodiments, the gene modifying polypeptide is capable of target primed reverse transcription. In some embodiments, the gene modifying polypeptide is capable of second-strand synthesis.

In some embodiments the gene modifying system is combined with a second polypeptide. In some embodiments, the second polypeptide may comprise an endonuclease domain. In some embodiments, the second polypeptide may comprise a polymerase domain, e.g., a reverse transcriptase domain. In some embodiments, the second polypeptide may comprise a DNA-dependent DNA polymerase domain. In some embodiments, the second polypeptide aids in completion of the genome edit, e.g., by contributing to second-strand synthesis or DNA repair resolution.

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

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

heterologous to the endonuclease domain; or the RT domain is heterologous to the endonuclease domain.

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

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

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

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

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

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

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

In some embodiments, a gene modifying polypeptide as described herein comprises a reverse transcriptase or RT domain (e.g., as described herein) that comprises a MoMLV RT sequence or variant thereof. In embodiments, the MoMLV RT sequence comprises one or more mutations selected from D200N, L603W, T330P, T306K, W313F, D524G, E562Q, D583N,

P51L, S67R, E67K, T197A, H204R, E302K, F309N, L435G, N454K, H594Q, D653N, R110S, and K103L. In embodiments, the MoMLV RT sequence comprises a combination of mutations, such as D200N, L603W, and T330P, optionally further including T306K and/or W313F.

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

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

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

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

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

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

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

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

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

In some embodiments, an insertion, deletion, substitution, or combination thereof, increases or decreases expression (e.g. transcription or translation) of a gene. In some embodiments, an insertion, deletion, substitution, or combination thereof, increases or decreases expression (e.g. transcription or translation) of a gene by altering, adding, or deleting sequences in a promoter or enhancer, e.g. sequences that bind transcription factors. In some embodiments, an insertion, deletion, substitution, or combination thereof alters translation of a gene (e.g. alters an amino acid sequence), inserts or deletes a start or stop codon, alters or fixes the translation frame of a gene. In some embodiments, an insertion, deletion, substitution, or combination

thereof alters splicing of a gene, e.g. by inserting, deleting, or altering a splice acceptor or donor site. In some embodiments, an insertion, deletion, substitution, or combination thereof alters transcript or protein half-life. In some embodiments, an insertion, deletion, substitution, or combination thereof alters protein localization in the cell (e.g. from the cytoplasm to a mitochondria, from the cytoplasm into the extracellular space (e.g. adds a secretion tag)). In some embodiments, an insertion, deletion, substitution, or combination thereof alters (e.g. improves) protein folding (e.g. to prevent accumulation of misfolded proteins). In some embodiments, an insertion, deletion, substitution, or combination thereof, alters, increases, decreases the activity of a gene, e.g. a protein encoded by the gene.

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

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

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

sequence consensus, e.g. using approaches described in Ivics et al., Cell 1997, 501 – 510 ; Wagstaff et al., Molecular Biology and Evolution 2013, 88-99.

Polypeptide components of gene modifying systems

In some embodiments, the gene modifying polypeptide possesses the functions of DNA target site binding, template nucleic acid (e.g., RNA) binding, DNA target site cleavage, and template nucleic acid (e.g., RNA) writing, e.g., reverse transcription. In some embodiments, each functions is contained within a distinct domain. In some embodiments, a function may be attributed to two or more domains (e.g., two or more domains, together, exhibit the functionality). In some embodiments, two or more domains may have the same or similar function (e.g., two or more domains each independently have DNA-binding functionality, e.g., for two different DNA sequences). In other embodiments, one or more domains may be capable of enabling one or more functions, e.g., a Cas9 domain enabling both DNA binding and target site cleavage. In some embodiments, the domains are all located within a single polypeptide. In some embodiments, a first domain is in one polypeptide and a second domain is in a second polypeptide. For example, in some embodiments, the sequences may be split between a first polypeptide and a second polypeptide, e.g., wherein the first polypeptide comprises a reverse transcriptase (RT) domain and wherein the second polypeptide comprises a DNA-binding domain and an endonuclease domain, e.g., a nickase domain. As a further example, in some embodiments, the first polypeptide and the second polypeptide each comprise a DNA binding domain (e.g., a first DNA binding domain and a second DNA binding domain). In some embodiments, the first and second polypeptide may be brought together post-translationally via a split-intein to form a single gene modifying polypeptide.

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

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

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

Exemplary N-terminal NLS-Cas9 domain

MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLF
DSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHP
IFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDV
DKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALS
LGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVN
TEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFY
KFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR
EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKN
LPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLK
EDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDR
EMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNF
MQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPE
NIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRD
MYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ
LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKL
IREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDY
KVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKG
RDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAY
SVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFE

LENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEI
IEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR
KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGG (SEQ ID NO: 4000)

Exemplary C-terminal sequence comprising an NLS

AGKRTADGSEFEKRTADGSEFESPKKKAKVE (SEQ ID NO: 4001)

Writing domain (RT Domain)

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

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

In some embodiments, the retroviral reverse transcriptase (RT) domain exhibits enhanced stringency of target-primed reverse transcription (TPRT) initiation, e.g., relative to an endogenous RT domain. In some embodiments, the RT domain initiates TPRT when the 3 nt in the target site immediately upstream of the first strand nick, e.g., the genomic DNA priming the RNA template, have at least 66% or 100% complementarity to the 3 nt of homology in the RNA template. In some embodiments, the RT domain initiates TPRT when there are less than 5 nt mismatched (e.g., less than 1, 2, 3, 4, or 5 nt mismatched) between the template RNA homology and the target DNA priming reverse transcription. In some embodiments, the RT domain is modified such that the stringency for mismatches in priming the TPRT reaction is increased, e.g., wherein the RT domain does not tolerate any mismatches or tolerates fewer mismatches in the priming region relative to a wild-type (e.g., unmodified) RT domain. In some embodiments, the

RT domain comprises a HIV-1 RT domain. In embodiments, the HIV-1 RT domain initiates lower levels of synthesis even with three nucleotide mismatches relative to an alternative RT domain (e.g., as described by Jamburuthugoda and Eickbush J Mol Biol 407(5):661-672 (2011); incorporated herein by reference in its entirety). In some embodiments, the RT domain forms a dimer (e.g., a heterodimer or homodimer). In some embodiments, the RT domain is monomeric. In some embodiments, an RT domain, naturally functions as a monomer or as a dimer (e.g., heterodimer or homodimer). In some embodiments, an RT domain naturally functions as a monomer, e.g., is derived from a virus wherein it functions as a monomer. In embodiments, the RT domain is selected from an RT domain from murine leukemia virus (MLV; sometimes referred to as MoMLV) (e.g., P03355), porcine endogenous retrovirus (PERV) (e.g., UniProt Q4VFZ2), mouse mammary tumor virus (MMTV) (e.g., UniProt P03365), Avian reticuloendotheliosis virus (AVIRE) (e.g., UniProtKB accession: P03360); Feline leukemia virus (FLV or FeLV) (e.g., e.g., UniProtKB accession: P10273); Mason-Pfizer monkey virus (MPMV) (e.g., UniProt P07572), bovine leukemia virus (BLV) (e.g., UniProt P03361), human T-cell leukemia virus-1 (HTLV-1) (e.g., UniProt P03362), human foamy virus (HFV) (e.g., UniProt P14350), simian foamy virus (SFV) (e.g., SFV3L) (e.g., UniProt P23074 or P27401), or bovine foamy/syncytial virus (BFV/BSV) (e.g., UniProt O41894), or a functional fragment or variant thereof (e.g., an amino acid sequence having at least 70%, 80%, 90%, 95%, or 99% identity thereto). In some embodiments, an RT domain is dimeric in its natural functioning. In some embodiments, the RT domain is derived from a virus wherein it functions as a dimer. In embodiments, the RT domain is selected from an RT domain from avian sarcoma/leukemia virus (ASLV) (e.g., UniProt A0A142BKH1), Rous sarcoma virus (RSV) (e.g., UniProt P03354), avian myeloblastosis virus (AMV) (e.g., UniProt Q83133), human immunodeficiency virus type I (HIV-1) (e.g., UniProt P03369), human immunodeficiency virus type II (HIV-2) (e.g., UniProt P15833), simian immunodeficiency virus (SIV) (e.g., UniProt P05896), bovine immunodeficiency virus (BIV) (e.g., UniProt P19560), equine infectious anemia virus (EIAV) (e.g., UniProt P03371), or feline immunodeficiency virus (FIV) (e.g., UniProt P16088) (Herschhorn and Hizi *Cell Mol Life Sci* 67(16):2717-2747 (2010)), or a functional fragment or variant thereof (e.g., an amino acid sequence having at least 70%, 80%, 90%, 95%, or 99% identity thereto). Naturally heterodimeric RT domains may, in some embodiments, also be functional as homodimers. In some embodiments, dimeric RT domains are expressed as fusion

proteins, e.g., as homodimeric fusion proteins or heterodimeric fusion proteins. In some embodiments, the RT function of the system is fulfilled by multiple RT domains (e.g., as described herein). In further embodiments, the multiple RT domains are fused or separate, e.g., may be on the same polypeptide or on different polypeptides.

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

In some embodiments, an RT domain is mutated to increase fidelity compared to an otherwise similar domain without the mutation. For instance, in some embodiments, a YADD or YMDD motif in an RT domain (e.g., in a reverse transcriptase) is replaced with YVDD. In embodiments, replacement of the YADD or YMDD or YVDD results in higher fidelity in

retroviral reverse transcriptase activity (e.g., as described in Jamburuthugoda and Eickbush J Mol Biol 2011; incorporated herein by reference in its entirety).

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

Table 6: Exemplary reverse transcriptase domains from retroviruses

RT Name	SEQ ID NO:	RT amino acid sequence
AVIRE_P03360	8,001	TAPLEEEYRLFLEAPIQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPV RKSGTSEYRMVQDLREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEEGESGQLTWTRLPQGFKNSPTLFD EALNRDLQGFRLDHPSVSLLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAILQIPVPKTKRQV REFLGTIGYCRLWIPGFAELAQPLYAATRGGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSK RLDPVAAGWPRCLRAIAAAALLTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLD TLDSLTSTRPDLTDQPLAQAEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIY RERGLLTAGGKAIKNAPEILALLTAVWLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATIS
AVIRE_P03360_3mut	8,002	TAPLEEEYRLFLEAPIQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPV RKSGTSEYRMVQDLREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEEGESGQLTWTRLPQGFKNSPTLFN EALNRDLQGFRLDHPSVSLLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAILQIPVPKTKRQV REFLGTIGYCRLWIPGFAELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSK RLDPVAAGWPRCLRAIAAAALLTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLD TLDSLTSTRPDLTDQPLAQAEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIY RERGWLTAGGKAIKNAPEILALLTAVWLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATIS
AVIRE_P03360_3mutA	8,003	TAPLEEEYRLFLEAPIQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPV RKSGTSEYRMVQDLREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEEGESGQLTWTRLPQGFKNSPTLFN EALNRDLQGFRLDHPSVSLLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAILQIPVPKTKRQV REFLGKIGYCRLFIPGFAELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSKR LDPVAAGWPRCLRAIAAAALLTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDT LDSLTSTRPDLTDQPLAQAEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIY RERGWLTAGGKAIKNAPEILALLTAVWLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATIS
BAEVM_P10272	8,004	TVSLQDEHRLFDIPVTTSLPDVWLQDFPQAWAETGGLGRAKCQAPIIIDLKPTAVPVSIKQYPMSLEAHMGIRQHIIKFLELGVLRPCRSPWNTPLLPVK KPGTQDYRPVQDLREINKRTVDIHPTVPNPYNLLSTLKPDYSWYTVLDLKDAFFCLPLAPQSQELFAFEWKDPERGISGQLTWTRLPQGFKNSPTLFD EALHRDLTDFRTQHPEVTLLQYVDDLLLAAPTKKACTQGTRHLLQELGEKGYRASAKKAQICQTKVTYLGYILSEGKRWLTPGRIETVARIPPPRNPRE VREFLGTAGFCRLWIPGFAELAAPLYALTKESTPFTWQTEHQLAFEALKKALLSAPALGLPDTSKPFTLFLDERQGIAKGVLTQKLGPWKRPVAYLSKK LDPVAAGWPPCLRIMAATAMLVKDSAKLTLGQPLTVITPHTLEAIVRQPPDRWITNARLTHYQALLLDTDRVQFGPPVTLNPATLLPVPENQPSPHDCR QVLAETHGTREDLKDQELPDADHTWYTDGSSYLDSGTRRAGAAVVDGHNTIWAQSLPPGTSAQKAELIALTKALELSKGKKANIYTDSRYAFATAHTH GSIYERRGLLTSEGKEIKNKAEIIALLKALFLPQEVAIIHCPGHQKGQDPVAVGNRQADRVARQAAMAEVLTLATEPDNTSHIT
BAEVM_P10272_3mut	8,005	TVSLQDEHRLFDIPVTTSLPDVWLQDFPQAWAETGGLGRAKCQAPIIIDLKPTAVPVSIKQYPMSLEAHMGIRQHIIKFLELGVLRPCRSPWNTPLLPVK KPGTQDYRPVQDLREINKRTVDIHPTVPNPYNLLSTLKPDYSWYTVLDLKDAFFCLPLAPQSQELFAFEWKDPERGISGQLTWTRLPQGFKNSPTLFN EALHRDLTDFRTQHPEVTLLQYVDDLLLAAPTKKACTQGTRHLLQELGEKGYRASAKKAQICQTKVTYLGYILSEGKRWLTPGRIETVARIPPPRNPRE VREFLGTAGFCRLWIPGFAELAAPLYALTKPSTPFTWQTEHQLAFEALKKALLSAPALGLPDTSKPFTLFLDERQGIAKGVLTQKLGPWKRPVAYLSKK LDPVAAGWPPCLRIMAATAMLVKDSAKLTLGQPLTVITPHTLEAIVRQPPDRWITNARLTHYQALLLDTDRVQFGPPVTLNPATLLPVPENQPSPHDCR QVLAETHGTREDLKDQELPDADHTWYTDGSSYLDSGTRRAGAAVVDGHNTIWAQSLPPGTSAQKAELIALTKALELSKGKKANIYTDSRYAFATAHTH GSIYERRGWLTSEGKEIKNKAEIIALLKALFLPQEVAIIHCPGHQKGQDPVAVGNRQADRVARQAAMAEVLTLATEPDNTSHIT
BAEVM_P10272_3mutA	8,006	TVSLQDEHRLFDIPVTTSLPDVWLQDFPQAWAETGGLGRAKCQAPIIIDLKPTAVPVSIKQYPMSLEAHMGIRQHIIKFLELGVLRPCRSPWNTPLLPVK KPGTQDYRPVQDLREINKRTVDIHPTVPNPYNLLSTLKPDYSWYTVLDLKDAFFCLPLAPQSQELFAFEWKDPERGISGQLTWTRLPQGFKNSPTLFN EALHRDLTDFRTQHPEVTLLQYVDDLLLAAPTKKACTQGTRHLLQELGEKGYRASAKKAQICQTKVTYLGYILSEGKRWLTPGRIETVARIPPPRNPRE VREFLGKAGFCRLFIPGFAELAAPLYALTKPSTPFTWQTEHQLAFEALKKALLSAPALGLPDTSKPFTLFLDERQGIAKGVLTQKLGPWKRPVAYLSKKL DPVAAGWPPCLRIMAATAMLVKDSAKLTLGQPLTVITPHTLEAIVRQPPDRWITNARLTHYQALLLDTDRVQFGPPVTLNPATLLPVPENQPSPHDCRQ VLAETHGTREDLKDQELPDADHTWYTDGSSYLDSGTRRAGAAVVDGHNTIWAQSLPPGTSAQKAELIALTKALELSKGKKANIYTDSRYAFATAHTHG SIYERRGWLTSEGKEIKNKAEIIALLKALFLPQEVAIIHCPGHQKGQDPVAVGNRQADRVARQAAMAEVLTLATEPDNTSHIT
BLVAU_P25059	8,007	GVLDAPPSHIGLEHLPPPPEVPQFPLNLERLQALQDLVHRSLEAGYISPWDGPGNNPVFPVRKPNGAWRFVHDLRVTNALTKPIPALSPGPPDLTAIPT HLPHIICLDLKDAFFQIPVEDRFRSYFAFTLPTPGGLQPHRRFAWRVLPQGFINSPALFERALQEPLRQVSAAFSQSLLVSYMDDILYVSPTEEQRLQCY QTMAAHLRDLGFQVASEKTRQTPSPVPFLGQMVHERMVTYQSLPTLQISSPISLHQLQTVLGDLQWVSRGTPTTRRPLQLLYSSLKGIDDPRAIIHLSP EQQQGIAELRQALSHNARSRYNEQEPLLAYVHLTRAGSTLVLFQKGAQFPLAYFQTPLTDNQASPWGLLLLLGCQYLQAQALSSYAKTILKYYHNLPK TSLDNWIQSSEDPRVQELLQLWPQISSQGIQPPGPWKTLVTRAEVFLTPQFSPEPIPAALCLFSDGAARRGAYCLWKDHLLDFQAVPAPESAQKGELA GLLAGLAAAPPEPLNIWVDSKYLYSLLRTLVLGAWLQPDPVPSYALLYKSLLRHPAIFVGHVRSHSSASHPIASLNNYVDQL

RT Name	SEQ ID NO:	RT amino acid sequence
BLVAU_P25059_2mut	8,008	GVLDAPPSHIGLEHLPPPPEVPQFPLNLERLQALQDLVHRSLEAGYISPWDGPGNNPVFPVRKPNGAWRFVHDLRVTNALTKPIPALSPGPPDLTAIPT HLPHIICLDLKDAFFQIPVEDRFRSYFAFTLPTPGGLQPHRRFAWRVLPQGFINSPALFQRALQEPLRQVSAAFSQSLLVSYMDDILYVSPTEEQRLQCY QTMAAHLRDLGFQVASEKTRQTPSPVPFLGQMVHERMVTYQSLPTLQISSPISLHQLQTVLGDLQWVSRGTPTTRRPLQLLYSSLKPIDDPRAIIHLSP EQQQGIAELRQALSHNARSRYNEQEPLLAYVHLTRAGSTLVLFQKGAQFPLAYFQTPLTDNQASPWGLLLLLGCQYLQAQALSSYAKTILKYYHNLPK TSLDNWIQSSEDPRVQELLQLWPQISSQGIQPPGPWKTLVTRAEVFLTPQFSPEPIPAALCLFSDGAARRGAYCLWKDHLLDFQAVPAPESAQKGELA GLLAGLAAAPPEPLNIWVDSKYLYSLLRTLVLGAWLQPDPVPSYALLYKSLLRHPAIFVGHVRSHSSASHPIASLNNYVDQL
BLVJ_P03361	8,009	GVLDTPPSHIGLEHLPPPPEVPQFPLNLERLQALQDLVHRSLEAGYISPWDGPGNNPVFPVRKPNGAWRFVHDLRATNALTKPIPALSPGPPDLTAIPT HPPHIICLDLKDAFFQIPVEDRFRFYLSFTLPSPGGLQPHRRFAWRVLPQGFINSPALFERALQEPLRQVSAAFSQSLLVSYMDDILYASPTEEQRSQCY QALAARLRDLGFQVASEKTSQTPSPVPFLGQMVHEQIVTYQSLPTLQISSPISLHQLQAVLGDLQWVSRGTPTTRRPLQLLYSSLKRHHDPRAIIQLSPE QLQGIAELRQALSHNARSRYNEQEPLLAYVHLTRAGSTLVLFQKGAQFPLAYFQTPLTDNQASPWGLLLLLGCQYLQTQALSSYAKPILKYYHNLPKTS LDNWIQSSEDPRVQELLQLWPQISSQGIQPPGPWKTLITRAEVFLTPQFSPDPIPAALCLFSDGATGRGAYCLWKDHLLDFQAVPAPESAQKGELAGL LAGLAAAPPEPVNIWVDSKYLYSLLRTLVLGAWLQPDPVPSYALLYKSLLRHPAIVVGHVRSHSSASHPIASLNNYVDQL
BLVJ_P03361_2mut	8,010	GVLDTPPSHIGLEHLPPPPEVPQFPLNLERLQALQDLVHRSLEAGYISPWDGPGNNPVFPVRKPNGAWRFVHDLRATNALTKPIPALSPGPPDLTAIPT HPPHIICLDLKDAFFQIPVEDRFRFYLSFTLPSPGGLQPHRRFAWRVLPQGFINSPALFNRALQEPLRQVSAAFSQSLLVSYMDDILYASPTEEQRSQCY QALAARLRDLGFQVASEKTSQTPSPVPFLGQMVHEQIVTYQSLPTLQISSPISLHQLQAVLGDLQWVSRGTPTTRRPLQLLYSSLKRHHDPRAIIQLSPE QLQGIAELRQALSHNARSRYNEQEPLLAYVHLTRAGSTLVLFQKGAQFPLAYFQTPLTDNQASPWGLLLLLGCQYLQTQALSSYAKPILKYYHNLPKTS LDNWIQSSEDPRVQELLQLWPQISSQGIQPPGPWKTLITRAEVFLTPQFSPDPIPAALCLFSDGATGRGAYCLWKDHLLDFQAVPAPESAQKGELAGL LAGLAAAPPEPVNIWVDSKYLYSLLRTWVLGAWLQPDPVPSYALLYKSLLRHPAIVVGHVRSHSSASHPIASLNNYVDQL
BLVJ_P03361_2mutB	8,011	GVLDTPPSHIGLEHLPPPPEVPQFPLNLERLQALQDLVHRSLEAGYISPWDGPGNNPVFPVRKPNGAWRFVHDLRATNALTKPIPALSPGPPDLTAPP THPPHIICLDLKDAFFQIPVEDRFRFYLSFTLPSPGGLQPHRRFAWRVLPQGFINSPALFQRALQEPLRQVSAAFSQSLLVSYMDDILYASPTEEQRSQC YQALAARLRDLGFQVASEKTSQTPSPVPFLGQMVHEQIVTYQSLPTLQISSPISLHQLQAVLGDLQWVSRGTPTTRRPLQLLYSSLKRHHDPRAIIQLSP EQLQGIAELRQALSHNARSRYNEQEPLLAYVHLTRAGSTLVLFQKGAQFPLAYFQTPLTDNQASPWGLLLLLGCQYLQTQALSSYAKPILKYYHNLPKT SLDNWIQSSEDPRVQELLQLWPQISSQGIQPPGPWKTLITRAEVFLTPQFSPDPIPAALCLFSDGATGRGAYCLWKDHLLDFQAVPAPESAQKGELAG LLAGLAAAPPEPVNIWVDSKYLYSLLRTWVLGAWLQPDPVPSYALLYKSLLRHPAIVVGHVRSHSSASHPIASLNNYVDQL
FFV_O93209	8,012	MDLLKPLTVERKGVKIKGYWNSQADITCVPKDLLQGEEPVRQQNVTTIHGTQEGDVYYVNLKIDGRRINTEVIGTTLDYAIITPGDVPWILKKPLELTIKLD LEEQQGTLLNNSILSKKGKEELKQLFEKYSALWQSWENQVGHRRIRPHKIATGTVKPTPQKQYHINPKAKPDIQIVINDLLKQGVLIQKESTMNTPVYPV PKPNGRWRMVLDYRAVNKVTPLIAVQNQHSYGILGSLFKGRYKTTIDLSNGFWAHPIVPEDYWITAFTWQGKQYCWTVLPQGFLNSPGLFTGDVVDL LQGIPNVEVYVDDVYISHDSEKEHLEYLDILFNRLKEAGYIISLKKSNIANSIVDFLGFQITNEGRGLTDTFKEKLENITAPTTLKQLQSILGLLNFARNFIPD FTELIAPLYALIPKSTKNYVPWQIEHSTTLETLITKLNGAEYLQGRKGDKTLIMKVNASYTTGYIRYYNEGEKKPISYVSIVFSKTELKFTELEKLLTTVHKG LLKALDLSMGQNIHVYSPIVSMQNIQKTPQTAKKALASRWLSWLSYLEDPRIRFFYDPQMPALKDLPAVDTGKDNKKHPSNFQHIFYTDGSAITSPTKE GHLNAGMGIVYFINKDGNLQKQQEWSISLGNHTAQFAEIAAFEFALKKCLPLGGNILVVTDSNYVAKAYNEELDVWASNGFVNNRKKPLKHISKWKSV ADLKRLRPDVVVTHEPGHQKLDSSPHAYGNNLADQLATQASFKVH
FFV_O93209_2mut	8,013	MDLLKPLTVERKGVKIKGYWNSQADITCVPKDLLQGEEPVRQQNVTTIHGTQEGDVYYVNLKIDGRRINTEVIGTTLDYAIITPGDVPWILKKPLELTIKLD LEEQQGTLLNNSILSKKGKEELKQLFEKYSALWQSWENQVGHRRIRPHKIATGTVKPTPQKQYHINPKAKPDIQIVINDLLKQGVLIQKESTMNTPVYPV PKPNGRWRMVLDYRAVNKVTPLIAVQNQHSYGILGSLFKGRYKTTIDLSNGFWAHPIVPEDYWITAFTWQGKQYCWTVLPQGFLNSPGLFNGDVVDL LQGIPNVEVYVDDVYISHDSEKEHLEYLDILFNRLKEAGYIISLKKSNIANSIVDFLGFQITNEGRGLTDTFKEKLENITAPTTLKQLQSILGLLNFARNFIPD FTELIAPLYALIPKSPKNYVPWQIEHSTTLETLITKLNGAEYLQGRKGDKTLIMKVNASYTTGYIRYYNEGEKKPISYVSIVFSKTELKFTELEKLLTTVHKG LLKALDLSMGQNIHVYSPIVSMQNIQKTPQTAKKALASRWLSWLSYLEDPRIRFFYDPQMPALKDLPAVDTGKDNKKHPSNFQHIFYTDGSAITSPTKE GHLNAGMGIVYFINKDGNLQKQQEWSISLGNHTAQFAEIAAFEFALKKCLPLGGNILVVTDSNYVAKAYNEELDVWASNGFVNNRKKPLKHISKWKSV ADLKRLRPDVVVTHEPGHQKLDSSPHAYGNNLADQLATQASFKVH
FFV_O93209_2mutA	8,014	MDLLKPLTVERKGVKIKGYWNSQADITCVPKDLLQGEEPVRQQNVTTIHGTQEGDVYYVNLKIDGRRINTEVIGTTLDYAIITPGDVPWILKKPLELTIKLD LEEQQGTLLNNSILSKKGKEELKQLFEKYSALWQSWENQVGHRRIRPHKIATGTVKPTPQKQYHINPKAKPDIQIVINDLLKQGVLIQKESTMNTPVYPV PKPNGRWRMVLDYRAVNKVTPLIAVQNQHSYGILGSLFKGRYKTTIDLSNGFWAHPIVPEDYWITAFTWQGKQYCWTVLPQGFLNSPGLFNGDVVDL LQGIPNVEVYVDDVYISHDSEKEHLEYLDILFNRLKEAGYIISLKKSNIANSIVDFLGFQITNEGRGLTDTFKEKLENITAPTTLKQLQSILGKLNFARNFIPD FTELIAPLYALIPKSPKNYVPWQIEHSTTLETLITKLNGAEYLQGRKGDKTLIMKVNASYTTGYIRYYNEGEKKPISYVSIVFSKTELKFTELEKLLTTVHKG LLKALDLSMGQNIHVYSPIVSMQNIQKTPQTAKKALASRWLSWLSYLEDPRIRFFYDPQMPALKDLPAVDTGKDNKKHPSNFQHIFYTDGSAITSPTKE GHLNAGMGIVYFINKDGNLQKQQEWSISLGNHTAQFAEIAAFEFALKKCLPLGGNILVVTDSNYVAKAYNEELDVWASNGFVNNRKKPLKHISKWKSV ADLKRLRPDVVVTHEPGHQKLDSSPHAYGNNLADQLATQASFKVH
FFV_O93209-Pro	8,015	VPWILKKPLELTIKLDLEEQQGTLLNNSILSKKGKEELKQLFEKYSALWQSWENQVGHRRIRPHKIATGTVKPTPQKQYHINPKAKPDIQIVINDLLKQGV LIQKESTMNTPVYPVPKPNGRWRMVLDYRAVNKVTPLIAVQNQHSYGILGSLFKGRYKTTIDLSNGFWAHPIVPEDYWITAFTWQGKQYCWTVLPQGF LNSPGLFTGDVVDLLQGIPNVEVYVDDVYISHDSEKEHLEYLDILFNRLKEAGYIISLKKSNIANSIVDFLGFQITNEGRGLTDTFKEKLENITAPTTLKQLQ SILGLLNFARNFIPDFTELIAPLYALIPKSTKNYVPWQIEHSTTLETLITKLNGAEYLQGRKGDKTLIMKVNASYTTGYIRYYNEGEKKPISYVSIVFSKTELK FTELEKLLTTVHKGLLKALDLSMGQNIHVYSPIVSMQNIQKTPQTAKKALASRWLSWLSYLEDPRIRFFYDPQMPALKDLPAVDTGKDNKKHPSNFQHI FYTDGSAITSPTKEGHLNAGMGIVYFINKDGNLQKQQEWSISLGNHTAQFAEIAAFEFALKKCLPLGGNILVVTDSNYVAKAYNEELDVWASNGFVNNR KKPLKHISKWKSVADLKRLRPDVVVTHEPGHQKLDSSPHAYGNNLADQLATQASFKVH
FFV_O93209-Pro_2mut	8,016	VPWILKKPLELTIKLDLEEQQGTLLNNSILSKKGKEELKQLFEKYSALWQSWENQVGHRRIRPHKIATGTVKPTPQKQYHINPKAKPDIQIVINDLLKQGV LIQKESTMNTPVYPVPKPNGRWRMVLDYRAVNKVTPLIAVQNQHSYGILGSLFKGRYKTTIDLSNGFWAHPIVPEDYWITAFTWQGKQYCWTVLPQGF LNSPGLFNGDVVDLLQGIPNVEVYVDDVYISHDSEKEHLEYLDILFNRLKEAGYIISLKKSNIANSIVDFLGFQITNEGRGLTDTFKEKLENITAPTTLKQLQ SILGLLNFARNFIPDFTELIAPLYALIPKSPKNYVPWQIEHSTTLETLITKLNGAEYLQGRKGDKTLIMKVNASYTTGYIRYYNEGEKKPISYVSIVFSKTELK FTELEKLLTTVHKGLLKALDLSMGQNIHVYSPIVSMQNIQKTPQTAKKALASRWLSWLSYLEDPRIRFFYDPQMPALKDLPAVDTGKDNKKHPSNFQHI FYTDGSAITSPTKEGHLNAGMGIVYFINKDGNLQKQQEWSISLGNHTAQFAEIAAFEFALKKCLPLGGNILVVTDSNYVAKAYNEELDVWASNGFVNNR KKPLKHISKWKSVADLKRLRPDVVVTHEPGHQKLDSSPHAYGNNLADQLATQASFKVH
FFV_O93209-Pro_2mutA	8,017	VPWILKKPLELTIKLDLEEQQGTLLNNSILSKKGKEELKQLFEKYSALWQSWENQVGHRRIRPHKIATGTVKPTPQKQYHINPKAKPDIQIVINDLLKQGV LIQKESTMNTPVYPVPKPNGRWRMVLDYRAVNKVTPLIAVQNQHSYGILGSLFKGRYKTTIDLSNGFWAHPIVPEDYWITAFTWQGKQYCWTVLPQGF LNSPGLFNGDVVDLLQGIPNVEVYVDDVYISHDSEKEHLEYLDILFNRLKEAGYIISLKKSNIANSIVDFLGFQITNEGRGLTDTFKEKLENITAPTTLKQLQ SILGKLNFARNFIPDFTELIAPLYALIPKSPKNYVPWQIEHSTTLETLITKLNGAEYLQGRKGDKTLIMKVNASYTTGYIRYYNEGEKKPISYVSIVFSKTELK FTELEKLLTTVHKGLLKALDLSMGQNIHVYSPIVSMQNIQKTPQTAKKALASRWLSWLSYLEDPRIRFFYDPQMPALKDLPAVDTGKDNKKHPSNFQHI

RT Name	SEQ ID NO:	RT amino acid sequence
		FYTDGSAITSPTKEGHLNAGMGIVYFINKDGNLQKQQEWSISLGNHTAQFAEIAAFEFALKKCLPLGGNILVVTDSNYVAKAYNEELDVWASNGFVNNR KKPLKHISKWKSVADLKRLRPDVVVTHEPGHQKLDSSPHAYGNNLADQLATQASFKVH
FLV_P 10273	8,018	TLQLEEEYRLFEPESTQKQEMDIWLKNFPQAWAETGGMGTAHCQAPVLIQLKATATPISIRQYPMPHEAYQGIKPHIRRMLDQGILKPCQSPWNTPLLP VKKPGTEDYRPVQDLREVNKRVEDIHPTVPNPYNLLSTLPPSHPWYTVLDLKDAFFCLRLHSESQLLFAFEWRDPEIGLSGQLTWTRLPQGFKNSPTL FDEALHSDLADFRVRYPALVLLQYVDDLLLAAATRTECLEGTKALLETLGNKGYRASAKKAQICLQEVTYLGYSLKDGQRWLTKARKEAILSIPVPKNSR QVREFLGTAGYCRLWIPGFAELAAPLYPLTRPGTLFQWGTEQQLAFEDIKKALLSSPALGLPDITKPFELFIDENSGFAKGVLVQKLGPWKRPVAYLSK KLDTVASGWPPCLRMVAAIAILVKDAGKLTLGQPLTILTSHPVEALVRQPPNKWLSNARMTHYQAMLLDAERVHFGPTVSLNPATLLPLPSGGNHHDC LQILAETHGTRPDLTDQPLPDADLTWYTDGSSFIRNGEREAGAAVTTESEVIWAAPLPPGTSAQRAELIALTQALKMAEGKKLTVYTDSRYAFATTHVH GEIYRRRGLLTSEGKEIKNKNEILALLEALFLPKRLSIIHCPGHQKGDSPQAKGNRLADDTAKKAATETHSSLTVLP
FLV_P 10273_ 3mut	8,019	TLQLEEEYRLFEPESTQKQEMDIWLKNFPQAWAETGGMGTAHCQAPVLIQLKATATPISIRQYPMPHEAYQGIKPHIRRMLDQGILKPCQSPWNTPLLP VKKPGTEDYRPVQDLREVNKRVEDIHPTVPNPYNLLSTLPPSHPWYTVLDLKDAFFCLRLHSESQLLFAFEWRDPEIGLSGQLTWTRLPQGFKNSPTL FNEALHSDLADFRVRYPALVLLQYVDDLLLAAATRTECLEGTKALLETLGNKGYRASAKKAQICLQEVTYLGYSLKDGQRWLTKARKEAILSIPVPKNSR QVREFLGTAGYCRLWIPGFAELAAPLYPLTRPGTLFQWGTEQQLAFEDIKKALLSSPALGLPDITKPFELFIDENSGFAKGVLVQKLGPWKRPVAYLSK KLDTVASGWPPCLRMVAAIAILVKDAGKLTLGQPLTILTSHPVEALVRQPPNKWLSNARMTHYQAMLLDAERVHFGPTVSLNPATLLPLPSGGNHHDC LQILAETHGTRPDLTDQPLPDADLTWYTDGSSFIRNGEREAGAAVTTESEVIWAAPLPPGTSAQRAELIALTQALKMAEGKKLTVYTDSRYAFATTHVH GEIYRRRGWLTSEGKEIKNKNEILALLEALFLPKRLSIIHCPGHQKGDSPQAKGNRLADDTAKKAATETHSSLTVLP
FLV_P 10273_ 3mutA	8,020	TLQLEEEYRLFEPESTQKQEMDIWLKNFPQAWAETGGMGTAHCQAPVLIQLKATATPISIRQYPMPHEAYQGIKPHIRRMLDQGILKPCQSPWNTPLLP VKKPGTEDYRPVQDLREVNKRVEDIHPTVPNPYNLLSTLPPSHPWYTVLDLKDAFFCLRLHSESQLLFAFEWRDPEIGLSGQLTWTRLPQGFKNSPTL FNEALHSDLADFRVRYPALVLLQYVDDLLLAAATRTECLEGTKALLETLGNKGYRASAKKAQICLQEVTYLGYSLKDGQRWLTKARKEAILSIPVPKNSR QVREFLGKAGYCRLFIPGFAELAAPLYPLTRPGTLFQWGTEQQLAFEDIKKALLSSPALGLPDITKPFELFIDENSGFAKGVLVQKLGPWKRPVAYLSKK LDTVASGWPPCLRMVAAIAILVKDAGKLTLGQPLTILTSHPVEALVRQPPNKWLSNARMTHYQAMLLDAERVHFGPTVSLNPATLLPLPSGGNHHDCL QILAETHGTRPDLTDQPLPDADLTWYTDGSSFIRNGEREAGAAVTTESEVIWAAPLPPGTSAQRAELIALTQALKMAEGKKLTVYTDSRYAFATTHVHG EIYRRRGWLTSEGKEIKNKNEILALLEALFLPKRLSIIHCPGHQKGDSPQAKGNRLADDTAKKAATETHSSLTVLP
FOAM V_P14 350	8,021	MNPLQLLQPLPAEIKGTKLLAHWNSGATITCIPESFLEDEQPIKKTLIKTIHGEKQQNVYYVTFKVKGRKVEAEVIASPYEYILLSPTDVPWLTQQPLQLTIL VPLQEYQEKILSKTALPEDQKQQLKTLFVKYDNLWQHWENQVGHRKIRPHNIATGDYPPRPQKQYPINPKAKPSIQIVIDDLLKQGVLTPQNSTMNTPV YPVPKPDGRWRMVLDYREVNKTIPLTAAQNQHSAGILATIVRQKYKTTLDLANGFWAHPITPESYWLTAFTWQGKQYCWTRLPQGFLNSPALFTADV VDLLKEIPNVQVYVDDIYLSHDDPKEHVQQLEKVFQILLQAGYVVSLKKSEIGQKTVEFLGFNITKEGRGLTDTFKTKLLNITPPKDLKQLQSILGLLNFAR NFIPNFAELVQPLYNLIASAKGKYIEWSEENTKQLNMVIEALNTASNLEERLPEQRLVIKVNTSPSAGYVRYYNETGKKPIMYLNYVFSKAELKFSMLEKL LTTMHKALIKAMDLAMGQEILVYSPIVSMTKIQKTPLPERKALPIRWITWMTYLEDPRIQFHYDKTLPELKHIPDVYTSSQSPVKHPSQYEGVFYTDGSAI KSPDPTKSNNAGMGIVHATYKPEYQVLNQWSIPLGNHTAQMAEIAAVEFACKKALKIPGPVLVITDSFYVAESANKELPYWKSNGFVNNKKKPLKHISK WKSIAECLSMKPDITIQHEKGISLQIPVFILKGNALADKLATQGSYVVN
FOAM V_P14 350_2 mut	8,022	MNPLQLLQPLPAEIKGTKLLAHWNSGATITCIPESFLEDEQPIKKTLIKTIHGEKQQNVYYVTFKVKGRKVEAEVIASPYEYILLSPTDVPWLTQQPLQLTIL VPLQEYQEKILSKTALPEDQKQQLKTLFVKYDNLWQHWENQVGHRKIRPHNIATGDYPPRPQKQYPINPKAKPSIQIVIDDLLKQGVLTPQNSTMNTPV YPVPKPDGRWRMVLDYREVNKTIPLTAAQNQHSAGILATIVRQKYKTTLDLANGFWAHPITPESYWLTAFTWQGKQYCWTRLPQGFLNSPALFNADV VDLLKEIPNVQVYVDDIYLSHDDPKEHVQQLEKVFQILLQAGYVVSLKKSEIGQKTVEFLGFNITKEGRGLTDTFKTKLLNITPPKDLKQLQSILGLLNFAR NFIPNFAELVQPLYNLIAPAKGKYIEWSEENTKQLNMVIEALNTASNLEERLPEQRLVIKVNTSPSAGYVRYYNETGKKPIMYLNYVFSKAELKFSMLEKL LTTMHKALIKAMDLAMGQEILVYSPIVSMTKIQKTPLPERKALPIRWITWMTYLEDPRIQFHYDKTLPELKHIPDVYTSSQSPVKHPSQYEGVFYTDGSAI KSPDPTKSNNAGMGIVHATYKPEYQVLNQWSIPLGNHTAQMAEIAAVEFACKKALKIPGPVLVITDSFYVAESANKELPYWKSNGFVNNKKKPLKHISK WKSIAECLSMKPDITIQHEKGISLQIPVFILKGNALADKLATQGSYVVN
FOAM V_P14 350_2 mutA	8,023	MNPLQLLQPLPAEIKGTKLLAHWNSGATITCIPESFLEDEQPIKKTLIKTIHGEKQQNVYYVTFKVKGRKVEAEVIASPYEYILLSPTDVPWLTQQPLQLTIL VPLQEYQEKILSKTALPEDQKQQLKTLFVKYDNLWQHWENQVGHRKIRPHNIATGDYPPRPQKQYPINPKAKPSIQIVIDDLLKQGVLTPQNSTMNTPV YPVPKPDGRWRMVLDYREVNKTIPLTAAQNQHSAGILATIVRQKYKTTLDLANGFWAHPITPESYWLTAFTWQGKQYCWTRLPQGFLNSPALFNADV VDLLKEIPNVQVYVDDIYLSHDDPKEHVQQLEKVFQILLQAGYVVSLKKSEIGQKTVEFLGFNITKEGRGLTDTFKTKLLNITPPKDLKQLQSILGKLNFAR NFIPNFAELVQPLYNLIAPAKGKYIEWSEENTKQLNMVIEALNTASNLEERLPEQRLVIKVNTSPSAGYVRYYNETGKKPIMYLNYVFSKAELKFSMLEKL LTTMHKALIKAMDLAMGQEILVYSPIVSMTKIQKTPLPERKALPIRWITWMTYLEDPRIQFHYDKTLPELKHIPDVYTSSQSPVKHPSQYEGVFYTDGSAI KSPDPTKSNNAGMGIVHATYKPEYQVLNQWSIPLGNHTAQMAEIAAVEFACKKALKIPGPVLVITDSFYVAESANKELPYWKSNGFVNNKKKPLKHISK WKSIAECLSMKPDITIQHEKGISLQIPVFILKGNALADKLATQGSYVVN
FOAM V_P14 350-Pro	8,024	VPWLTQQPLQLTILVPLQEYQEKILSKTALPEDQKQQLKTLFVKYDNLWQHWENQVGHRKIRPHNIATGDYPPRPQKQYPINPKAKPSIQIVIDDLLKQG VLTPQNSTMNTPVYPVPKPDGRWRMVLDYREVNKTIPLTAAQNQHSAGILATIVRQKYKTTLDLANGFWAHPITPESYWLTAFTWQGKQYCWTRLPQ GFLNSPALFTADVVDLLKEIPNVQVYVDDIYLSHDDPKEHVQQLEKVFQILLQAGYVVSLKKSEIGQKTVEFLGFNITKEGRGLTDTFKTKLLNITPPKDLK QLQSILGLLNFARNFIPNFAELVQPLYNLIASAKGKYIEWSEENTKQLNMVIEALNTASNLEERLPEQRLVIKVNTSPSAGYVRYYNETGKKPIMYLNYVF SKAELKFSMLEKLLTTMHKALIKAMDLAMGQEILVYSPIVSMTKIQKTPLPERKALPIRWITWMTYLEDPRIQFHYDKTLPELKHIPDVYTSSQSPVKHPS QYEGVFYTDGSAIKSPDPTKSNNAGMGIVHATYKPEYQVLNQWSIPLGNHTAQMAEIAAVEFACKKALKIPGPVLVITDSFYVAESANKELPYWKSNGF VNNKKKPLKHISKWKSIAECLSMKPDITIQHEKGISLQIPVFILKGNALADKLATQGSYVVN
FOAM V_P14 350-Pro_2mut	8,025	VPWLTQQPLQLTILVPLQEYQEKILSKTALPEDQKQQLKTLFVKYDNLWQHWENQVGHRKIRPHNIATGDYPPRPQKQYPINPKAKPSIQIVIDDLLKQG VLTPQNSTMNTPVYPVPKPDGRWRMVLDYREVNKTIPLTAAQNQHSAGILATIVRQKYKTTLDLANGFWAHPITPESYWLTAFTWQGKQYCWTRLPQ GFLNSPALFNADVVDLLKEIPNVQVYVDDIYLSHDDPKEHVQQLEKVFQILLQAGYVVSLKKSEIGQKTVEFLGFNITKEGRGLTDTFKTKLLNITPPKDL KQLQSILGLLNFARNFIPNFAELVQPLYNLIAPAKGKYIEWSEENTKQLNMVIEALNTASNLEERLPEQRLVIKVNTSPSAGYVRYYNETGKKPIMYLNYV FSKAELKFSMLEKLLTTMHKALIKAMDLAMGQEILVYSPIVSMTKIQKTPLPERKALPIRWITWMTYLEDPRIQFHYDKTLPELKHIPDVYTSSQSPVKHP SQYEGVFYTDGSAIKSPDPTKSNNAGMGIVHATYKPEYQVLNQWSIPLGNHTAQMAEIAAVEFACKKALKIPGPVLVITDSFYVAESANKELPYWKSNG FVNNKKKPLKHISKWKSIAECLSMKPDITIQHEKGISLQIPVFILKGNALADKLATQGSYVVN
FOAM V_P14 350-Pro_2mutA	8,026	VPWLTQQPLQLTILVPLQEYQEKILSKTALPEDQKQQLKTLFVKYDNLWQHWENQVGHRKIRPHNIATGDYPPRPQKQYPINPKAKPSIQIVIDDLLKQG VLTPQNSTMNTPVYPVPKPDGRWRMVLDYREVNKTIPLTAAQNQHSAGILATIVRQKYKTTLDLANGFWAHPITPESYWLTAFTWQGKQYCWTRLPQ GFLNSPALFNADVVDLLKEIPNVQVYVDDIYLSHDDPKEHVQQLEKVFQILLQAGYVVSLKKSEIGQKTVEFLGFNITKEGRGLTDTFKTKLLNITPPKDL KQLQSILGKLNFARNFIPNFAELVQPLYNLIAPAKGKYIEWSEENTKQLNMVIEALNTASNLEERLPEQRLVIKVNTSPSAGYVRYYNETGKKPIMYLNYV FSKAELKFSMLEKLLTTMHKALIKAMDLAMGQEILVYSPIVSMTKIQKTPLPERKALPIRWITWMTYLEDPRIQFHYDKTLPELKHIPDVYTSSQSPVKHP

RT Name	SEQ ID NO:	RT amino acid sequence
		SQYEGVFYTDGSAIKSPDPTKSNNAGMGIVHATYKPEYQVLNQWSIPLGNHTAQMAEIAAVEFACKKALKIPGPVLVITDSFYVAESANKELPYWKSNG FVNNKKKPLKHISKWKSIAECLSMKPDITIQHEKGISLQIPVFILKGNALADKLATQGSYVVN
GALV_P21414	8,027	VLNLEEEYRLHEKPVPSSIDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMSKEAREGIRPHIQKFLDLGVLVPCRSPWNTPLL PVKKPGTNDYRPVQDLREINKRVQDIHPTVPNPYNLLSSLPPSYTWYSVLDLKDAFFCLRLHPNSQPLFAFEWKDPEKGNTGQLTWTRLPQGFKNSP TLFDEALHRDLAPFRALNPQVVLLQYVDDLLVAAPTYEDCKKGTQKLLQELSKLGYRVSAKKAQLCQREVTYLGYLLKEGKRWLTPARKATVMKIPVP TTPRQVREFLGTAGFCRLWIPGFASLAAPLYPLTKESIPFIWTEEHQQAFDHIKKALLSAPALALPDLTKPFTLYIDERAGVARGVLTQTLGPWRRPVAY LSKKLDPVASGWPTCLKAVAAVALLLKDADKLTLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVH RCSEILAEETGTRRDLEDQPLPGVPTWYTDGSSFITEGKRRAGAPIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKNINIYTDSRYAFATAHIH GAIYKQRGLLTSAGKDIKNKEEILALLEAIHLPRRVAIIHCPGHQRGSNPVATGNRRADEAAKQAALSTRVLAGTTKP
GALV_P21414_3mut	8,028	VLNLEEEYRLHEKPVPSSIDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMSKEAREGIRPHIQKFLDLGVLVPCRSPWNTPLL PVKKPGTNDYRPVQDLREINKRVQDIHPTVPNPYNLLSSLPPSYTWYSVLDLKDAFFCLRLHPNSQPLFAFEWKDPEKGNTGQLTWTRLPQGFKNSP TLFNEALHRDLAPFRALNPQVVLLQYVDDLLVAAPTYEDCKKGTQKLLQELSKLGYRVSAKKAQLCQREVTYLGYLLKEGKRWLTPARKATVMKIPVP TTPRQVREFLGTAGFCRLWIPGFASLAAPLYPLTKPSIPFIWTEEHQQAFDHIKKALLSAPALALPDLTKPFTLYIDERAGVARGVLTQTLGPWRRPVAY LSKKLDPVASGWPTCLKAVAAVALLLKDADKLTLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVH RCSEILAEETGTRRDLEDQPLPGVPTWYTDGSSFITEGKRRAGAPIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKNINIYTDSRYAFATAHIH GAIYKQRGWLTSAGKDIKNKEEILALLEAIHLPRRVAIIHCPGHQRGSNPVATGNRRADEAAKQAALSTRVLAGTTKP
GALV_P21414_3mutA	8,029	VLNLEEEYRLHEKPVPSSIDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMSKEAREGIRPHIQKFLDLGVLVPCRSPWNTPLL PVKKPGTNDYRPVQDLREINKRVQDIHPTVPNPYNLLSSLPPSYTWYSVLDLKDAFFCLRLHPNSQPLFAFEWKDPEKGNTGQLTWTRLPQGFKNSP TLFNEALHRDLAPFRALNPQVVLLQYVDDLLVAAPTYEDCKKGTQKLLQELSKLGYRVSAKKAQLCQREVTYLGYLLKEGKRWLTPARKATVMKIPVP TTPRQVREFLGKAGFCRLFIPGFASLAAPLYPLTKPSIPFIWTEEHQQAFDHIKKALLSAPALALPDLTKPFTLYIDERAGVARGVLTQTLGPWRRPVAYL SKKLDPVASGWPTCLKAVAAVALLLKDADKLTLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVH RCSEILAEETGTRRDLEDQPLPGVPTWYTDGSSFITEGKRRAGAPIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKNINIYTDSRYAFATAHIH GAIYKQRGWLTSAGKDIKNKEEILALLEAIHLPRRVAIIHCPGHQRGSNPVATGNRRADEAAKQAALSTRVLAGTTKP
HTL1A_P03362	8,030	AVLGLEHLPRPPQISQFPLNPERLQALQHLVRKALEAGHIEPYTGPGNNPVFPVKKANGTWRFIHDLRATNSLTIDLSSSSPGPPDLSSLPTTLAHLQTI DLRDAFFQIPLPKQFQPYFAFTVPQQCNYGPGTRYAWKVLPQGFKNSPTLFEMQLAHILQPIRQAFPQCTILQYMDDILLASPSHEDLLLLSEATMASLI SHGLPVSENKTQQTPGTIKFLGQIISPNHLTYDAVPTVPIRSRWALPELQALLGEIQWVSKGTPTLRQPLHSLYCALQRHTDPRDQIYLNPSQVQSLVQL RQALSQNCRSRLVQTLPLLGAIMLTLTGTTTVVFQSKEQWPLVWLHAPLPHTSQCPWGQLLASAVLLLDKYTLQSYGLLCQTIHHNISTQTFNQFIQTS DHPSVPILLHHSHRFKNLGAQTGELWNTFLKTAAPLAPVKALMPVFTLSPVIINTAPCLFSDGSTSRAAYILWDKQILSQRSFPLPPPHKSAQRAELLGLL HGLSSARSWRCLNIFLDSKYLYHYLRTLALGTFQGRSSQAPFQALLPRLLSRKVVYLHHVRSHTNLPDPISRLNALTDALLITPVLQL
HTL1A_P03362_2mut	8,031	AVLGLEHLPRPPQISQFPLNPERLQALQHLVRKALEAGHIEPYTGPGNNPVFPVKKANGTWRFIHDLRATNSLTIDLSSSSPGPPDLSSLPTTLAHLQTI DLRDAFFQIPLPKQFQPYFAFTVPQQCNYGPGTRYAWKVLPQGFKNSPTLFEMQLAHILQPIRQAFPQCTILQYMDDILLASPSHEDLLLLSEATMASLI SHGLPVSENKTQQTPGTIKFLGQIISPNHLTYDAVPTVPIRSRWALPELQALLGEIQWVSKGTPTLRQPLHSLYCALQPHTDPRDQIYLNPSQVQSLVQL RQALSQNCRSRLVQTLPLLGAIMLTLTGTTTVVFQSKEQWPLVWLHAPLPHTSQCPWGQLLASAVLLLDKYTLQSYGLLCQTIHHNISTQTFNQFIQTS DHPSVPILLHHSHRFKNLGAQTGELWNTFLKTAAPLAPVKALMPVFTLSPVIINTAPCLFSDGSTSRAAYILWDKQILSQRSFPLPPPHKSAQRAELLGLL HGLSSARSWRCLNIFLDSKYLYHYLRTLALGTFQGRSSQAPFQALLPRLLSRKVVYLHHVRSHTNLPDPISRLNALTDALLITPVLQL
HTL1A_P03362_2mutB	8,032	AVLGLEHLPRPPQISQFPLNPERLQALQHLVRKALEAGHIEPYTGPGNNPVFPVKKANGTWRFIHDLRATNSLTIDLSSSSPGPPDLSSPPTTLAHLQTI DLRDAFFQIPLPKQFQPYFAFTVPQQCNYGPGTRYAWKVLPQGFKNSPTLFQMQLAHILQPIRQAFPQCTILQYMDDILLASPSHEDLLLLSEATMASLI SHGLPVSENKTQQTPGTIKFLGQIISPNHLTYDAVPTVPIRSRWALPELQALLGEIQWVSKGTPTLRQPLHSLYCALQPHTDPRDQIYLNPSQVQSLVQL RQALSQNCRSRLVQTLPLLGAIMLTLTGTTTVVFQSKEQWPLVWLHAPLPHTSQCPWGQLLASAVLLLDKYTLQSYGLLCQTIHHNISTQTFNQFIQTS DHPSVPILLHHSHRFKNLGAQTGELWNTFLKTAAPLAPVKALMPVFTLSPVIINTAPCLFSDGSTSRAAYILWDKQILSQRSFPLPPPHKSAQRAELLGLL HGLSSARSWRCLNIFLDSKYLYHYLRTLALGTFQGRSSQAPFQALLPRLLSRKVVYLHHVRSHTNLPDPISRLNALTDALLITPVLQL
HTL1C_P14078	8,033	AVLGLEHLPRPPEISQFPLNPERLQALQHLVRKALEAGHIEPYTGPGNNPVFPVKKANGTWRFIHDLRATNSLTIDLSSSSPGPPDLSSLPTTLAHLQTI DLKDAFFQIPLPKQFQPYFAFTVPQQCNYGPGTRYAWRVLPQGFKNSPTLFEMQLAHILQPIRQAFPQCTILQYMDDILLASPSHADLQLLSEATMASLI SHGLPVSENKTQQTPGTIKFLGQIISPNHLTYDAVPKVPIRSRWALPELQALLGEIQWVSKGTPTLRQPLHSLYCALQRHTDPRDQIYLNPSQVQSLVQL RQALSQNCRSRLVQTLPLLGAIMLTLTGTTTVVFQSKQQWPLVWLHAPLPHTSQCPWGQLLASAVLLLDKYTLQSYGLLCQTIHHNISTQTFNQFIQTS DHPSVPILLHHSHRFKNLGAQTGELWNTFLKTTAPLAPVKALMPVFTLSPVIINTAPCLFSDGSTSQAAYILWDKHILSQRSFPLPPPHKSAQRAELLGLL HGLSSARSWRCLNIFLDSKYLYHYLRTLALGTFQGRSSQAPFQALLPRLLSRKVVYLHHVRSHTNLPDPISRLNALTDALLITPVLQL
HTL1C_P14078_2mut	8,034	AVLGLEHLPRPPEISQFPLNPERLQALQHLVRKALEAGHIEPYTGPGNNPVFPVKKANGTWRFIHDLRATNSLTIDLSSSSPGPPDLSSLPTTLAHLQTI DLKDAFFQIPLPKQFQPYFAFTVPQQCNYGPGTRYAWRVLPQGFKNSPTLFQMQLAHILQPIRQAFPQCTILQYMDDILLASPSHADLQLLSEATMASLI SHGLPVSENKTQQTPGTIKFLGQIISPNHLTYDAVPKVPIRSRWALPELQALLGEIQWVSKGTPTLRQPLHSLYCALQPHTDPRDQIYLNPSQVQSLVQL RQALSQNCRSRLVQTLPLLGAIMLTLTGTTTVVFQSKQQWPLVWLHAPLPHTSQCPWGQLLASAVLLLDKYTLQSYGLLCQTIHHNISTQTFNQFIQTS DHPSVPILLHHSHRFKNLGAQTGELWNTFLKTTAPLAPVKALMPVFTLSPVIINTAPCLFSDGSTSQAAYILWDKHILSQRSFPLPPPHKSAQRAELLGLL HGLSSARSWRCLNIFLDSKYLYHYLRTLALGTFQGRSSQAPFQALLPRLLSRKVVYLHHVRSHTNLPDPISRLNALTDALLITPVLQL
HTL1L_P0C211	8,035	GLEHLPRPPEISQFPLNPERLQALQHLVRKALEAGHIEPYTGPGNNPVFPVKKANGTWRFIHDLRATNSLTVDLSSSSPGPPDLSSLPTTLAHLQTIDLK DAFFQIPLPKQFQPYFAFTVPQQCNYGPGTRYAWKVLPQGFKNSPTLFEMQLASILQPIRQAFPQCVILQYMDDILLASPSPEDLQQLSEATMASLISH GLPVSQDKTQQTPGTIKFLGQIISPNHITYDAVPTVPIRSRWALPELQALLGEIQWVSKGTPTLRQPLHSLYCALQGHTDPRDQIYLNPSQVQSLMQLQ QALSQNCRSRLAQTLPLLGAIMLTLTGTTTVVFQSKQQWPLVWLHAPLPHTSQCPWGQLLASAVLLLDKYTLQSYGLLCQTIHHNISIQTFNQFIQTSD HPSVPILLHHSHRFKNLGAQTGELWNTFLKTAAPLAPVKALTPVFTLSPIIINTAPCLFSDGSTSQAAYILWDKHILSQRSFPLPPPHKSAQQAELLGLLH GLSSARSWHCLNIFLDSKYLYHYLRTLALGTFQGKSSQAPFQALLPRLLAHKVIYLHHVRSHTNLPDPISKLNALTDALLITPIL
HTL1L_P0C211_2mut	8,036	GLEHLPRPPEISQFPLNPERLQALQHLVRKALEAGHIEPYTGPGNNPVFPVKKANGTWRFIHDLRATNSLTVDLSSSSPGPPDLSSLPTTLAHLQTIDLK DAFFQIPLPKQFQPYFAFTVPQQCNYGPGTRYAWKVLPQGFKNSPTLFQMQLASILQPIRQAFPQCVILQYMDDILLASPSPEDLQQLSEATMASLISH GLPVSQDKTQQTPGTIKFLGQIISPNHITYDAVPTVPIRSRWALPELQALLGEIQWVSKGTPTLRQPLHSLYCALQGHTDPRDQIYLNPSQVQSLMQLQ QALSQNCRSRLAQTLPLLGAIMLTLTGTTTVVFQSKQQWPLVWLHAPLPHTSQCPWGQLLASAVLLLDKYTLQSYGLLCQTIHHNISIQTFNQFIQTSD HPSVPILLHHSHRFKNLGAQTGELWNTFLKTAAPLAPVKALTPVFTLSPIIINTAPCLFSDGSTSQAAYILWDKHILSQRSFPLPPPHKSAQQAELLGLLH GLSSARSWHCLNIFLDSKYLYHYLRTLAWGTFQGKSSQAPFQALLPRLLAHKVIYLHHVRSHTNLPDPISKLNALTDALLITPIL
HTL1L_P0C2	8,037	GLEHLPRPPEISQFPLNPERLQALQHLVRKALEAGHIEPYTGPGNNPVFPVKKANGTWRFIHDLRATNSLTVDLSSSSPGPPDLSSPPTTLAHLQTIDLK DAFFQIPLPKQFQPYFAFTVPQQCNYGPGTRYAWKVLPQGFKNSPTLFQMQLASILQPIRQAFPQCVILQYMDDILLASPSPEDLQQLSEATMASLISH

RT Name	SEQ ID NO:	RT amino acid sequence
11_2mutB		GLPVSQDKTQQTPGTIKFLGQIISPNHITYDAVPTVPIRSRWALPELQALLGEIQWVSKGTPTLRQPLHSLYCALQGHTDPRDQIYLNPSQVQSLMQLQ QALSQNCRSRLAQTLPLLGAIMLTLTGTTTVVFQSKQQWPLVWLHAPLPHTSQCPWGQLLASAVLLLDKYTLQSYGLLCQTIHHNISIQTFNQFIQTSD HPSVPILLHHSHRFKNLGAQTGELWNTFLKTAAPLAPVKALTPVFTLSPIIINTAPCLFSDGSTSQAAYILWDKHILSQRSFPLPPPHKSAQQAELLGLLH GLSSARSWHCLNIFLDSKYLYHYLRTLAWGTFQGKSSQAPFQALLPRLLAHKVIYLHHVRSHTNLPDPISKLNALTDALLITPIL
HTL32_Q0R5R2	8,038	GLEHLPPPPEVSQFPLNPERLQALTDLVSRALEAKHIEPYQGPGNNPIFPVKKPNGKWRFIHDLRATNSVTRDLASPSPGPPDLTSLPQGLPHLRTIDLT DAFFQIPLPTIFQPYFAFTLPQPNNYGPGTRYSWRVLPQGFKNSPTLFEQQLSHILTPVRKTFPNSLIIQYMDDILLASPAPGELAALTDKVTNALTKEGL PLSPEKTQATPGPIHFLGQVISQDCITYETLPSINVKSTWSLAELQSMLGELQWVSKGTPVLRSSLHQLYLALRGHRDPRDTIKLTSIQVQALRTIQKALT LNCRSRLVNQLPILALIMLRPTGTTAVLFQTKQKWPLVWLHTPHPATSLRPWGQLLANAVIILDKYSLQHYGQVCKSFHHNISNQALTYYLHTSDQSSV AILLQHSHRFHNLGAQPSGPWRSLLQMPQIFQNIDVLRPPFTISPVVINHAPCLFSDGSASKAAFIIWDRQVIHQQVLSLPSTCSAQAGELFGLLAGLQK SQPWVALNIFLDSKFLIGHLRRMALGAFPGPSTQCELHTQLLPLLQGKTVYVHHVRSHTLLQDPISRLNEATDALMLAPLLPL
HTL32_Q0R5R2_2mut	8,039	GLEHLPPPPEVSQFPLNPERLQALTDLVSRALEAKHIEPYQGPGNNPIFPVKKPNGKWRFIHDLRATNSVTRDLASPSPGPPDLTSLPQGLPHLRTIDLT DAFFQIPLPTIFQPYFAFTLPQPNNYGPGTRYSWRVLPQGFKNSPTLFQQQLSHILTPVRKTFPNSLIIQYMDDILLASPAPGELAALTDKVTNALTKEGL PLSPEKTQATPGPIHFLGQVISQDCITYETLPSINVKSTWSLAELQSMLGELQWVSKGTPVLRSSLHQLYLALRGHRDPRDTIKLTSIQVQALRTIQKALT LNCRSRLVNQLPILALIMLRPTGTTAVLFQTKQKWPLVWLHTPHPATSLRPWGQLLANAVIILDKYSLQHYGQVCKSFHHNISNQALTYYLHTSDQSSV AILLQHSHRFHNLGAQPSGPWRSLLQMPQIFQNIDVLRPPFTISPVVINHAPCLFSDGSASKAAFIIWDRQVIHQQVLSLPSTCSAQAGELFGLLAGLQK SQPWVALNIFLDSKFLIGHLRRMAWGAFPGPSTQCELHTQLLPLLQGKTVYVHHVRSHTLLQDPISRLNEATDALMLAPLLPL
HTL32_Q0R5R2_2mutB	8,040	GLEHLPPPPEVSQFPLNPERLQALTDLVSRALEAKHIEPYQGPGNNPIFPVKKPNGKWRFIHDLRATNSVTRDLASPSPGPPDLTSPPQGLPHLRTIDL TDAFFQIPLPTIFQPYFAFTLPQPNNYGPGTRYSWRVLPQGFKNSPTLFQQQLSHILTPVRKTFPNSLIIQYMDDILLASPAPGELAALTDKVTNALTKEG LPLSPEKTQATPGPIHFLGQVISQDCITYETLPSINVKSTWSLAELQSMLGELQWVSKGTPVLRSSLHQLYLALRGHRDPRDTIKLTSIQVQALRTIQKAL TLNCRSRLVNQLPILALIMLRPTGTTAVLFQTKQKWPLVWLHTPHPATSLRPWGQLLANAVIILDKYSLQHYGQVCKSFHHNISNQALTYYLHTSDQSS VAILLQHSHRFHNLGAQPSGPWRSLLQMPQIFQNIDVLRPPFTISPVVINHAPCLFSDGSASKAAFIIWDRQVIHQQVLSLPSTCSAQAGELFGLLAGLQ KSQPWVALNIFLDSKFLIGHLRRMAWGAFPGPSTQCELHTQLLPLLQGKTVYVHHVRSHTLLQDPISRLNEATDALMLAPLLPL
HTL3P_Q4U0X6	8,041	GLEHLPPPPEVSQFPLNPERLQALTDLVSRALEAKHIEPYQGPGNNPIFPVKKPNGKWRFIHDLRATNSLTRDLASPSPGPPDLTSLPQDLPHLRTIDLT DAFFQIPLPAVFQPYFAFTLPQPNNHGPGTRYSWRVLPQGFKNSPTLFEQQLSHILAPVRKAFPNSLIIQYMDDILLASPALRELTALTDKVTNALTKEGL PMSLEKTQATPGSIHFLGQVISPDCITYETLPSIHVKSIWSLAELQSMLGELQWVSKGTPVLRSSLHQLYLALRGHRDPRDTIELTSTQVQALKTIQKALA LNCRSRLVSQLPILALIILRPTGTTAVLFQTKQKWPLVWLHTPHPATSLRPWGQLLANAIITLDKYSLQHYGQICKSFHHNISNQALTYYLHTSDQSSVAIL LQHSHRFHNLGAQPSGPWRSLLQVPQIFQNIDVLRPPFIISPVVIDHAPCLFSDGATSKAAFILWDKQVIHQQVLPLPSTCSAQAGELFGLLAGLQKSKP WPALNIFLDSKFLIGHLRRMALGAFLGPSTQCDLHARLFPLLQGKTVYVHHVRSHTLLQDPISRLNEATDALMLAPLLPL
HTL3P_Q4U0X6_2mut	8,042	GLEHLPPPPEVSQFPLNPERLQALTDLVSRALEAKHIEPYQGPGNNPIFPVKKPNGKWRFIHDLRATNSLTRDLASPSPGPPDLTSLPQDLPHLRTIDLT DAFFQIPLPAVFQPYFAFTLPQPNNHGPGTRYSWRVLPQGFKNSPTLFQQQLSHILAPVRKAFPNSLIIQYMDDILLASPALRELTALTDKVTNALTKEG LPMSLEKTQATPGSIHFLGQVISPDCITYETLPSIHVKSIWSLAELQSMLGELQWVSKGTPVLRSSLHQLYLALRGHRDPRDTIELTSTQVQALKTIQKAL ALNCRSRLVSQLPILALIILRPTGTTAVLFQTKQKWPLVWLHTPHPATSLRPWGQLLANAIITLDKYSLQHYGQICKSFHHNISNQALTYYLHTSDQSSVAI LLQHSHRFHNLGAQPSGPWRSLLQVPQIFQNIDVLRPPFIISPVVIDHAPCLFSDGATSKAAFILWDKQVIHQQVLPLPSTCSAQAGELFGLLAGLQKSK PWPALNIFLDSKFLIGHLRRMAWGAFLGPSTQCDLHARLFPLLQGKTVYVHHVRSHTLLQDPISRLNEATDALMLAPLLPL
HTL3P_Q4U0X6_2mutB	8,043	GLEHLPPPPEVSQFPLNPERLQALTDLVSRALEAKHIEPYQGPGNNPIFPVKKPNGKWRFIHDLRATNSLTRDLASPSPGPPDLTSPPQDLPHLRTIDLT DAFFQIPLPAVFQPYFAFTLPQPNNHGPGTRYSWRVLPQGFKNSPTLFQQQLSHILAPVRKAFPNSLIIQYMDDILLASPALRELTALTDKVTNALTKEG LPMSLEKTQATPGSIHFLGQVISPDCITYETLPSIHVKSIWSLAELQSMLGELQWVSKGTPVLRSSLHQLYLALRGHRDPRDTIELTSTQVQALKTIQKAL ALNCRSRLVSQLPILALIILRPTGTTAVLFQTKQKWPLVWLHTPHPATSLRPWGQLLANAIITLDKYSLQHYGQICKSFHHNISNQALTYYLHTSDQSSVAI LLQHSHRFHNLGAQPSGPWRSLLQVPQIFQNIDVLRPPFIISPVVIDHAPCLFSDGATSKAAFILWDKQVIHQQVLPLPSTCSAQAGELFGLLAGLQKSK PWPALNIFLDSKFLIGHLRRMAWGAFLGPSTQCDLHARLFPLLQGKTVYVHHVRSHTLLQDPISRLNEATDALMLAPLLPL
HTLV2_P03363_2mut	8,044	HLPPPPQVDQFPLNLPERLQALNDLVSKALEAGHIEPYSGPGNNPVFPVKKPNGKWRFIHDLRATNAITTTLTSPSPGPPDLTSLPTALPHLQTIDLTDA FFQIPLPKQYQPYFAFTIPQPCNYGPGTRYAWTVLPQGFKNSPTLFQQQLAAVLNPMRKMFPTSTIVQYMDDILLASPTNEELQQLSQLTLQALTTHGL PISQEKTQQTPGQIRFLGQVISPNHITYESTPTIPIKSQWTLTELQVILGEIQWVSKGTPILRKHLQSLYSALHPYRDPRACITLTPQQLHALHAIQQALQH NCRGRLNPALPLLGLISLSTSGTTSVIFQPKQNWPLAWLHTPHPPTSLCPWGHLLACTILTLDKYTLQHYGQLCQSFHHNMSKQALCDFLRNSPHPSV GILIHHMGRFHNLGSQPSGPWKTLLHLPTLLQEPRLLRPIFTLSPVVLDTAPCLFSDGSPQKAAYVLWDQTILQQDITPLPSHETHSAQKGELLALICGLR AAKPWPSLNIFLDSKYLIKYLHSLAIGAFLGTSAHQTLQAALPPLLQGKTIYLHHVRSHTNLPDPISTFNEYTDSLILAPLVPL
JSRV_P31623	8,045	PLGTSDSPVTHADPIDWKSEEPVWVDQWPLTQEKLSAAQQLVQEQLRLGHIEPSTSAWNSPIFVIKKKSGKWRLLQDLRKVNETMMHMGALQPGLPT PSAIPDKSYIIVIDLKDCFYTIPLAPQDCKRFAFSLPSVNFKEPMQRYQWRVLPQGMTNSPTLCQKFVATAIAPVRQRFPQLYLVHYMDDILLAHTDEHLL YQAFSILKQHLSLNGLVIADEKIQTHFPYNYLGFSLYPRVVYNTQLVKLQTDHLKTLNDFQKLLGDINWIRPYLKLPTYTLQPLFDILKGDSDPASPRTLSLE GRTALQSIEEAIRQQQITYCDYQRSWGLYILPTPRAPTGVLYQDKPLRWIYLSATPTKHLLPYYELVAKIIAKGRHEAIQYFGMEPPFICVPYALEQQDWL FQFSDNWSIAFANYPGQITHHYPSDKLLQFASSHAFIFPKIVRRQPIPEATLIFTDGSSNGTAALIINHQTYYAQTSFSSAQVVELFAVHQALLTVPTSFNL FTDSSYVVGALQMIETVPIIGTTSPEVLNLFTLIQQVLHCRQHPCFFGHIRAHSTLPGALVQGNHTADVLTKQVFFQS
JSRV_P31623_2mutB	8,046	PLGTSDSPVTHADPIDWKSEEPVWVDQWPLTQEKLSAAQQLVQEQLRLGHIEPSTSAWNSPIFVIKKKSGKWRLLQDLRKVNETMMHMGALQPGLPT PSPIPDKSYIIVIDLKDCFYTIPLAPQDCKRFAFSLPSVNFKEPMQRYQWRVLPQGMTNSPTLCQKFVATAIAPVRQRFPQLYLVHYMDDILLAHTDEHLL YQAFSILKQHLSLNGLVIADEKIQTHFPYNYLGFSLYPRVVYNTQLVKLQTDHLKTLNDFQKLLGDINWIRPYLKLPTYTLQPLFDILKGDSDPASPRTLSLE GRTALQSIEEAIRQQQITYCDYQRSWGLYILPTPRAPTGVLYQDKPLRWIYLSATPTKHLLPYYELVAKIIAKGRHEAIQYFGMEPPFICVPYALEQQDWL FQFSDNWSIAFANYPGQITHHYPSDKLLQFASSHAFIFPKIVRRQPIPEATLIFTDGSSNGTAALIINHQTYYAQTSFSSAQVVELFAVHQALLTVPTSFNL FTDSSYVVGALQMIETVPIIGTTSPEVLNLFTLIQQVLHCRQHPCFFGHIRAHSTLPGALVQGNHTADVLTKQVFFQS
KORV_Q9TTC1	8,047	TLGDQGSRGSDPLPEPRVTLTVEGIPTEFLVNTGAEHSVLTKPMGKMGSKRTVVAGATGSKVYPWTTKRLLKIGQKQVTHSFLVIPECPAPLLGRDLLT KLKAQIQFSTEGPQVTWEDRPAMCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPMVWAEKAGMGLANQVPPVVVELKSDASPVAVRQYPMSKEAREGI RPHIQRFLDLGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEW RDPEKGNTGQLTWTRLPQGFKNSPTLFDEALHRDLASFRALNPQVVMLQYVDDLLVAAPTYRDCKEGTRRLLQELSKLGYRVSAKKAQLCREEVTYL GYLLKGGKRWLTPARKATVMKIPTPTTPRQVREFLGTAGFCRLWIPGFASLAAPLYPLTREKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFAL YVDEKEGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLN ERVSFAPPAILNPATLLPVESDDTPIHICSEILAEETGTRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALT QALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGLLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTET TKN

RT Name	SEQ ID NO:	RT amino acid sequence
KORV_Q9TTC1_3mut	8,048	TLGDQGSRGSDPLPEPRVTLTVEGIPTEFLVNTGAEHSVLTKPMGKMGSKRTVVAGATGSKVYPWTTKRLLKIGQKQVTHSFLVIPECPAPLLGRDLLTKLKAQIQFSTEGPQVTWEDRPAMCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPMVWAEKAGMGLANQVPPVVVELKSDASPVAVRQYPMSKEAREGIRPHIQRFLDLGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLASFRALNPQVVMLQYVDDLLVAAPTYRDCKEGTRRLLQELSKLGYRVSAKKAQLCREEVTYLGYLLKGGKRWLTPARKATVMKIPTPTTPRQVREFLGTAGFCRLWIPGFASLAAPLYPLTRPKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFALYVDEKEGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAILNPATLLPVESDDTPIHICSEILAEETGTRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTETTKN
KORV_Q9TTC1_3mutA	8,049	TLGDQGSRGSDPLPEPRVTLTVEGIPTEFLVNTGAEHSVLTKPMGKMGSKRTVVAGATGSKVYPWTTKRLLKIGQKQVTHSFLVIPECPAPLLGRDLLTKLKAQIQFSTEGPQVTWEDRPAMCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPMVWAEKAGMGLANQVPPVVVELKSDASPVAVRQYPMSKEAREGIRPHIQRFLDLGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLASFRALNPQVVMLQYVDDLLVAAPTYRDCKEGTRRLLQELSKLGYRVSAKKAQLCREEVTYLGYLLKGGKRWLTPARKATVMKIPTPTTPRQVREFLGKAGFCRLFIPGFASLAAPLYPLTRPKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFALYVDEKEGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAILNPATLLPVESDDTPIHICSEILAEETGTRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTETTKN
KORV_Q9TTC1-Pro	8,050	LLGRDLLTKLKAQIQFSTEGPQVTWEDRPAMCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPMVWAEKAGMGLANQVPPVVVELKSDASPVAVRQYPMSKEAREGIRPHIQRFLDLGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFDEALHRDLASFRALNPQVVMLQYVDDLLVAAPTYRDCKEGTRRLLQELSKLGYRVSAKKAQLCREEVTYLGYLLKGGKRWLTPARKATVMKIPTPTTPRQVREFLGTAGFCRLWIPGFASLAAPLYPLTREKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFALYVDEKEGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAILNPATLLPVESDDTPIHICSEILAEETGTRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGLLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTETTKN
KORV_Q9TTC1-Pro_3mut	8,051	LLGRDLLTKLKAQIQFSTEGPQVTWEDRPAMCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPMVWAEKAGMGLANQVPPVVVELKSDASPVAVRQYPMSKEAREGIRPHIQRFLDLGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLASFRALNPQVVMLQYVDDLLVAAPTYRDCKEGTRRLLQELSKLGYRVSAKKAQLCREEVTYLGYLLKGGKRWLTPARKATVMKIPTPTTPRQVREFLGTAGFCRLWIPGFASLAAPLYPLTRPKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFALYVDEKEGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAILNPATLLPVESDDTPIHICSEILAEETGTRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTETTKN
KORV_Q9TTC1-Pro_3mutA	8,052	LLGRDLLTKLKAQIQFSTEGPQVTWEDRPAMCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPMVWAEKAGMGLANQVPPVVVELKSDASPVAVRQYPMSKEAREGIRPHIQRFLDLGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLASFRALNPQVVMLQYVDDLLVAAPTYRDCKEGTRRLLQELSKLGYRVSAKKAQLCREEVTYLGYLLKGGKRWLTPARKATVMKIPTPTTPRQVREFLGKAGFCRLFIPGFASLAAPLYPLTRPKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFALYVDEKEGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAILNPATLLPVESDDTPIHICSEILAEETGTRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTETTKN
MLVAV_P03356	8,053	TLNLEDEYRLYETSAEPEVSPGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEAKLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHRWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFDEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLLTLGNLGYRASAKKAQLCQKQVKYLGYLLKEGQRWLTEARKETVMGQPTKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKTGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLRKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGLLTSEGREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLL
MLVAV_P03356_3mut	8,054	TLNLEDEYRLYETSAEPEVSPGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEAKLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHRWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLLTLGNLGYRASAKKAQLCQKQVKYLGYLLKEGQRWLTEARKETVMGQPTKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKTGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLRKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGLLTSEGREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLL
MLVAV_P03356_3mutA	8,055	TLNLEDEYRLYETSAEPEVSPGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEAKLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHRWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFDEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLLTLGNLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKTGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLRKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLL
MLVBM_Q7SVK7	8,056	TLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFDEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKTGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAY

RT Name	SEQ ID NO:	RT amino acid sequence
		LSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAP HDCLEILAETHGTRPDLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFAT AHIHGEIYRRRGLLTSEGREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLL
MLVBM_Q7SVK7	8,057	TLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLP VKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPT LFDEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKT PRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKTGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAY LSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAP HDCLEILAETHGTRPDLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFAT AHIHGEIYRRRGLLTSEGREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLL
MLVBM_Q7SVK7_3mut	8,058	TLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLP VKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPT LFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKT PRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVA YLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGA PHDCLEILAETHGTRPDLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFA TAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLL
MLVBM_Q7SVK7_3mut	8,059	TLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLP VKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPT LFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKT PRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVA YLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGA PHDCLEILAETHGTRPDLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFA TAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLL
MLVBM_Q7SVK7_3mutA_WS	8,060	LGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPV KKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTL FNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTP RQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYL SKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAP HDCLEILAETHGTRPDLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFAT AHIHGEIYRRRGWLTSEGREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLI
MLVBM_Q7SVK7_3mutA_WS	8,061	LGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPV KKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTL FNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTP RQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYL SKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAP HDCLEILAETHGTRPDLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFAT AHIHGEIYRRRGWLTSEGREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLI
MLVCB_P08361	8,062	TLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLP VKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPT LFDEALHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKT PRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKTGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAY LSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQ HDCLDILAEAHGTRSDLMDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFAT AHIHGEIYRRRGLLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLL
MLVCB_P08361_3mut	8,063	TLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLP VKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPT LFNEALHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKT PRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKTGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVA YLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGL QHDCLDILAEAHGTRSDLMDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAF ATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLL
MLVCB_P08361_3mutA	8,064	TLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLP VKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPT LFNEALHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKT PRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVA YLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQ HDCLDILAEAHGTRSDLMDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFAT AHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLL
MLVF5_P26810	8,065	TLNIEDEYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAFRQAPLIISLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLP VKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWKDPEMGISGQLTWTRLPQGFKNSPT LFDEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKT PRQLREFLGTAGLCRLWIPGFAEMAAPLYPLTKTGTLFKWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAY LSKKLDPVAAGWPPCLRMVAAIAVLTKDVGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQ HDCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSFLQEGQRRAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAAGKKLNVYTDSRYAFAT AHIHGEIYRRRGLLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNHAEARGNRMADQAAREVATRETPETSTLL

RT Name	SEQ ID NO:	RT amino acid sequence
MLVF5_P26810_3mut	8,066	TLNIEDEYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAFRQAPLIISLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLP VKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWKDPEMGISGQLTWTRLPQGFKNSPT LFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKT PRQLREFLGTAGLCRLWIPGFAEMAAPLYPLTKPGTLFKWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAY LSKKLDPVAAGWPPCLRMVAAIAVLTKDVGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQ HDCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSFLQEGQRRAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAAGKKLNVYTDSRYAFAT AHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNHAEARGNRMADQAARE VATRETPETSTLL
MLVF5_P26810_3mutA	8,067	TLNIEDEYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAFRQAPLIISLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLP VKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWKDPEMGISGQLTWTRLPQGFKNSPT LFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKT PRQLREFLGKAGLCRLFIPGFAEMAAPLYPLTKPGTLFKWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAY LSKKLDPVAAGWPPCLRMVAAIAVLTKDVGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQ HDCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSFLQEGQRRAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAAGKKLNVYTDSRYAFAT AHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNHAEARGNRMADQAARE VATRETPETSTLL
MLVFF_P26809_3mut	8,068	TLNIEDEYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLP VKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPT LFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKT PRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVA YLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQ HDCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFA TAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAARE VATRETPETSTLL
MLVFF_P26809_3mutA	8,069	TLNIEDEYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLP VKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPT LFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKT PRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAY LSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQ HDCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFA TAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAARE VATRETPETSTLL
MLVMS_P03355	8,070	TLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLP VKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPT LFDEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKT PRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKTGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVA YLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGL QHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFA TAHIHGEIYRRRGLLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLL
MLVMS_reference	8,137	TLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLP VKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPT LFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKT PRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAY LSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQ HNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFAT AHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSP
MLVMS_P03355	8,071	TLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLP VKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPT LFDEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKT PRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKTGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVA YLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGL QHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFA TAHIHGEIYRRRGLLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLL
MLVMS_P03355_3mut	8,072	TLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLP VKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPT LFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKT PRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKTGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVA YLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGL QHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFA TAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLL
MLVMS_P03355_3mut	8,073	TLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLP VKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPT LFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKT PRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKTGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVA YLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGL QHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFA TAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLL
MLVMS_P03355_3	8,074	TLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLP VKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPT LFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKT PRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAY

RT Name	SEQ ID NO:	RT amino acid sequence
mutA_WS		LSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQ HNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFAT AHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLL
MLVM S_P03 355_3 mutA_ WS	8,075	TLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLP VKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPT LFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKT PRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAY LSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQ HNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFAT AHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLL
MLVM S_P03 355_PL V919	8,076	TLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLP VKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPT LFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKT PRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAY LSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQ HNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFAT AHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEF E
MLVM S_P03 355_PL V919	8,077	TLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLP VKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPT LFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKT PRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAY LSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQ HNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFAT AHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEF E
MLVRD_P1122 7	8,078	TLNIEDEYRLHEISTEPDVSPGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEAKLGIKPHIQRLLDQGILVPCQSPWNTPLLP VKKPGTNDYRPVQGLREVNKRVEDIHPTVPNPYNLLSGLPTSHRWYTVLDLKDAFFCLRLHPTSQPLFASEWRDPGMGISGQLTWTRLPQGFKNSPT LFDEALHRGLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLKTLGNLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPTPKT PRQLREFLGTAGFCRLWIPRFAEMAAPLYPLTKTGTLFNWGPDQQKAYHEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAY LSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAP HDCLEILAETHGTEPDLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATA HIHGEIYKRRGLLTSEGREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLL
MLVRD_P1122 7_3mut	8,079	TLNIEDEYRLHEISTEPDVSPGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEAKLGIKPHIQRLLDQGILVPCQSPWNTPLLP VKKPGTNDYRPVQGLREVNKRVEDIHPTVPNPYNLLSGLPTSHRWYTVLDLKDAFFCLRLHPTSQPLFASEWRDPGMGISGQLTWTRLPQGFKNSPT LFNEALHRGLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLKTLGNLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPTPKT PRQLREFLGTAGFCRLWIPRFAEMAAPLYPLTKPGTLFNWGPDQQKAYHEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAY LSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAP HDCLEILAETHGTEPDLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATA HIHGEIYKRRGWLTSEGREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLL
MMTV B_P03 365	8,080	WVQEISDSRPMLHIYLNGRRFLGLLNTGADKTCIAGRDWPANWPIHQTESSLQGLGMACGVARSSQPLRWQHEDKSGIIHPFVIPTLPFTLWGRDIMK DIKVRLMTDSPDDSQDLMIGAIESNLFADQISWKSDQPVWLNQWPLKQEKLQALQQLVTEQLQLGHLEESNSPWNTPVFVIKKKSGKWRLLQDLRAV NATMHDMGALQPGLPSPVAVPKGWEIIIIDLQDCFFNIKLHPEDCKRFAFSVPSPNFKRPYQRFQWKVLPQGMKNSPTLCQKFVDKAILTVRDKYQDS YIVHYMDDILLAHPSRSIVDEILTSMIQALNKHGLVVSTEKIQKYDNLKYLGTHIQGDSVSYQKLQIRTDKLRTLNDFQKLLGNINWIRPFLKLTTGELKPLF EILNGDSNPISTRKLTPEACKALQLMNERLSTARVKRLDLSQPWSLCILKTEYTPTACLWQDGVVEWIHLPHISPKVITPYDIFCTQLIIKGRHRSKELFSK DPDYIVVPYTKVQFDLLLQEKEDWPISLLGFLGEVHFHLPKDPLLTFTLQTAIIFPHMTSTTPLEKGIVIFTDGSANGRSVTYIQGREPIIKENTQNTAQQA EIVAVITAFEEVSQPFNLYTDSKYVTGLFPEIETATLSPRTKIYTELKHLQRLIHKRQEKFYIGHIRGHTGLPGPLAQGNAYADSLTRILT
MMTV B_P03 365	8,081	WVQEISDSRPMLHIYLNGRRFLGLLNTGADKTCIAGRDWPANWPIHQTESSLQGLGMACGVARSSQPLRWQHEDKSGIIHPFVIPTLPFTLWGRDIMK DIKVRLMTDSPDDSQDLMIGAIESNLFADQISWKSDQPVWLNQWPLKQEKLQALQQLVTEQLQLGHLEESNSPWNTPVFVIKKKSGKWRLLQDLRAV NATMHDMGALQPGLPSPVAVPKGWEIIIIDLQDCFFNIKLHPEDCKRFAFSVPSPNFKRPYQRFQWKVLPQGMKNSPTLCQKFVDKAILTVRDKYQDS YIVHYMDDILLAHPSRSIVDEILTSMIQALNKHGLVVSTEKIQKYDNLKYLGTHIQGDSVSYQKLQIRTDKLRTLNDFQKLLGNINWIRPFLKLTTGELKPLF EILNGDSNPISTRKLTPEACKALQLMNERLSTARVKRLDLSQPWSLCILKTEYTPTACLWQDGVVEWIHLPHISPKVITPYDIFCTQLIIKGRHRSKELFSK DPDYIVVPYTKVQFDLLLQEKEDWPISLLGFLGEVHFHLPKDPLLTFTLQTAIIFPHMTSTTPLEKGIVIFTDGSANGRSVTYIQGREPIIKENTQNTAQQA EIVAVITAFEEVSQPFNLYTDSKYVTGLFPEIETATLSPRTKIYTELKHLQRLIHKRQEKFYIGHIRGHTGLPGPLAQGNAYADSLTRILT
MMTV B_P03 365_2 mut	8,082	WVQEISDSRPMLHIYLNGRRFLGLLNTGADKTCIAGRDWPANWPIHQTESSLQGLGMACGVARSSQPLRWQHEDKSGIIHPFVIPTLPFTLWGRDIMK DIKVRLMTDSPDDSQDLMIGAIESNLFADQISWKSDQPVWLNQWPLKQEKLQALQQLVTEQLQLGHLEESNSPWNTPVFVIKKKSGKWRLLQDLRAV NATMHDMGALQPGLPSPVAVPKGWEIIIIDLQDCFFNIKLHPEDCKRFAFSVPSPNFKRPYQRFQWKVLPQGMKNSPTLCQKFVDKAILTVRDKYQDS YIVHYMDDILLAHPSRSIVDEILTSMIQALNKHGLVVSTEKIQKYDNLKYLGTHIQGDSVSYQKLQIRTDKLRTLNDFQKLLGNINWIRPFLKLTTGELKPLF EILNPDSNPISTRKLTPEACKALQLMNERLSTARVKRLDLSQPWSLCILKTEYTPTACLWQDGVVEWIHLPHISPKVITPYDIFCTQLIIKGRHRSKELFSK DPDYIVVPYTKVQFDLLLQEKEDWPISLLGFLGEVHFHLPKDPLLTFTLQTAIIFPHMTSTTPLEKGIVIFTDGSANGRSVTYIQGREPIIKENTQNTAQQA EIVAVITAFEEVSQPFNLYTDSKYVTGLFPEIETATLSPRTKIYTELKHLQRLIHKRQEKFYIGHIRGHTGLPGPLAQGNAYADSLTRILT
MMTV B_P03 365_2 mut_W S	8,083	VQEISDSRPMLHIYLNGRRFLGLLDTGADKTCIAGRDWPANWPIHQTESSLQGLGMACGVARSSQPLRWQHEDKSGIIHPFVIPTLPFTLWGRDIMKDI KVRLMTDSPDDSQDLMIGAIESNLFADQISWKSDQPVWLNQWPLKQEKLQALQQLVTEQLQLGHLEESNSPWNTPVFVIKKKSGKWRLLQDLRAVNA TMHDMGALQPGLPSPVAVPKGWEIIIIDLQDCFFNIKLHPEDCKRFAFSVPSPNFKRPYQRFQWKVLPQGMKNSPTLCQKFVDKAILTVRDKYQDSYIV HYMDDILLAHPSRSIVDEILTSMIQALNKHGLVVSTEKIQKYDNLKYLGTHIQGDSVSYQKLQIRTDKLRTLNDFQKLLGNINWIRPFLKLTTGELKPLFEIL NPDSNPISTRKLTPEACKALQLMNERLSTARVKRLDLSQPWSLCILKTEYTPTACLWQDGVVEWIHLPHISPKVITPYDIFCTQLIIKGRHRSKELFSKDP

RT Name	SEQ ID NO:	RT amino acid sequence
		DYIVVPYTKVQFDLLLQEKEDWPISLLGFLGEVHFHLPKDPLLTFTLQTAIIFPHMTSTTPLEKGIVIFTDGSANGRSVTYIQGREPIIKENTQNTAQQAEIV AVITAFEEVSQPFNLYTDSKYVTGLFPEIETATLSPRTKIYTELKHLQRLIHKRQEKFYIGHIRGHTGLPGPLAQGNAYADSLTRILTA
MMTV B_P03 365_2 mut_W S	8,084	VQEISDSRPMLHIYLNGRRFLGLLDTGADKTCIAGRDWPANWPIHQTESSLQGLGMACGVARSSQPLRWQHEDKSGIIHPFVIPTLPFTLWGRDIMKDI KVRLMTDSPDDSQDLMIGAIESNLFADQISWKSDQPVWLNQWPLKQEKLQALQQLVTEQLQLGHLEESNSPWNTPVFVIKKKSGKWRLLQDLRAVNA TMHDMGALQPGLPSPVAVPKGWEIIIIDLQDCFFNIKLHPEDCKRFAFSVPSPNFKRPYQRFQWKVLPQGMKNSPTLCQKFVDKAILTVRDKYQDSYIV HYMDDILLAHPSRSIVDEILTSMIQALNKHGLVVSTEKIQKYDNLKYLGTHIQGDSVSYQKLQIRTDKLRTLNDFQKLLGNINWIRPFLKLTTGELKPLFEIL NPDSNPISTRKLTPEACKALQLMNERLSTARVKRLDLSQPWSLCILKTEYTPTACLWQDGVVEWIHLPHISPKVITPYDIFCTQLIIKGRHRSKELFSKDP DYIVVPYTKVQFDLLLQEKEDWPISLLGFLGEVHFHLPKDPLLTFTLQTAIIFPHMTSTTPLEKGIVIFTDGSANGRSVTYIQGREPIIKENTQNTAQQAEIV AVITAFEEVSQPFNLYTDSKYVTGLFPEIETATLSPRTKIYTELKHLQRLIHKRQEKFYIGHIRGHTGLPGPLAQGNAYADSLTRILTA
MMTV B_P03 365_2 mutB	8,085	WVQEISDSRPMLHIYLNGRRFLGLLNTGADKTCIAGRDWPANWPIHQTESSLQGLGMACGVARSSQPLRWQHEDKSGIIHPFVIPTLPFTLWGRDIMK DIKVRLMTDSPDDSQDLMIGAIESNLFADQISWKSDQPVWLNQWPLKQEKLQALQQLVTEQLQLGHLEESNSPWNTPVFVIKKKSGKWRLLQDLRAV NATMHDMGALQPGLPSPVAPPKGWEIIIIDLQDCFFNIKLHPEDCKRFAFSVPSPNFKRPYQRFQWKVLPQGMKNSPTLCQKFVDKAILTVRDKYQDS YIVHYMDDILLAHPSRSIVDEILTSMIQALNKHGLVVSTEKIQKYDNLKYLGTHIQGDSVSYQKLQIRTDKLRTLNDFQKLLGNINWIRPFLKLTTGELKPLF EILNPDSNPISTRKLTPEACKALQLMNERLSTARVKRLDLSQPWSLCILKTEYTPTACLWQDGVVEWIHLPHISPKVITPYDIFCTQLIIKGRHRSKELFSK DPDYIVVPYTKVQFDLLLQEKEDWPISLLGFLGEVHFHLPKDPLLTFTLQTAIIFPHMTSTTPLEKGIVIFTDGSANGRSVTYIQGREPIIKENTQNTAQQA EIVAVITAFEEVSQPFNLYTDSKYVTGLFPEIETATLSPRTKIYTELKHLQRLIHKRQEKFYIGHIRGHTGLPGPLAQGNAYADSLTRILT
MMTV B_P03 365_2 mutB	8,086	WVQEISDSRPMLHIYLNGRRFLGLLNTGADKTCIAGRDWPANWPIHQTESSLQGLGMACGVARSSQPLRWQHEDKSGIIHPFVIPTLPFTLWGRDIMK DIKVRLMTDSPDDSQDLMIGAIESNLFADQISWKSDQPVWLNQWPLKQEKLQALQQLVTEQLQLGHLEESNSPWNTPVFVIKKKSGKWRLLQDLRAV NATMHDMGALQPGLPSPVAPPKGWEIIIIDLQDCFFNIKLHPEDCKRFAFSVPSPNFKRPYQRFQWKVLPQGMKNSPTLCQKFVDKAILTVRDKYQDS YIVHYMDDILLAHPSRSIVDEILTSMIQALNKHGLVVSTEKIQKYDNLKYLGTHIQGDSVSYQKLQIRTDKLRTLNDFQKLLGNINWIRPFLKLTTGELKPLF EILNPDSNPISTRKLTPEACKALQLMNERLSTARVKRLDLSQPWSLCILKTEYTPTACLWQDGVVEWIHLPHISPKVITPYDIFCTQLIIKGRHRSKELFSK DPDYIVVPYTKVQFDLLLQEKEDWPISLLGFLGEVHFHLPKDPLLTFTLQTAIIFPHMTSTTPLEKGIVIFTDGSANGRSVTYIQGREPIIKENTQNTAQQA EIVAVITAFEEVSQPFNLYTDSKYVTGLFPEIETATLSPRTKIYTELKHLQRLIHKRQEKFYIGHIRGHTGLPGPLAQGNAYADSLTRILT
MMTV B_P03 365_2 mutB_ WS	8,087	VQEISDSRPMLHIYLNGRRFLGLLDTGADKTCIAGRDWPANWPIHQTESSLQGLGMACGVARSSQPLRWQHEDKSGIIHPFVIPTLPFTLWGRDIMKDI KVRLMTDSPDDSQDLMIGAIESNLFADQISWKSDQPVWLNQWPLKQEKLQALQQLVTEQLQLGHLEESNSPWNTPVFVIKKKSGKWRLLQDLRAVNA TMHDMGALQPGLPSPPAVPKGWEIIIIDLQDCFFNIKLHPEDCKRFAFSVPSPNFKRPYQRFQWKVLPQGMKNSPTLCQKFVDKAILTVRDKYQDSYIV HYMDDILLAHPSRSIVDEILTSMIQALNKHGLVVSTEKIQKYDNLKYLGTHIQGDSVSYQKLQIRTDKLRTLNDFQKLLGNINWIRPFLKLTTGELKPLFEIL NPDSNPISTRKLTPEACKALQLMNERLSTARVKRLDLSQPWSLCILKTEYTPTACLWQDGVVEWIHLPHISPKVITPYDIFCTQLIIKGRHRSKELFSKDP DYIVVPYTKVQFDLLLQEKEDWPISLLGFLGEVHFHLPKDPLLTFTLQTAIIFPHMTSTTPLEKGIVIFTDGSANGRSVTYIQGREPIIKENTQNTAQQAEIV AVITAFEEVSQPFNLYTDSKYVTGLFPEIETATLSPRTKIYTELKHLQRLIHKRQEKFYIGHIRGHTGLPGPLAQGNAYADSLTRILTA
MMTV B_P03 365_2 mutB_ WS	8,088	VQEISDSRPMLHIYLNGRRFLGLLDTGADKTCIAGRDWPANWPIHQTESSLQGLGMACGVARSSQPLRWQHEDKSGIIHPFVIPTLPFTLWGRDIMKDI KVRLMTDSPDDSQDLMIGAIESNLFADQISWKSDQPVWLNQWPLKQEKLQALQQLVTEQLQLGHLEESNSPWNTPVFVIKKKSGKWRLLQDLRAVNA TMHDMGALQPGLPSPPAVPKGWEIIIIDLQDCFFNIKLHPEDCKRFAFSVPSPNFKRPYQRFQWKVLPQGMKNSPTLCQKFVDKAILTVRDKYQDSYIV HYMDDILLAHPSRSIVDEILTSMIQALNKHGLVVSTEKIQKYDNLKYLGTHIQGDSVSYQKLQIRTDKLRTLNDFQKLLGNINWIRPFLKLTTGELKPLFEIL NPDSNPISTRKLTPEACKALQLMNERLSTARVKRLDLSQPWSLCILKTEYTPTACLWQDGVVEWIHLPHISPKVITPYDIFCTQLIIKGRHRSKELFSKDP DYIVVPYTKVQFDLLLQEKEDWPISLLGFLGEVHFHLPKDPLLTFTLQTAIIFPHMTSTTPLEKGIVIFTDGSANGRSVTYIQGREPIIKENTQNTAQQAEIV AVITAFEEVSQPFNLYTDSKYVTGLFPEIETATLSPRTKIYTELKHLQRLIHKRQEKFYIGHIRGHTGLPGPLAQGNAYADSLTRILTA
MMTV B_P03 365_W S	8,089	VQEISDSRPMLHIYLNGRRFLGLLDTGADKTCIAGRDWPANWPIHQTESSLQGLGMACGVARSSQPLRWQHEDKSGIIHPFVIPTLPFTLWGRDIMKDI KVRLMTDSPDDSQDLMIGAIESNLFADQISWKSDQPVWLNQWPLKQEKLQALQQLVTEQLQLGHLEESNSPWNTPVFVIKKKSGKWRLLQDLRAVNA TMHDMGALQPGLPSPVAVPKGWEIIIIDLQDCFFNIKLHPEDCKRFAFSVPSPNFKRPYQRFQWKVLPQGMKNSPTLCQKFVDKAILTVRDKYQDSYIV HYMDDILLAHPSRSIVDEILTSMIQALNKHGLVVSTEKIQKYDNLKYLGTHIQGDSVSYQKLQIRTDKLRTLNDFQKLLGNINWIRPFLKLTTGELKPLFEIL NGDSNPISTRKLTPEACKALQLMNERLSTARVKRLDLSQPWSLCILKTEYTPTACLWQDGVVEWIHLPHISPKVITPYDIFCTQLIIKGRHRSKELFSKDP DYIVVPYTKVQFDLLLQEKEDWPISLLGFLGEVHFHLPKDPLLTFTLQTAIIFPHMTSTTPLEKGIVIFTDGSANGRSVTYIQGREPIIKENTQNTAQQAEIV AVITAFEEVSQPFNLYTDSKYVTGLFPEIETATLSPRTKIYTELKHLQRLIHKRQEKFYIGHIRGHTGLPGPLAQGNAYADSLTRILTA
MMTV B_P03 365_W S	8,090	VQEISDSRPMLHIYLNGRRFLGLLDTGADKTCIAGRDWPANWPIHQTESSLQGLGMACGVARSSQPLRWQHEDKSGIIHPFVIPTLPFTLWGRDIMKDI KVRLMTDSPDDSQDLMIGAIESNLFADQISWKSDQPVWLNQWPLKQEKLQALQQLVTEQLQLGHLEESNSPWNTPVFVIKKKSGKWRLLQDLRAVNA TMHDMGALQPGLPSPVAVPKGWEIIIIDLQDCFFNIKLHPEDCKRFAFSVPSPNFKRPYQRFQWKVLPQGMKNSPTLCQKFVDKAILTVRDKYQDSYIV HYMDDILLAHPSRSIVDEILTSMIQALNKHGLVVSTEKIQKYDNLKYLGTHIQGDSVSYQKLQIRTDKLRTLNDFQKLLGNINWIRPFLKLTTGELKPLFEIL NGDSNPISTRKLTPEACKALQLMNERLSTARVKRLDLSQPWSLCILKTEYTPTACLWQDGVVEWIHLPHISPKVITPYDIFCTQLIIKGRHRSKELFSKDP DYIVVPYTKVQFDLLLQEKEDWPISLLGFLGEVHFHLPKDPLLTFTLQTAIIFPHMTSTTPLEKGIVIFTDGSANGRSVTYIQGREPIIKENTQNTAQQAEIV AVITAFEEVSQPFNLYTDSKYVTGLFPEIETATLSPRTKIYTELKHLQRLIHKRQEKFYIGHIRGHTGLPGPLAQGNAYADSLTRILTA
MMTV B_P03 365-Pro	8,091	GRDIMKDIKVRLMTDSPDDSQDLMIGAIESNLFADQISWKSDQPVWLNQWPLKQEKLQALQQLVTEQLQLGHLEESNSPWNTPVFVIKKKSGKWRLL QDLRAVNATMHDMGALQPGLPSPVAVPKGWEIIIIDLQDCFFNIKLHPEDCKRFAFSVPSPNFKRPYQRFQWKVLPQGMKNSPTLCQKFVDKAILTVR DKYQDSYIVHYMDDILLAHPSRSIVDEILTSMIQALNKHGLVVSTEKIQKYDNLKYLGTHIQGDSVSYQKLQIRTDKLRTLNDFQKLLGNINWIRPFLKLTT GELKPLFEILNGDSNPISTRKLTPEACKALQLMNERLSTARVKRLDLSQPWSLCILKTEYTPTACLWQDGVVEWIHLPHISPKVITPYDIFCTQLIIKGRHR SKELFSKDPDYIVVPYTKVQFDLLLQEKEDWPISLLGFLGEVHFHLPKDPLLTFTLQTAIIFPHMTSTTPLEKGIVIFTDGSANGRSVTYIQGREPIIKENTQ NTAQQAEIVAVITAFEEVSQPFNLYTDSKYVTGLFPEIETATLSPRTKIYTELKHLQRLIHKRQEKFYIGHIRGHTGLPGPLAQGNAYADSLTRILT
MMTV B_P03 365-Pro	8,092	GRDIMKDIKVRLMTDSPDDSQDLMIGAIESNLFADQISWKSDQPVWLNQWPLKQEKLQALQQLVTEQLQLGHLEESNSPWNTPVFVIKKKSGKWRLL QDLRAVNATMHDMGALQPGLPSPVAVPKGWEIIIIDLQDCFFNIKLHPEDCKRFAFSVPSPNFKRPYQRFQWKVLPQGMKNSPTLCQKFVDKAILTVR DKYQDSYIVHYMDDILLAHPSRSIVDEILTSMIQALNKHGLVVSTEKIQKYDNLKYLGTHIQGDSVSYQKLQIRTDKLRTLNDFQKLLGNINWIRPFLKLTT GELKPLFEILNGDSNPISTRKLTPEACKALQLMNERLSTARVKRLDLSQPWSLCILKTEYTPTACLWQDGVVEWIHLPHISPKVITPYDIFCTQLIIKGRHR SKELFSKDPDYIVVPYTKVQFDLLLQEKEDWPISLLGFLGEVHFHLPKDPLLTFTLQTAIIFPHMTSTTPLEKGIVIFTDGSANGRSVTYIQGREPIIKENTQ NTAQQAEIVAVITAFEEVSQPFNLYTDSKYVTGLFPEIETATLSPRTKIYTELKHLQRLIHKRQEKFYIGHIRGHTGLPGPLAQGNAYADSLTRILT
MMTV B_P03 365-	8,093	GRDIMKDIKVRLMTDSPDDSQDLMIGAIESNLFADQISWKSDQPVWLNQWPLKQEKLQALQQLVTEQLQLGHLEESNSPWNTPVFVIKKKSGKWRLL QDLRAVNATMHDMGALQPGLPSPVAVPKGWEIIIIDLQDCFFNIKLHPEDCKRFAFSVPSPNFKRPYQRFQWKVLPQGMKNSPTLCQKFVDKAILTVR DKYQDSYIVHYMDDILLAHPSRSIVDEILTSMIQALNKHGLVVSTEKIQKYDNLKYLGTHIQGDSVSYQKLQIRTDKLRTLNDFQKLLGNINWIRPFLKLTT GELKPLFEILNPDSNPISTRKLTPEACKALQLMNERLSTARVKRLDLSQPWSLCILKTEYTPTACLWQDGVVEWIHLPHISPKVITPYDIFCTQLIIKGRHR

RT Name	SEQ ID NO:	RT amino acid sequence
Pro_2mut		SKELFSKDPDYIVVPYTKVQFDLLLQEKEDWPISLLGFLGEVHFHLPKDPLLTFTLQTAIIFPHMTSTTPLEKGIVIFTDGSANGRSVTYIQGREPIIKENTQ NTAQQAEIVAVITAFEEVSQPFNLYTDSKYVTGLFPEIETATLSPRTKIYTELKHLQRLIHKRQEKFYIGHIRGHTGLPGPLAQGNAYADSLTRILT
MMTV B_P0365-Pro_2mut	8,094	GRDIMKDIKVRLMTDSPDDSQDLMIGAIESNLFADQISWKSDQPVWLNQWPLKQEKLQALQQLVTEQLQLGHLEESNSPWNTPVFVIKKKSGKWRLL QDLRAVNATMHDMGALQPGLPSPVAVPKGWEIIIIDLQDCFFNIKLHPEDCKRFAFSVPSPNFKRPYQRFQWKVLPQGMKNSPTLCQKFVDKAILTVR DKYQDSYIVHYMDDILLAHPSRSIVDEILTSMIQALNKHGLVVSTEKIQKYDNLKYLGTHIQGDSVSYQKLQIRTDKLRTLNDFQKLLGNINWIRPFLKLTT GELKPLFEILNPDSNPISTRKLTPEACKALQLMNERLSTARVKRLDLSQPWSLCILKTEYTPTACLWQDGVVEWIHLPHISPKVITPYDIFCTQLIIKGRHR SKELFSKDPDYIVVPYTKVQFDLLLQEKEDWPISLLGFLGEVHFHLPKDPLLTFTLQTAIIFPHMTSTTPLEKGIVIFTDGSANGRSVTYIQGREPIIKENTQ NTAQQAEIVAVITAFEEVSQPFNLYTDSKYVTGLFPEIETATLSPRTKIYTELKHLQRLIHKRQEKFYIGHIRGHTGLPGPLAQGNAYADSLTRILT
MMTV B_P0365-Pro_2mutB	8,095	GRDIMKDIKVRLMTDSPDDSQDLMIGAIESNLFADQISWKSDQPVWLNQWPLKQEKLQALQQLVTEQLQLGHLEESNSPWNTPVFVIKKKSGKWRLL QDLRAVNATMHDMGALQPGLPSPVAPPKGWEIIIIDLQDCFFNIKLHPEDCKRFAFSVPSPNFKRPYQRFQWKVLPQGMKNSPTLCQKFVDKAILTVR DKYQDSYIVHYMDDILLAHPSRSIVDEILTSMIQALNKHGLVVSTEKIQKYDNLKYLGTHIQGDSVSYQKLQIRTDKLRTLNDFQKLLGNINWIRPFLKLTT GELKPLFEILNPDSNPISTRKLTPEACKALQLMNERLSTARVKRLDLSQPWSLCILKTEYTPTACLWQDGVVEWIHLPHISPKVITPYDIFCTQLIIKGRHR SKELFSKDPDYIVVPYTKVQFDLLLQEKEDWPISLLGFLGEVHFHLPKDPLLTFTLQTAIIFPHMTSTTPLEKGIVIFTDGSANGRSVTYIQGREPIIKENTQ NTAQQAEIVAVITAFEEVSQPFNLYTDSKYVTGLFPEIETATLSPRTKIYTELKHLQRLIHKRQEKFYIGHIRGHTGLPGPLAQGNAYADSLTRILT
MMTV B_P0365-Pro_2mutB	8,096	GRDIMKDIKVRLMTDSPDDSQDLMIGAIESNLFADQISWKSDQPVWLNQWPLKQEKLQALQQLVTEQLQLGHLEESNSPWNTPVFVIKKKSGKWRLL QDLRAVNATMHDMGALQPGLPSPVAPPKGWEIIIIDLQDCFFNIKLHPEDCKRFAFSVPSPNFKRPYQRFQWKVLPQGMKNSPTLCQKFVDKAILTVR DKYQDSYIVHYMDDILLAHPSRSIVDEILTSMIQALNKHGLVVSTEKIQKYDNLKYLGTHIQGDSVSYQKLQIRTDKLRTLNDFQKLLGNINWIRPFLKLTT GELKPLFEILNPDSNPISTRKLTPEACKALQLMNERLSTARVKRLDLSQPWSLCILKTEYTPTACLWQDGVVEWIHLPHISPKVITPYDIFCTQLIIKGRHR SKELFSKDPDYIVVPYTKVQFDLLLQEKEDWPISLLGFLGEVHFHLPKDPLLTFTLQTAIIFPHMTSTTPLEKGIVIFTDGSANGRSVTYIQGREPIIKENTQ NTAQQAEIVAVITAFEEVSQPFNLYTDSKYVTGLFPEIETATLSPRTKIYTELKHLQRLIHKRQEKFYIGHIRGHTGLPGPLAQGNAYADSLTRILT
MPMV_P07572	8,097	LTAAIDILAPQQCAEPITWKSDEPVWVDQWPLTNDKLAAAQQLVQEQLEAGHITESSSPWNTPIFVIKKKSGKWRLLQDLRAVNATMVLMGALQPGLP SPVAIPQGYLKIIIDLKDCFFSIPLHPSDQKRFAFSLPSTNFKEPMQRFQWKVLPQGMANSPTLCQKYVATAIHKVRHAWKQMYIIHYMDDILIAGKDGQ QVLQCFDQLKQELTAAGLHIAPEKVQLQDPYTYLGFELNGPKITNQKAVIRKDKLQTLNDFQKLLGDINWLRPYLKLTTGDLKPLFDTLKGDSDPNSHR SLSKEALASLEKVETAIAEQFVTHINYSLPLIFLIFNTALTPTGLFWQDNPIMWIHLPASPKKVLLPYYDAIADLIILGRDHSKKYFGIEPSTIIQPYSKSQIDW LMQNTEMWPIACASFVGILDNHYPPNKLIQFCKLHTFVFPQIISKTPLNNALLVFTDGSSTGMAAYTLTDTTIKFQTNLNSAQLVELQALIAVLSAFPNQPL NIYTDSAYLAHSIPLLETVAQIKHISETAKLFLQCQQLIYNRSIPFYIGHVRAHSGLPGPIAQGNQRADLATKIVASNINT
MPMV_P07572_2mutB	8,098	LTAAIDILAPQQCAEPITWKSDEPVWVDQWPLTNDKLAAAQQLVQEQLEAGHITESSSPWNTPIFVIKKKSGKWRLLQDLRAVNATMVLMGALQPGLP SPVAPPQGYLKIIIDLKDCFFSIPLHPSDQKRFAFSLPSTNFKEPMQRFQWKVLPQGMANSPTLCQKYVATAIHKVRHAWKQMYIIHYMDDILIAGKDGQ QVLQCFDQLKQELTAAGLHIAPEKVQLQDPYTYLGFELNGPKITNQKAVIRKDKLQTLNDFQKLLGDINWLRPYLKLTTGDLKPLFDTLKPDSDPNSHRS LSKEALASLEKVETAIAEQFVTHINYSLPLIFLIFNTALTPTGLFWQDNPIMWIHLPASPKKVLLPYYDAIADLIILGRDHSKKYFGIEPSTIIQPYSKSQIDWL MQNTEMWPIACASFVGILDNHYPPNKLIQFCKLHTFVFPQIISKTPLNNALLVFTDGSSTGMAAYTLTDTTIKFQTNLNSAQLVELQALIAVLSAFPNQPL NIYTDSAYLAHSIPLLETVAQIKHISETAKLFLQCQQLIYNRSIPFYIGHVRAHSGLPGPIAQGNQRADLATKIVASNINT
PERV_Q4VFZ2	8,099	TLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLL PVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNS PTIFDEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPT TAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKEKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVA YLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTH DCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAH VHGAIYKQRGLLTSAGREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLL
PERV_Q4VFZ2	8,100	TLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLL PVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNS PTIFDEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPT TAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKEKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVA YLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTH DCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAH VHGAIYKQRGLLTSAGREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLL
PERV_Q4VFZ2_3mut	8,101	TLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLL PVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNS PTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPT TAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVA YLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTH DCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAH VHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLL
PERV_Q4VFZ2_3mut	8,102	TLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLL PVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNS PTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPT TAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVA YLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTH DCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAH VHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLL
PERV_Q4VFZ2_3mutA_WS	8,103	LDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVR KPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIF NEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAK QVREFLGKAGFCRLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSK KLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQ LLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAI YKQRGWLTSAGREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLP

RT Name	SEQ ID NO:	RT amino acid sequence
PERV_Q4VFZ2_3mutA_WS	8,104	LDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVR KPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIF NEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAK QVREFLGKAGFCRLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSK KLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQ LLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAI YKQRGWLTSAGREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLP
SFV1_P23074	8,105	MDPLQLLQPLEAEIKGTKLKAHWNSGATITCVPEAFLEDERPIQTMLIKTIHGEKQQDVYYLTFKVQGRKVEAEVLASPYDYILLNPSDVPWLMKKPLQL TVLVPLHEYQERLLQQTALPKEQKELLQKLFLKYDALWQHWENQVGHRRIKPHNIATGTLAPRPQKQYPINPKAKPSIQIVIDDLLKQGVLIQQNSTMNT PVYPVPKPDGKWRMVLDYREVNKTIPLIAAQNQHSAGILSSIYRGKYKTTLDLTNGFWAHPITPESYWLTAFTWQGKQYCWTRLPQGFLNSPALFTAD VVDLLKEIPNVQAYVDDIYISHDDPQEHLEQLEKIFSILLNAGYVVSLKKSEIAQREVEFLGFNITKEGRGLTDTFKQKLLNITPPKDLKQLQSILGLLNFAR NFIPNYSELVKPLYTIVANANGKFISWTEDNSNQLQHIISVLNQADNLEERNPETRLIIKVNSSPSAGYIRYYNEGSKRPIMYVNYIFSKAEAKFTQTEKLL TTMHKGLIKAMDLAMGQEILVYSPIVSMTKIQRTPLPERKALPVRWITWMTYLEDPRIQFHYDKSLPELQQIPNVTEDVIAKTKHPSEFAMVFYTDGSAIK HPDVNKSHSAGMGIAQVQFIPEYKIVHQWSIPLGDHTAQLAEIAAVEFACKKALKISGPVLIVTDSFYVAESANKELPYWKSNGFLNNKKKPLRHVSKW KSIAECLQLKPDIIIMHEKGHQQPMTTLHTEGNNLADKLATQGSYVVH
SFV1_P23074_2mut	8,106	MDPLQLLQPLEAEIKGTKLKAHWNSGATITCVPEAFLEDERPIQTMLIKTIHGEKQQDVYYLTFKVQGRKVEAEVLASPYDYILLNPSDVPWLMKKPLQL TVLVPLHEYQERLLQQTALPKEQKELLQKLFLKYDALWQHWENQVGHRRIKPHNIATGTLAPRPQKQYPINPKAKPSIQIVIDDLLKQGVLIQQNSTMNT PVYPVPKPDGKWRMVLDYREVNKTIPLIAAQNQHSAGILSSIYRGKYKTTLDLTNGFWAHPITPESYWLTAFTWQGKQYCWTRLPQGFLNSPALFNAD VVDLLKEIPNVQAYVDDIYISHDDPQEHLEQLEKIFSILLNAGYVVSLKKSEIAQREVEFLGFNITKEGRGLTDTFKQKLLNITPPKDLKQLQSILGLLNFAR NFIPNYSELVKPLYTIVAPANGKFISWTEDNSNQLQHIISVLNQADNLEERNPETRLIIKVNSSPSAGYIRYYNEGSKRPIMYVNYIFSKAEAKFTQTEKLLT TMHKGLIKAMDLAMGQEILVYSPIVSMTKIQRTPLPERKALPVRWITWMTYLEDPRIQFHYDKSLPELQQIPNVTEDVIAKTKHPSEFAMVFYTDGSAIKH PDVNKSHSAGMGIAQVQFIPEYKIVHQWSIPLGDHTAQLAEIAAVEFACKKALKISGPVLIVTDSFYVAESANKELPYWKSNGFLNNKKKPLRHVSKWK SIAECLQLKPDIIIMHEKGHQQPMTTLHTEGNNLADKLATQGSYVVH
SFV1_P23074_2mutA	8,107	MDPLQLLQPLEAEIKGTKLKAHWNSGATITCVPEAFLEDERPIQTMLIKTIHGEKQQDVYYLTFKVQGRKVEAEVLASPYDYILLNPSDVPWLMKKPLQL TVLVPLHEYQERLLQQTALPKEQKELLQKLFLKYDALWQHWENQVGHRRIKPHNIATGTLAPRPQKQYPINPKAKPSIQIVIDDLLKQGVLIQQNSTMNT PVYPVPKPDGKWRMVLDYREVNKTIPLIAAQNQHSAGILSSIYRGKYKTTLDLTNGFWAHPITPESYWLTAFTWQGKQYCWTRLPQGFLNSPALFNAD VVDLLKEIPNVQAYVDDIYISHDDPQEHLEQLEKIFSILLNAGYVVSLKKSEIAQREVEFLGFNITKEGRGLTDTFKQKLLNITPPKDLKQLQSILGKLNFAR NFIPNYSELVKPLYTIVAPANGKFISWTEDNSNQLQHIISVLNQADNLEERNPETRLIIKVNSSPSAGYIRYYNEGSKRPIMYVNYIFSKAEAKFTQTEKLLT TMHKGLIKAMDLAMGQEILVYSPIVSMTKIQRTPLPERKALPVRWITWMTYLEDPRIQFHYDKSLPELQQIPNVTEDVIAKTKHPSEFAMVFYTDGSAIKH PDVNKSHSAGMGIAQVQFIPEYKIVHQWSIPLGDHTAQLAEIAAVEFACKKALKISGPVLIVTDSFYVAESANKELPYWKSNGFLNNKKKPLRHVSKWK SIAECLQLKPDIIIMHEKGHQQPMTTLHTEGNNLADKLATQGSYVVH
SFV1_P23074-Pro	8,108	VPWLMKKPLQLTVLVPLHEYQERLLQQTALPKEQKELLQKLFLKYDALWQHWENQVGHRRIKPHNIATGTLAPRPQKQYPINPKAKPSIQIVIDDLLKQ GVLIQQNSTMNTPVYPVPKPDGKWRMVLDYREVNKTIPLIAAQNQHSAGILSSIYRGKYKTTLDLTNGFWAHPITPESYWLTAFTWQGKQYCWTRLPQ GFLNSPALFTADVVDLLKEIPNVQAYVDDIYISHDDPQEHLEQLEKIFSILLNAGYVVSLKKSEIAQREVEFLGFNITKEGRGLTDTFKQKLLNITPPKDLKQ LQSILGLLNFARNFIPNYSELVKPLYTIVANANGKFISWTEDNSNQLQHIISVLNQADNLEERNPETRLIIKVNSSPSAGYIRYYNEGSKRPIMYVNYIFSKA EAKFTQTEKLLTTMHKGLIKAMDLAMGQEILVYSPIVSMTKIQRTPLPERKALPVRWITWMTYLEDPRIQFHYDKSLPELQQIPNVTEDVIAKTKHPSEFA MVFYTDGSAIKHPDVNKSHSAGMGIAQVQFIPEYKIVHQWSIPLGDHTAQLAEIAAVEFACKKALKISGPVLIVTDSFYVAESANKELPYWKSNGFLNNK KKPLRHVSKWKSIAECLQLKPDIIIMHEKGHQQPMTTLHTEGNNLADKLATQGSYVVH
SFV1_P23074-Pro_2mut	8,109	VPWLMKKPLQLTVLVPLHEYQERLLQQTALPKEQKELLQKLFLKYDALWQHWENQVGHRRIKPHNIATGTLAPRPQKQYPINPKAKPSIQIVIDDLLKQ GVLIQQNSTMNTPVYPVPKPDGKWRMVLDYREVNKTIPLIAAQNQHSAGILSSIYRGKYKTTLDLTNGFWAHPITPESYWLTAFTWQGKQYCWTRLPQ GFLNSPALFNADVVDLLKEIPNVQAYVDDIYISHDDPQEHLEQLEKIFSILLNAGYVVSLKKSEIAQREVEFLGFNITKEGRGLTDTFKQKLLNITPPKDLK QLQSILGLLNFARNFIPNYSELVKPLYTIVAPANGKFISWTEDNSNQLQHIISVLNQADNLEERNPETRLIIKVNSSPSAGYIRYYNEGSKRPIMYVNYIFSK AEAKFTQTEKLLTTMHKGLIKAMDLAMGQEILVYSPIVSMTKIQRTPLPERKALPVRWITWMTYLEDPRIQFHYDKSLPELQQIPNVTEDVIAKTKHPSEF AMVFYTDGSAIKHPDVNKSHSAGMGIAQVQFIPEYKIVHQWSIPLGDHTAQLAEIAAVEFACKKALKISGPVLIVTDSFYVAESANKELPYWKSNGFLNN KKKPLRHVSKWKSIAECLQLKPDIIIMHEKGHQQPMTTLHTEGNNLADKLATQGSYVVH
SFV1_P23074-Pro_2mutA	8,110	VPWLMKKPLQLTVLVPLHEYQERLLQQTALPKEQKELLQKLFLKYDALWQHWENQVGHRRIKPHNIATGTLAPRPQKQYPINPKAKPSIQIVIDDLLKQ GVLIQQNSTMNTPVYPVPKPDGKWRMVLDYREVNKTIPLIAAQNQHSAGILSSIYRGKYKTTLDLTNGFWAHPITPESYWLTAFTWQGKQYCWTRLPQ GFLNSPALFNADVVDLLKEIPNVQAYVDDIYISHDDPQEHLEQLEKIFSILLNAGYVVSLKKSEIAQREVEFLGFNITKEGRGLTDTFKQKLLNITPPKDLK QLQSILGLNFARNFIPNYSELVKPLYTIVAPANGKFISWTEDNSNQLQHIISVLNQADNLEERNPETRLIIKVNSSPSAGYIRYYNEGSKRPIMYVNYIFSK AEAKFTQTEKLLTTMHKGLIKAMDLAMGQEILVYSPIVSMTKIQRTPLPERKALPVRWITWMTYLEDPRIQFHYDKSLPELQQIPNVTEDVIAKTKHPSEF AMVFYTDGSAIKHPDVNKSHSAGMGIAQVQFIPEYKIVHQWSIPLGDHTAQLAEIAAVEFACKKALKISGPVLIVTDSFYVAESANKELPYWKSNGFLNN KKKPLRHVSKWKSIAECLQLKPDIIIMHEKGHQQPMTTLHTEGNNLADKLATQGSYVVH
SFV3L_P27401	8,111	MDPLQLLQPLEAEIKGTKLKAHWNSGATITCVPQAFLEEEVPIKNIWIKTIHGEKEQPVYYLTFKIQGRKVEAEVISSPYDYILVSPSDIPWLMKKPLQLTT LVPLQEYEERLLKQTMLTGSYKEKLQSLFLKYDALWQHWENQVGHRRIKPHHIATGTVNPRPQKQYPINPKAKASIQTVINDLLKQGVLIQQNSIMNTP VYPVPKPDGKWRMVLDYREVNKTIPLIAAQNQHSAGILSSIFRGKYKTTLDLSNGFWAHSITPESYWLTAFTWLGQQYCWTRLPQGFLNSPALFTADV VDLLKEVPNVQVYVDDIYISHDDPREHLEQLEKVFSLLLNAGYVVSLKKSEIAQHEVEFLGFNITKEGRGLTETFKQKLLNITPPRDLKQLQSILGLLNFAR NFIPNFSELVKPLYNIIATANGKYITWTTDNSQQLQNIISMLNSAENLEERNPEVRLIMKVNTSPSAGYIRFYNEFAKRPIMYLNYVYTKAEVKFTNTEKLL TTIHKGLIKALDLGMGQEILVYSPIVSMTKIQKTPLPERKALPIRWITWMSYLEDPRIQFHYDKTLPELQQVPTVTDDIIAKIKHPSEFSMVFYTDGSAIKHP NVNKSHNAGMGIAQVQFKPEFTVINTWSIPLGDHTAQLAEVAAVEFACKKALKIDGPVLIVTDSFYVAESVNKELPYWQSNGFFNNKKKPLKHVSKWK SIADCIQLKPDIIIIHEKGHQPTASTFHTEGNNLADKLATQGSYVVN
SFV3L_P27401_2mut	8,112	MDPLQLLQPLEAEIKGTKLKAHWNSGATITCVPQAFLEEEVPIKNIWIKTIHGEKEQPVYYLTFKIQGRKVEAEVISSPYDYILVSPSDIPWLMKKPLQLTT LVPLQEYEERLLKQTMLTGSYKEKLQSLFLKYDALWQHWENQVGHRRIKPHHIATGTVNPRPQKQYPINPKAKASIQTVINDLLKQGVLIQQNSIMNTP VYPVPKPDGKWRMVLDYREVNKTIPLIAAQNQHSAGILSSIFRGKYKTTLDLSNGFWAHSITPESYWLTAFTWLGQQYCWTRLPQGFLNSPALFNADV VDLLKEVPNVQVYVDDIYISHDDPREHLEQLEKVFSLLLNAGYVVSLKKSEIAQHEVEFLGFNITKEGRGLTETFKQKLLNITPPRDLKQLQSILGLLNFAR NFIPNFSELVKPLYNIIATAPGKYITWTTDNSQQLQNIISMLNSAENLEERNPEVRLIMKVNTSPSAGYIRFYNEFAKRPIMYLNYVYTKAEVKFTNTEKLL TTIHKGLIKALDLGMGQEILVYSPIVSMTKIQKTPLPERKALPIRWITWMSYLEDPRIQFHYDKTLPELQQVPTVTDDIIAKIKHPSEFSMVFYTDGSAIKHP

RT Name	SEQ ID NO:	RT amino acid sequence
		NVNKSHNAGMGIAQVQFKPEFTVINTWSIPLGDHTAQLAEVAAVEFACKKALKIDGPVLIVTDSFYVAESVNKELPYWQSNGFFNNKKKPLKHVSKWK SIADCIQLKPDIIIIHEKGHQPTASTFHTEGNNLADKLATQGSYVVN
SFV3L_P27401_2mutA	8,113	MDPLQLLQPLEAEIKGTKLKAHWNSGATITCVPQAFLEEEVPIKNIWIKTIHGEKEQPVYYLTFKIQGRKVEAEVISSPYDYILVSPSDIPWLMKKPLQLTT LVPLQEYEERLLKQTMLTGSYKEKLQSLFLKYDALWQHWENQVGHRRIKPHHIATGTVNPRPQKQYPINPKAKASIQTVINDLLKQGVLIQQNSIMNTP VYPVPKPDGKWRMVLDYREVNKTIPLIAAQNQHSAGILSSIFRGKYKTTLDLSNGFWAHSITPESYWLTAFTWLGQQYCWTRLPQGFLNSPALFNADV VDLLKEVPNVQVYVDDIYISHDDPREHLEQLEKVFSLLLNAGYVVSLKKSEIAQHEVEFLGFNITKEGRGLTETFKQKLLNITPPRDLKQLQSILGKLNFA RNFIPNFSELVKPLYNIIATAPGKYITWTTDNSQQLQNIISMLNSAENLEERNPEVRLIMKVNTSPSAGYIRFYNEFAKRPIMYLNYVYTKAEVKFTNTEKL LTTIHKGLIKALDLGMGQEILVYSPIVSMTKIQKTPLPERKALPIRWITWMSYLEDPRIQFHYDKTLPELQQVPTVTDDIIAKIKHPSEFSMVFYTDGSAIKH PNVNKSHNAGMGIAQVQFKPEFTVINTWSIPLGDHTAQLAEVAAVEFACKKALKIDGPVLIVTDSFYVAESVNKELPYWQSNGFFNNKKKPLKHVSKW KSIADCIQLKPDIIIIHEKGHQPTASTFHTEGNNLADKLATQGSYVVN
SFV3L_P27401-Pro	8,114	IPWLMKKPLQLTTLVPLQEYEERLLKQTMLTGSYKEKLQSLFLKYDALWQHWENQVGHRRIKPHHIATGTVNPRPQKQYPINPKAKASIQTVINDLLKQ GVLIQQNSIMNTPVYPVPKPDGKWRMVLDYREVNKTIPLIAAQNQHSAGILSSIFRGKYKTTLDLSNGFWAHSITPESYWLTAFTWLGQQYCWTRLPQ GFLNSPALFTADVVDLLKEVPNVQVYVDDIYISHDDPREHLEQLEKVFSLLLNAGYVVSLKKSEIAQHEVEFLGFNITKEGRGLTETFKQKLLNITPPRDL KQLQSILGLLNFARNFIPNFSELVKPLYNIIATANGKYITWTTDNSQQLQNIISMLNSAENLEERNPEVRLIMKVNTSPSAGYIRFYNEFAKRPIMYLNYVY TKAEVKFTNTEKLLTTIHKGLIKALDLGMGQEILVYSPIVSMTKIQKTPLPERKALPIRWITWMSYLEDPRIQFHYDKTLPELQQVPTVTDDIIAKIKHPSEF SMVFYTDGSAIKHPNVNKSHNAGMGIAQVQFKPEFTVINTWSIPLGDHTAQLAEVAAVEFACKKALKIDGPVLIVTDSFYVAESVNKELPYWQSNGFFN NKKKPLKHVSKWKSIADCIQLKPDIIIIHEKGHQPTASTFHTEGNNLADKLATQGSYVVN
SFV3L_P27401-Pro_2mut	8,115	IPWLMKKPLQLTTLVPLQEYEERLLKQTMLTGSYKEKLQSLFLKYDALWQHWENQVGHRRIKPHHIATGTVNPRPQKQYPINPKAKASIQTVINDLLKQ GVLIQQNSIMNTPVYPVPKPDGKWRMVLDYREVNKTIPLIAAQNQHSAGILSSIFRGKYKTTLDLSNGFWAHSITPESYWLTAFTWLGQQYCWTRLPQ GFLNSPALFNADVVDLLKEVPNVQVYVDDIYISHDDPREHLEQLEKVFSLLLNAGYVVSLKKSEIAQHEVEFLGFNITKEGRGLTETFKQKLLNITPPRDL KQLQSILGLLNFARNFIPNFSELVKPLYNIIATAPGKYITWTTDNSQQLQNIISMLNSAENLEERNPEVRLIMKVNTSPSAGYIRFYNEFAKRPIMYLNYVY TKAEVKFTNTEKLLTTIHKGLIKALDLGMGQEILVYSPIVSMTKIQKTPLPERKALPIRWITWMSYLEDPRIQFHYDKTLPELQQVPTVTDDIIAKIKHPSEF SMVFYTDGSAIKHPNVNKSHNAGMGIAQVQFKPEFTVINTWSIPLGDHTAQLAEVAAVEFACKKALKIDGPVLIVTDSFYVAESVNKELPYWQSNGFFN NKKKPLKHVSKWKSIADCIQLKPDIIIIHEKGHQPTASTFHTEGNNLADKLATQGSYVVN
SFV3L_P27401-Pro_2mutA	8,116	IPWLMKKPLQLTTLVPLQEYEERLLKQTMLTGSYKEKLQSLFLKYDALWQHWENQVGHRRIKPHHIATGTVNPRPQKQYPINPKAKASIQTVINDLLKQ GVLIQQNSIMNTPVYPVPKPDGKWRMVLDYREVNKTIPLIAAQNQHSAGILSSIFRGKYKTTLDLSNGFWAHSITPESYWLTAFTWLGQQYCWTRLPQ GFLNSPALFNADVVDLLKEVPNVQVYVDDIYISHDDPREHLEQLEKVFSLLLNAGYVVSLKKSEIAQHEVEFLGFNITKEGRGLTETFKQKLLNITPPRDL KQLQSILGKLNFARNFIPNFSELVKPLYNIIATAPGKYITWTTDNSQQLQNIISMLNSAENLEERNPEVRLIMKVNTSPSAGYIRFYNEFAKRPIMYLNYVY TKAEVKFTNTEKLLTTIHKGLIKALDLGMGQEILVYSPIVSMTKIQKTPLPERKALPIRWITWMSYLEDPRIQFHYDKTLPELQQVPTVTDDIIAKIKHPSEF SMVFYTDGSAIKHPNVNKSHNAGMGIAQVQFKPEFTVINTWSIPLGDHTAQLAEVAAVEFACKKALKIDGPVLIVTDSFYVAESVNKELPYWQSNGFFN NKKKPLKHVSKWKSIADCIQLKPDIIIIHEKGHQPTASTFHTEGNNLADKLATQGSYVVN
SFVCP_Q87040	8,117	MNPLQLLQPLPAEVKGTKLLAHWNSGATITCIPESFLEDEQPIKQTLIKTIHGEKQQNVYYLTFKVKGRKVEAEVIASPYEYILLSPTDVPWLTQQPLQLTI LVPLQEYQDRILNKTALPEEQKQQLKALFTKYDNLWQHWENQVGHRKIRPHNIATGDYPPRPQKQYPINPKAKPSIQIVIDDLLKQGVLTPQNSTMNTP VYPVPKPDGRWRMVLDYREVNKTIPLTAAQNQHSAGILATIVRQKYKTTLDLANGFWAHPITPDSYWLTAFTWQGKQYCWTRLPQGFLNSPALFTAD AVDLLKEVPNVQVYVDDIYLSHDNPHEHIQQLEKVFQILLQAGYVVSLKKSEIGQRTVEFLGFNITKEGRGLTDTFKTKLLNVTPPKDLKQLQSILGLLNF ARNFIPNFAELVQTLYNLIASSKGKYIEWTEDNTKQLNKVIEALNTASNLEERLPDQRLVIKVNTSPSAGYVRYYNESGKKPIMYLNYVFSKAELKFSMLE KLLTTMHKALIKAMDLAMGQEILVYSPIVSMTKIQKTPLPERKALPIRWITWMTYLEDPRIQFHYDKTLPELKHIPDVYTSSIPPLKHPSQYEGVFCTDGSA IKSPDPTKSNNAGMGIVHAIYNPEYKILNQWSIPLGHHTAQMAEIAAVEFACKKALKVPGPVLVITDSFYVAESANKELPYWKSNGFVNNKKEPLKHISK WKSIAECLSIKPDITIQHEKGHQPINTSIHTEGNALADKLATQGSYVVN
SFVCP_Q87040_2mut	8,118	MNPLQLLQPLPAEVKGTKLLAHWNSGATITCIPESFLEDEQPIKQTLIKTIHGEKQQNVYYLTFKVKGRKVEAEVIASPYEYILLSPTDVPWLTQQPLQLTI LVPLQEYQDRILNKTALPEEQKQQLKALFTKYDNLWQHWENQVGHRKIRPHNIATGDYPPRPQKQYPINPKAKPSIQIVIDDLLKQGVLTPQNSTMNTP VYPVPKPDGRWRMVLDYREVNKTIPLTAAQNQHSAGILATIVRQKYKTTLDLANGFWAHPITPDSYWLTAFTWQGKQYCWTRLPQGFLNSPALFNAD AVDLLKEVPNVQVYVDDIYLSHDNPHEHIQQLEKVFQILLQAGYVVSLKKSEIGQRTVEFLGFNITKEGRGLTDTFKTKLLNVTPPKDLKQLQSILGLLNF ARNFIPNFAELVQTLYNLIASSPGKYIEWTEDNTKQLNKVIEALNTASNLEERLPDQRLVIKVNTSPSAGYVRYYNESGKKPIMYLNYVFSKAELKFSMLE KLLTTMHKALIKAMDLAMGQEILVYSPIVSMTKIQKTPLPERKALPIRWITWMTYLEDPRIQFHYDKTLPELKHIPDVYTSSIPPLKHPSQYEGVFCTDGSA IKSPDPTKSNNAGMGIVHAIYNPEYKILNQWSIPLGHHTAQMAEIAAVEFACKKALKVPGPVLVITDSFYVAESANKELPYWKSNGFVNNKKEPLKHISK WKSIAECLSIKPDITIQHEKGHQPINTSIHTEGNALADKLATQGSYVVN
SFVCP_Q87040_2mutA	8,119	MNPLQLLQPLPAEVKGTKLLAHWNSGATITCIPESFLEDEQPIKQTLIKTIHGEKQQNVYYLTFKVKGRKVEAEVIASPYEYILLSPTDVPWLTQQPLQLTI LVPLQEYQDRILNKTALPEEQKQQLKALFTKYDNLWQHWENQVGHRKIRPHNIATGDYPPRPQKQYPINPKAKPSIQIVIDDLLKQGVLTPQNSTMNTP VYPVPKPDGRWRMVLDYREVNKTIPLTAAQNQHSAGILATIVRQKYKTTLDLANGFWAHPITPDSYWLTAFTWQGKQYCWTRLPQGFLNSPALFNAD AVDLLKEVPNVQVYVDDIYLSHDNPHEHIQQLEKVFQILLQAGYVVSLKKSEIGQRTVEFLGFNITKEGRGLTDTFKTKLLNVTPPKDLKQLQSILGKLNF ARNFIPNFAELVQTLYNLIASSPGKYIEWTEDNTKQLNKVIEALNTASNLEERLPDQRLVIKVNTSPSAGYVRYYNESGKKPIMYLNYVFSKAELKFSMLE KLLTTMHKALIKAMDLAMGQEILVYSPIVSMTKIQKTPLPERKALPIRWITWMTYLEDPRIQFHYDKTLPELKHIPDVYTSSIPPLKHPSQYEGVFCTDGSA IKSPDPTKSNNAGMGIVHAIYNPEYKILNQWSIPLGHHTAQMAEIAAVEFACKKALKVPGPVLVITDSFYVAESANKELPYWKSNGFVNNKKEPLKHISK WKSIAECLSIKPDITIQHEKGHQPINTSIHTEGNALADKLATQGSYVVN
SFVCP_Q87040-Pro	8,120	VPWLTQQPLQLTILVPLQEYQDRILNKTALPEEQKQQLKALFTKYDNLWQHWENQVGHRKIRPHNIATGDYPPRPQKQYPINPKAKPSIQIVIDDLLKQG VLTPQNSTMNTPVYPVPKPDGRWRMVLDYREVNKTIPLTAAQNQHSAGILATIVRQKYKTTLDLANGFWAHPITPDSYWLTAFTWQGKQYCWTRLPQ GFLNSPALFTADAVDLLKEVPNVQVYVDDIYLSHDNPHEHIQQLEKVFQILLQAGYVVSLKKSEIGQRTVEFLGFNITKEGRGLTDTFKTKLLNVTPPKDL KQLQSILGLLNFARNFIPNFAELVQTLYNLIASSKGKYIEWTEDNTKQLNKVIEALNTASNLEERLPDQRLVIKVNTSPSAGYVRYYNESGKKPIMYLNYV FSKAELKFSMLEKLLTTMHKALIKAMDLAMGQEILVYSPIVSMTKIQKTPLPERKALPIRWITWMTYLEDPRIQFHYDKTLPELKHIPDVYTSSIPPLKHPS QYEGVFCTDGSAIKSPDPTKSNNAGMGIVHAIYNPEYKILNQWSIPLGHHTAQMAEIAAVEFACKKALKVPGPVLVITDSFYVAESANKELPYWKSNGF VNNKKEPLKHISKWKSIAECLSIKPDITIQHEKGHQPINTSIHTEGNALADKLATQGSYVVN
SFVCP_Q87040-Pro_2mut	8,121	VPWLTQQPLQLTILVPLQEYQDRILNKTALPEEQKQQLKALFTKYDNLWQHWENQVGHRKIRPHNIATGDYPPRPQKQYPINPKAKPSIQIVIDDLLKQG VLTPQNSTMNTPVYPVPKPDGRWRMVLDYREVNKTIPLTAAQNQHSAGILATIVRQKYKTTLDLANGFWAHPITPDSYWLTAFTWQGKQYCWTRLPQ GFLNSPALFNADAVDLLKEVPNVQVYVDDIYLSHDNPHEHIQQLEKVFQILLQAGYVVSLKKSEIGQRTVEFLGFNITKEGRGLTDTFKTKLLNVTPPKDL KQLQSILGLLNFARNFIPNFAELVQTLYNLIASSPGKYIEWTEDNTKQLNKVIEALNTASNLEERLPDQRLVIKVNTSPSAGYVRYYNESGKKPIMYLNYV FSKAELKFSMLEKLLTTMHKALIKAMDLAMGQEILVYSPIVSMTKIQKTPLPERKALPIRWITWMTYLEDPRIQFHYDKTLPELKHIPDVYTSSIPPLKHPS

RT Name	SEQ ID NO:	RT amino acid sequence
		QYEGVFCTDGSAIKSPDPTKSNNAGMGIVHAIYNPEYKILNQWSIPLGHHTAQMAEIAAVEFACKKALKVPGPVLVITDSFYVAESANKELPYWKSNGF VNNKKEPLKHISKWKSIAECLSIKPDITIQHEKGHQPINTSIHTEGNALADKLATQGSYVVN
SFVCP_Q87040-Pro_2mutA	8,122	VPWLTQQPLQLTILVPLQEYQDRILNKTALPEEQKQQLKALFTKYDNLWQHWENQVGHRKIRPHNIATGDYPPRPQKQYPINPKAKPSIQIVIDDLLKQG VLTPQNSTMNTPVYPVPKPDGRWRMVLDYREVNKTIPLTAAQNQHSAGILATIVRQKYKTTLDLANGFWAHPITPDSYWLTAFTWQGKQYCWTRLPQ GFLNSPALFNADAVDLLKEVPNVQVYVDDIYLSHDNPHEHIQQLEKVFQILLQAGYVVSLKKSEIGQRTVEFLGFNITKEGRGLTDTFKTKLLNVTPPKDL KQLQSILGKLNFARNFIPNFAELVQTLYNLIASSPGKYIEWTEDNTKQLNKVIEALNTASNLEERLPDQRLVIKVNTSPSAGYVRYYNESGKKPIMYLNYV FSKAELKFSMLEKLLTTMHKALIKAMDLAMGQEILVYSPIVSMTKIQKTPLPERKALPIRWITWMTYLEDPRIQFHYDKTLPELKHIPDVYTSSIPPLKHPS QYEGVFCTDGSAIKSPDPTKSNNAGMGIVHAIYNPEYKILNQWSIPLGHHTAQMAEIAAVEFACKKALKVPGPVLVITDSFYVAESANKELPYWKSNGF VNNKKEPLKHISKWKSIAECLSIKPDITIQHEKGHQPINTSIHTEGNALADKLATQGSYVVN
SMRVH_P03364	8,123	PRSRAIDIPVPHADKISWKITDPVWVDQWPLTYEKTLAAIALVQEQLAAGHIEPTNSPWNTPIFIIKKKSGSWRLLQDLRAVNKVMVPMGALQPGLPSPV AIPLNYHKIVIDLKDCFFTIPLHPEDRPYFAFSVPQINFQSPMPRYQWKVLPQGMANSPTLCQKFVAAAIAPVRSQWPEAYILHYMDDILLACDSAEAAK ACYAHIISCLTSYGLKIAPDKVQVSEPFSYLGFELHHQQVFTPRVCLKTDHLKTLNDFQKLLGDIQWLRPYLKLPTSALVPLNNILKGDPNPLSVRALTPE AKQSLALINKAIQNQSVQQISYNLPLVLLLLPTPHTPTAVFWQPNGTDPTKNGSPLLWLHLPASPSKVLLTYPSLLAMLIIKGRYTGRQLFGRDPHSIIIPY TQDQLTWLLQTSDEWAIALSSFTGDIDNHYPSDPVIQFAKLHQFIFPKITKCAPIPQATLVFTDGSSNGIAAYVIDNQPISIKSPYLSAQLVELYAILQVFTV LAHQPFNLYTDSAYIAQSVPLLETVPFIKSSTNATPLFSKLQQLILNRQHPFFIGHLRAHLNLPGPLAEGNALADAATQIFPIISD
SMRVH_P03364_2mut	8,124	PRSRAIDIPVPHADKISWKITDPVWVDQWPLTYEKTLAAIALVQEQLAAGHIEPTNSPWNTPIFIIKKKSGSWRLLQDLRAVNKVMVPMGALQPGLPSPV AIPLNYHKIVIDLKDCFFTIPLHPEDRPYFAFSVPQINFQSPMPRYQWKVLPQGMANSPTLCQKFVAAAIAPVRSQWPEAYILHYMDDILLACDSAEAAK ACYAHIISCLTSYGLKIAPDKVQVSEPFSYLGFELHHQQVFTPRVCLKTDHLKTLNDFQKLLGDIQWLRPYLKLPTSALVPLNNILKPDPNPLSVRALTPE AKQSLALINKAIQNQSVQQISYNLPLVLLLLPTPHTPTAVFWQPNGTDPTKNGSPLLWLHLPASPSKVLLTYPSLLAMLIIKGRYTGRQLFGRDPHSIIIPY TQDQLTWLLQTSDEWAIALSSFTGDIDNHYPSDPVIQFAKLHQFIFPKITKCAPIPQATLVFTDGSSNGIAAYVIDNQPISIKSPYLSAQLVELYAILQVFTV LAHQPFNLYTDSAYIAQSVPLLETVPFIKSSTNATPLFSKLQQLILNRQHPFFIGHLRAHLNLPGPLAEGNALADAATQIFPIISD
SMRVH_P03364_2mutB	8,125	PRSRAIDIPVPHADKISWKITDPVWVDQWPLTYEKTLAAIALVQEQLAAGHIEPTNSPWNTPIFIIKKKSGSWRLLQDLRAVNKVMVPMGALQPGLPSPV APPLNYHKIVIDLKDCFFTIPLHPEDRPYFAFSVPQINFQSPMPRYQWKVLPQGMANSPTLCQKFVAAAIAPVRSQWPEAYILHYMDDILLACDSAEAAK ACYAHIISCLTSYGLKIAPDKVQVSEPFSYLGFELHHQQVFTPRVCLKTDHLKTLNDFQKLLGDIQWLRPYLKLPTSALVPLNNILKPDPNPLSVRALTPE AKQSLALINKAIQNQSVQQISYNLPLVLLLLPTPHTPTAVFWQPNGTDPTKNGSPLLWLHLPASPSKVLLTYPSLLAMLIIKGRYTGRQLFGRDPHSIIIPY TQDQLTWLLQTSDEWAIALSSFTGDIDNHYPSDPVIQFAKLHQFIFPKITKCAPIPQATLVFTDGSSNGIAAYVIDNQPISIKSPYLSAQLVELYAILQVFTV LAHQPFNLYTDSAYIAQSVPLLETVPFIKSSTNATPLFSKLQQLILNRQHPFFIGHLRAHLNLPGPLAEGNALADAATQIFPIISD
SRV2_P51517	8,126	LATAVDILAPQRYADPITWKSDEPVWVDQWPLTQEKLAAAQQLVQEQLQAGHIIESNSPWNTPIFVIKKKSGKWRLLQDLRAVNATMVLMGALQPGLP SPVAIPQGYFKIVIDLKDCFFTIPLQPVDQKRFAFSLPSTNFKQPMKRYQWKVLPQGMANSPTLCQKYVAAAIEPVRKSWAQMYIIHYMDDILIAGKLGE QVLQCFAQLKQALTTTGLQIAPEKVQLQDPYTYLGFQINGPKITNQKAVIRRDKLQTLNDFQKLLGDINWLRPYLHLTTGDLKPLFDILKGDSNPNSPRS LSEAALASLQKVETAIAEQFVTQIDYTQPLTFLIFNTTLTPTGLFWQNNPVMWVHLPASPKKVLLPYYDAIADLIILGRDNSKKYFGLEPSTIIQPYSKSQIH WLMQNTETWPIACASYAGNIDNHYPPNKLIQFCKLHAVVFPRIISKTPLDNALLVFTDGSSTGIAAYTFEKTTVRFKTSHTSAQLVELQALIAVLSAFPHR ALNVYTDSAYLAHSIPLLETVSHIKHISDTAKFFLQCQQLIYNRSIPFYLGHIRAHSGLPGPLSQGNHITDLATKVVATTLTT
SRV2_P51517_2mutB	8,127	LATAVDILAPQRYADPITWKSDEPVWVDQWPLTQEKLAAAQQLVQEQLQAGHIIESNSPWNTPIFVIKKKSGKWRLLQDLRAVNATMVLMGALQPGLP SPVAPPQGYFKIVIDLKDCFFTIPLQPVDQKRFAFSLPSTNFKQPMKRYQWKVLPQGMANSPTLCQKYVAAAIEPVRKSWAQMYIIHYMDDILIAGKLGE QVLQCFAQLKQALTTTGLQIAPEKVQLQDPYTYLGFQINGPKITNQKAVIRRDKLQTLNDFQKLLGDINWLRPYLHLTTGDLKPLFDILKGDSNPNSPRS LSEAALASLQKVETAIAEQFVTQIDYTQPLTFLIFNTTLTPTGLFWQNNPVMWVHLPASPKKVLLPYYDAIADLIILGRDNSKKYFGLEPSTIIQPYSKSQIH WLMQNTETWPIACASYAGNIDNHYPPNKLIQFCKLHAVVFPRIISKTPLDNALLVFTDGSSTGIAAYTFEKTTVRFKTSHTSAQLVELQALIAVLSAFPHR ALNVYTDSAYLAHSIPLLETVSHIKHISDTAKFFLQCQQLIYNRSIPFYLGHIRAHSGLPGPLSQGNHITDLATKVVATTLTT
WDSV_O92815	8,128	SCQTKNTLNIDEYLLQFPDQLWASLPTDIGRMLVPPITIKIKDNASLPSIRQYPLPKDKTEGLRPLISSLENQGILIKCHSPCNTPIFPIKKAGRDEYRMIHD LRAINNIVAPLTAVVASPTTVLSNLAPSLHWFTVIDLSNAFFSVPIHKDSQYLFAFTFEGHQYTWTVLPQGFIHSPTLFSQALYQSLHKIKFKISSEICIYMD DVLIASKDRDTNLKDTAVMLQHLASEGHKVSKKKLQLCQQEVVYLGQLLTPEGRKILPDRKVTVSQFQQPTTIRQIRAFLGLVGYCRHWIPEFSIHSKFL EKQLKKDTAEPFQLDDQQVEAFNKLKHAITTAPVLVVPDPAKPFQLYTSHSEHASIAVLTQKHAGRTRPIAFLSSKFDAIESGLPPCLKACASIHRSLTQA DSFILGAPLIIYTTHAICTLLQRDRSQLVTASRFSKWEADLLRPELTFVACSAVSPAHLYMQSCENNIPPHDCVLLTHTISRPRPDLSDLPIPDPDMTLFSD GSYTTGRGGAAVVMHRPVTDDFIIIHQQPGGASAQTAELLALAAACHLATDKTVNIYTDSRYAYGVVHDFGHLWMHRGFVTSAGTPIKNHKEIEYLLKQ IMKPKQVSVIKIEAHTKGVSMEVRGNAAADEAAKNAVFLVQR
WDSV_O92815_2mut	8,129	SCQTKNTLNIDEYLLQFPDQLWASLPTDIGRMLVPPITIKIKDNASLPSIRQYPLPKDKTEGLRPLISSLENQGILIKCHSPCNTPIFPIKKAGRDEYRMIHD LRAINNIVAPLTAVVASPTTVLSNLAPSLHWFTVIDLSNAFFSVPIHKDSQYLFAFTFEGHQYTWTVLPQGFIHSPTLFNQALYQSLHKIKFKISSEICIYMD DVLIASKDRDTNLKDTAVMLQHLASEGHKVSKKKLQLCQQEVVYLGQLLTPEGRKILPDRKVTVSQFQQPTTIRQIRAFLGLVGYCRHWIPEFSIHSKFL EKQLKPDTAEPFQLDDQQVEAFNKLKHAITTAPVLVVPDPAKPFQLYTSHSEHASIAVLTQKHAGRTRPIAFLSSKFDAIESGLPPCLKACASIHRSLTQA DSFILGAPLIIYTTHAICTLLQRDRSQLVTASRFSKWEADLLRPELTFVACSAVSPAHLYMQSCENNIPPHDCVLLTHTISRPRPDLSDLPIPDPDMTLFSD GSYTTGRGGAAVVMHRPVTDDFIIIHQQPGGASAQTAELLALAAACHLATDKTVNIYTDSRYAYGVVHDFGHLWMHRGFVTSAGTPIKNHKEIEYLLKQ IMKPKQVSVIKIEAHTKGVSMEVRGNAAADEAAKNAVFLVQR
WDSV_O92815_2mutA	8,130	SCQTKNTLNIDEYLLQFPDQLWASLPTDIGRMLVPPITIKIKDNASLPSIRQYPLPKDKTEGLRPLISSLENQGILIKCHSPCNTPIFPIKKAGRDEYRMIHD LRAINNIVAPLTAVVASPTTVLSNLAPSLHWFTVIDLSNAFFSVPIHKDSQYLFAFTFEGHQYTWTVLPQGFIHSPTLFNQALYQSLHKIKFKISSEICIYMD DVLIASKDRDTNLKDTAVMLQHLASEGHKVSKKKLQLCQQEVVYLGQLLTPEGRKILPDRKVTVSQFQQPTTIRQIRAFLGKVGYCRHFIPEFSIHSKFL EKQLKPDTAEPFQLDDQQVEAFNKLKHAITTAPVLVVPDPAKPFQLYTSHSEHASIAVLTQKHAGRTRPIAFLSSKFDAIESGLPPCLKACASIHRSLTQA DSFILGAPLIIYTTHAICTLLQRDRSQLVTASRFSKWEADLLRPELTFVACSAVSPAHLYMQSCENNIPPHDCVLLTHTISRPRPDLSDLPIPDPDMTLFSD GSYTTGRGGAAVVMHRPVTDDFIIIHQQPGGASAQTAELLALAAACHLATDKTVNIYTDSRYAYGVVHDFGHLWMHRGFVTSAGTPIKNHKEIEYLLKQ IMKPKQVSVIKIEAHTKGVSMEVRGNAAADEAAKNAVFLVQR
WMSV_P03359	8,131	VLNLEEEYRLHEKPVPSSIDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMSKEAREGIRPHIQRFLDLGVLVPCQSPWNTPLL PVKKPGTNDYRPVQDLREINKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSP TLFDEALHRDLAPFRALNPQVVLLQYVDDLLVAAPTYRDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLLKEGKRWLTPARKATVMKIPPP TTPRQVREFLGTAGFCRLWIPGFASLAAPLYPLTKESIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVAY LSKKLDPVASGWPTCLKAVAAVALLLKDADKLTLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVH RCSEILAEETGTRRDLKDQPLPGVPAWYTDGSSFIAEGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDINIYTDSRYAFATAHI HGAIYKQRGLLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKP

RT Name	SEQ ID NO:	RT amino acid sequence
WMSV_P03359_3mut	8,132	VLNLEEEYRLHEKPVPSSIDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMSKEAREGIRPHIQRFLDLGVLVPCQSPWNTPLL PVKKPGTNDYRPVQDLREINKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSP TLFNEALHRDLAPFRALNPQVVLLQYVDDLLVAAPTYRDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLLKEGKRWLTPARKATVMKIPPP TTPRQVREFLGTAGFCRLWIPGFASLAAPLYPLTKPSIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVAY LSKKLDPVASGWPTCLKAVAAVALLLKDADKLTLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVH RCSEILAEETGTRRDLKDQPLPGVPAWYTDGSSFIAEGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDINIYTDSRYAFATAHI HGAIYKQRGWLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKP
WMSV_P03359_3mutA	8,133	VLNLEEEYRLHEKPVPSSIDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMSKEAREGIRPHIQRFLDLGVLVPCQSPWNTPLL PVKKPGTNDYRPVQDLREINKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSP TLFNEALHRDLAPFRALNPQVVLLQYVDDLLVAAPTYRDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLLKEGKRWLTPARKATVMKIPPP TTPRQVREFLGKAGFCRLFIPGFASLAAPLYPLTKPSIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVAY LSKKLDPVASGWPTCLKAVAAVALLLKDADKLTLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVH RCSEILAEETGTRRDLKDQPLPGVPAWYTDGSSFIAEGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDINIYTDSRYAFATAHI HGAIYKQRGWLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKP
XMRV6_A1Z651	8,134	TLNIEDEYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLP VKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPT LFDEALHRDLADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPK TPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKTGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVA YLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEA PHDCLEILAETHGTRPDLTDQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFAT AHVHGEIYRRRGLLTSEGREIKNKNEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLL
XMRV6_A1Z651_3mut	8,135	TLNIEDEYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLP VKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPT LFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPK TPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPV AYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKE APHDCLEILAETHGTRPDLTDQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAF ATAHVHGEIYRRRGWLTSEGREIKNKNEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLL
XMRV6_A1Z651_3mutA	8,136	TLNIEDEYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLP VKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPT LFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPK TPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVA YLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEA PHDCLEILAETHGTRPDLTDQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFAT AHVHGEIYRRRGWLTSEGREIKNKNEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLL

In some embodiments, reverse transcriptase domains are modified, for example by site-specific mutation. In some embodiments, reverse transcriptase domains are engineered to have improved properties, e.g. SuperScript IV (SSIV) reverse transcriptase derived from the MMLV RT. In some embodiments, the reverse transcriptase domain may be engineered to have lower error rates, e.g., as described in WO2001068895, incorporated herein by reference. In some embodiments, the reverse transcriptase domain may be engineered to be more thermostable. In some embodiments, the reverse transcriptase domain may be engineered to be more processive. In some embodiments, the reverse transcriptase domain may be engineered to have tolerance to inhibitors. In some embodiments, the reverse transcriptase domain may be engineered to be faster. In some embodiments, the reverse transcriptase domain may be engineered to better tolerate modified nucleotides in the RNA template. In some embodiments, the reverse transcriptase domain may be engineered to insert modified DNA nucleotides. In some embodiments, the reverse transcriptase domain is engineered to bind a template RNA. In some embodiments, one or more mutations are chosen from D200N, L603W, T330P, D524G, E562Q,

D583N, P51L, S67R, E67K, T197A, H204R, E302K, F309N, W313F, L435G, N454K, H594Q, L671P, E69K, H8Y, T306K, or D653N in the RT domain of murine leukemia virus reverse transcriptase or a corresponding mutation at a corresponding position of another RT domain.

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

M-MLV (WT):

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

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

TLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSI
KQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNK
RVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGIS
GQLTWTRLPQGFKNSPTLFDEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQG
TRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKT
PRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKTGTLFNWGPDQQKAYQEIKQALLTAP
ALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRM
VAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDR

VQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSL LQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRY AFATAHIHGEIYRRRGLLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEAR GNRMADQAARKAAITETPDTSTLL (SEQ ID NO: 5003)

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

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

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

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

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

including T306K and W313F. In some embodiments, an M-MLV RT used herein comprises the mutations D200N, L603W, T330P, T306K and W313F. In embodiments, the mutant M-MLV RT comprises the following amino acid sequence:

M-MLV (PE2):
TLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSI
KQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNK
RVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGIS
GQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQG
TRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKT
PRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAP
ALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRM
VAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDR
VQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSL
LQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRY
AFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEAR
GNRMADQAARKAAITETPDTSTLLI (SEQ ID NO: 5005)

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

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

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

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

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

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

In embodiments, quantifying integrations in cells comprises counting the fraction of integrations that contain at least about 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% of the DNA sequence corresponding to the template RNA (e.g., a template RNA having a

length of at least 0.05, 0.1, 0.5, 0.6, 0.7, 0.8, 0.9, 1, 1.5, 2, 3, 4, or 5 kb, e.g., a length between 0.5-0.6, 0.6-0.7, 0.7-0.8, 0.8-0.9, 1.0-1.2, 1.2-1.4, 1.4-1.6, 1.6-1.8, 1.8-2.0, 2-3, 3-4, or 4-5 kb).

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

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

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

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

In some embodiments, the reverse transcriptase domain specifically binds a specific RNA template with higher frequency (e.g., about 5 or 10-fold higher frequency) than any endogenous

cellular RNA, e.g., when expressed in cells (e.g., HEK293T cells). In embodiments, frequency of specific binding between the reverse transcriptase domain and the template RNA are measured by CLIP-seq, e.g., as described in Lin and Miles (2019) *Nucleic Acids Res* 47(11):5490-5501 (incorporated herein by reference in its entirety).

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

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

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

FOAMV_P14350-Pro_2mut	T207N	S331P				
FOAMV_P14350-Pro_2mutA	T207N	S331P	L307K			
GALV_P21414						
GALV_P21414_3mut	D198N	E328P	L600W			
GALV_P21414_3mutA	D198N	E328P	L600W	T304K	W311F	
HTL1A_P03362						
HTL1A_P03362_2mut	E152Q	R279P				
HTL1A_P03362_2mutB	E152Q	R279P	L90P			
HTL1C_P14078						
HTL1C_P14078_2mut	E152Q	R279P				
HTL1L_P0C211						
HTL1L_P0C211_2mut	E149Q	L527W				
HTL1L_P0C211_2mutB	E149Q	L527W	L87P			
HTL32_Q0R5R2						
HTL32_Q0R5R2_2mut	E149Q	L526W				
HTL32_Q0R5R2_2mutB	E149Q	L526W	L87P			
HTL3P_Q4U0X6						
HTL3P_Q4U0X6_2mut	E149Q	L526W				
HTL3P_Q4U0X6_2mutB	E149Q	L526W	L87P			
HTLV2_P03363_2mut	E147Q	G274P				
JSRV_P31623						
JSRV_P31623_2mutB	A100P					
KORV_Q9TTC1	D32N					
KORV_Q9TTC1_3mut	D32N	D322N	E452P	L724W		
KORV_Q9TTC1_3mutA	D32N	D322N	E452P	L724W	T428K	W435F
KORV_Q9TTC1-Pro						
KORV_Q9TTC1-Pro_3mut	D231N	E361P	L633W			
KORV_Q9TTC1-Pro_3mutA	D231N	E361P	L633W	T337K	W344F	
MLVAV_P03356						
MLVAV_P03356_3mut	D200N	T330P	L603W			
MLVAV_P03356_3mutA	D200N	T330P	L603W	T306K	W313F	
MLVBM_Q7SVK7						
MLVBM_Q7SVK7						
MLVBM_Q7SVK7_3mut	D200N	T330P	L603W			
MLVBM_Q7SVK7_3mut	D200N	T330P	L603W			
MLVBM_Q7SVK7_3mutA_WS	D199N	T329P	L602W	T305K	W312F	
MLVBM_Q7SVK7_3mutA_WS	D199N	T329P	L602W	T305K	W312F	
MLVCB_P08361						
MLVCB_P08361_3mut	D200N	T330P	L603W			

MLVCB_P08361_3mutA	D200N	T330P	L603W	T306K	W313F	
MLVF5_P26810						
MLVF5_P26810_3mut	D200N	T330P	L603W			
MLVF5_P26810_3mutA	D200N	T330P	L603W	T306K	W313F	
MLVFF_P26809_3mut	D200N	T330P	L603W			
MLVFF_P26809_3mutA	D200N	T330P	L603W	T306K	W313F	
MLVMS_P03355						
MLVMS_P03355						
MLVMS_P03355_3mut	D200N	T330P	L603W			
MLVMS_P03355_3mut	D200N	T330P	L603W			
MLVMS_P03355_3mutA_WS	D200N	T330P	L603W	T306K	W313F	
MLVMS_P03355_3mutA_WS	D200N	T330P	L603W	T306K	W313F	
MLVMS_P03355_PLV919	D200N	T330P	L603W	T306K	W313F	H8Y
MLVMS_P03355_PLV919	D200N	T330P	L603W	T306K	W313F	H8Y
MLVRD_P11227						
MLVRD_P11227_3mut	D200N	T330P	L603W			
MMTVB_P03365	D26N					
MMTVB_P03365	D26N					
MMTVB_P03365_2mut	D26N	G401P				
MMTVB_P03365_2mut_WS	G400P					
MMTVB_P03365_2mut_WS	G400P					
MMTVB_P03365_2mutB	D26N	G401P	V215P			
MMTVB_P03365_2mutB	D26N	G401P	V215P			
MMTVB_P03365_2mutB_WS	G400P	V212P				
MMTVB_P03365_2mutB_WS	G400P	V212P				
MMTVB_P03365_WS						
MMTVB_P03365_WS						
MMTVB_P03365-Pro						
MMTVB_P03365-Pro						
MMTVB_P03365-Pro_2mut	G309P					
MMTVB_P03365-Pro_2mut	G309P					
MMTVB_P03365-Pro_2mutB	G309P	V123P				
MMTVB_P03365-Pro_2mutB	G309P	V123P				
MPMV_P07572						
MPMV_P07572_2mutB	G289P	I103P				
PERV_Q4VFZ2						
PERV_Q4VFZ2						
PERV_Q4VFZ2_3mut	D199N	E329P	L602W			
PERV_Q4VFZ2_3mut	D199N	E329P	L602W			

PERV_Q4VFZ2_3mutA_WS	D196N	E326P	L599W	T302K	W309F	
PERV_Q4VFZ2_3mutA_WS	D196N	E326P	L599W	T302K	W309F	
SFV1_P23074	D24N					
SFV1_P23074_2mut	D24N	T296N	N420P			
SFV1_P23074_2mutA	D24N	T296N	N420P	L396K		
SFV1_P23074-Pro						
SFV1_P23074-Pro_2mut	T207N	N331P				
SFV1_P23074-Pro_2mutA	T207N	N331P	L307K			
SFV3L_P27401	D24N					
SFV3L_P27401_2mut	D24N	T296N	N422P			
SFV3L_P27401_2mutA	D24N	T296N	N422P	L396K		
SFV3L_P27401-Pro						
SFV3L_P27401-Pro_2mut	T307N	N333P				
SFV3L_P27401-Pro_2mutA	T307N	N333P	L307K			
SFVCP_Q87040	D24N					
SFVCP_Q87040_2mut	D24N	T296N	K422P			
SFVCP_Q87040_2mutA	D24N	T296N	K422P	L396K		
SFVCP_Q87040-Pro						
SFVCP_Q87040-Pro_2mut	T207N	K333P				
SFVCP_Q87040-Pro_2mutA	T207N	K333P	L307K			
SMRVH_P03364						
SMRVH_P03364_2mut	G288P					
SMRVH_P03364_2mutB	G288P	I102P				
SRV2_P51517						
SRV2_P51517_2mutB	I103P					
WDSV_O92815						
WDSV_O92815_2mut	S183N	K312P				
WDSV_O92815_2mutA	S183N	K312P	L288K	W295F		
WMSV_P03359						
WMSV_P03359_3mut	D198N	E328P	L600W			
WMSV_P03359_3mutA	D198N	E328P	L600W	T304K	W311F	
XMRV6_A1Z651						
XMRV6_A1Z651_3mut	D200N	T330P	L603W			
XMRV6_A1Z651_3mutA	D200N	T330P	L603W	T306K	W313F	

Template nucleic acid binding domain

The gene modifying polypeptide typically contains regions capable of associating with the template nucleic acid (e.g., template RNA). In some embodiments, the template nucleic acid binding domain is an RNA binding domain. In some embodiments, the RNA binding domain is

a modular domain that can associate with RNA molecules containing specific signatures, e.g., structural motifs. In other embodiments, the template nucleic acid binding domain (e.g., RNA binding domain) is contained within the reverse transcription domain, e.g., the reverse transcriptase-derived component has a known signature for RNA preference.

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

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

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

embodiments, the RNA binding domain is associated with the template RNA in cells (e.g., in HEK293T cells) at a frequency at least about 5-fold or 10-fold higher than with a scrambled RNA. In some embodiments, the frequency of association between the RNA binding domain and the template RNA or scrambled RNA is measured by CLIP-seq, e.g., as described in Lin and Miles (2019), *supra.*

Endonuclease domains and DNA binding domains

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

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

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

In certain aspects, the DNA-binding domain of a gene modifying polypeptide described herein is selected, designed, or constructed for binding to a desired host DNA target sequence. In certain embodiments, the DNA-binding domain of the polypeptide is a heterologous DNA-binding element. In some embodiments the heterologous DNA binding element is a zinc-finger

element or a TAL effector element, e.g., a zinc-finger or TAL polypeptide or functional fragment thereof. In some embodiments the heterologous DNA binding element is a sequence-guided DNA binding element, such as Cas9, Cpf1, or other CRISPR-related protein that has been altered to have no endonuclease activity. In some embodiments the heterologous DNA binding element retains endonuclease activity. In some embodiments, the heterologous DNA binding element retains partial endonuclease activity to cleave ssDNA, e.g., possesses nickase activity. In specific embodiments, the heterologous DNA-binding domain can be any one or more of Cas9, TAL domain, ZF domain, Myb domain, combinations thereof, or multiples thereof.

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

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

In some embodiments, a gene modifying polypeptide comprises a modification to a DNA-binding domain, e.g., relative to the wild-type polypeptide. In some embodiments, the DNA-binding domain comprises an addition, deletion, replacement, or modification to the amino acid sequence of the original DNA-binding domain. In some embodiments, the DNA-binding domain is modified to include a heterologous functional domain that binds specifically to a target nucleic acid (e.g., DNA) sequence of interest. In some embodiments, the functional domain replaces at least a portion (e.g., the entirety of) the prior DNA-binding domain of the

polypeptide. In some embodiments, the functional domain comprises a zinc finger (e.g., a zinc finger that specifically binds to the target nucleic acid (e.g., DNA) sequence of interest. In some embodiments, the functional domain comprises a Cas domain (e.g., a Cas domain that specifically binds to the target nucleic acid (e.g., DNA) sequence of interest. In some embodiments, the Cas domain comprises a Cas9 or a mutant or variant thereof (e.g., as described herein). In embodiments, the Cas domain is associated with a guide RNA (gRNA), e.g., as described herein. In embodiments, the Cas domain is directed to a target nucleic acid (e.g., DNA) sequence of interest by the gRNA. In embodiments, the Cas domain is encoded in the same nucleic acid (e.g., RNA) molecule as the gRNA. In embodiments, the Cas domain is encoded in a different nucleic acid (e.g., RNA) molecule from the gRNA.

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

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

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

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

In some embodiments, the endonuclease domain has nickase activity and cleaves one strand of a target DNA. In some embodiments, nickase activity reduces the formation of double-stranded breaks at the target site. In some embodiments, the endonuclease domain creates a staggered nick structure in the first and second strands of a target DNA. In some embodiments, a staggered nick structure generates free 3' overhangs at the target site. In some embodiments, free 3' overhangs at the target site improve editing efficiency, e.g., by enhancing access and annealing of a 3' homology region of a template nucleic acid. In some embodiments, a staggered nick structure reduces the formation of double-stranded breaks at the target site.

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

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

In some embodiments, the endonuclease domain has nickase activity and does not form double-stranded breaks. In some embodiments, the endonuclease domain forms single-stranded breaks at a higher frequency than double-stranded breaks, e.g., at least 90%, 95%, 96%, 97%, 98%, or 99% of the breaks are single-stranded breaks, or less than 10%, 5%, 4%, 3%, 2%, or 1% of the breaks are double-stranded breaks. In some embodiments, the endonuclease forms substantially no double-stranded breaks. In some embodiments, the endonuclease does not form detectable levels of double-stranded breaks.

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

In some other embodiments, the endonuclease domain has nickase activity that nicks the target site DNA of the first strand and the second strand. Without wishing to be bound by theory, after a writing domain (e.g., RT domain) of a polypeptide described herein polymerizes (e.g., reverse transcribes) from the heterologous object sequence of a template nucleic acid (e.g., template RNA), the cellular DNA repair machinery must repair the nick on the first DNA strand. The target site DNA now contains two different sequences for the first DNA strand: one corresponding to the original genomic DNA (e.g., having a free 5′ end) and a second corresponding to that polymerized from the heterologous object sequence (e.g., having a free 3′ end). It is thought that the two different sequences equilibrate with one another, first one hybridizing the second strand, then the other, and which sequence the cellular DNA repair apparatus incorporates into its repaired target site may be a stochastic process. Without wishing

to be bound by theory, it is thought that introducing an additional nick to the second-strand may bias the cellular DNA repair machinery to adopt the heterologous object sequence-based sequence more frequently than the original genomic sequence (Anzalone et al. Nature 576:149-157 (2019)). In some embodiments, the additional nick is positioned at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135, 140, 145, or 150 nucleotides 5′ or 3′ of the target site modification (e.g., the insertion, deletion, or substitution) or to the nick on the first strand.

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

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

In some embodiments, the endonuclease domain is capable of nicking a first strand and a second strand. In some embodiments, the first and second strand nicks occur at the same position in the target site but on opposite strands. In some embodiments, the second strand nick occurs in a staggered location, e.g., upstream or downstream, from the first nick. In some embodiments, the endonuclease domain generates a target site deletion if the second strand nick is upstream of the first strand nick. In some embodiments, the endonuclease domain generates a target site duplication if the second strand nick is downstream of the first strand nick. In some embodiments, the endonuclease domain generates no duplication and/or deletion if the first and second strand nicks occur in the same position of the target site. In some embodiments, the

endonuclease domain has altered activity depending on protein conformation or RNA-binding status, e.g., which promotes the nicking of the first or second strand (e.g., as described in Christensen et al. PNAS 2006; incorporated by reference herein in its entirety).

In some embodiments, the endonuclease domain comprises a meganuclease, or a functional fragment thereof. In some embodiments, the endonuclease domain comprises a homing endonuclease, or a functional fragment thereof. In some embodiments, the endonuclease domain comprises a meganuclease from the LAGLIDADG, GIY-YIG, HNH, His-Cys Box, or PD-(D/E) XK families, or a functional fragment or variant thereof, e.g., which possess conserved amino acid motifs, e.g., as indicated in the family names. In some embodiments, the endonuclease domain comprises a meganuclease, or fragment thereof, chosen from, e.g., I-SmaMI (Uniprot F7WD42), I-SceI (Uniprot P03882), I-AniI (Uniprot P03880), I-DmoI (Uniprot P21505), I-CreI (Uniprot P05725), I-TevI (Uniprot P13299), I-OnuI (Uniprot Q4VWW5), or I-BmoI (Uniprot Q9ANR6). In some embodiments, the meganuclease is naturally monomeric, e.g., I-SceI, I-TevI, or dimeric, e.g., I-CreI, in its functional form. For example, the LAGLIDADG meganucleases with a single copy of the LAGLIDADG motif generally form homodimers, whereas members with two copies of the LAGLIDADG motif are generally found as monomers. In some embodiments, a meganuclease that normally forms as a dimer is expressed as a fusion, e.g., the two subunits are expressed as a single ORF and, optionally, connected by a linker, e.g., an I-CreI dimer fusion (Rodriguez-Fornes et al. Gene Therapy 2020; incorporated by reference herein in its entirety). In some embodiments, a meganuclease, or a functional fragment thereof, is altered to favor nickase activity for one strand of a double-stranded DNA molecule, e.g., I-SceI (K122I and/or K223I) (Niu et al. J Mol Biol 2008), I-AniI (K227M) (McConnell Smith et al. PNAS 2009), I-DmoI (Q42A and/or K120M) (Molina et al. J Biol Chem 2015). In some embodiments, a meganuclease or functional fragment thereof possessing this preference for single-strand cleavage is used as an endonuclease domain, e.g., with nickase activity. In some embodiments, an endonuclease domain comprises a meganuclease, or a functional fragment thereof, which naturally targets or is engineered to target a safe harbor site, e.g., an I-CreI targeting SH6 site (Rodriguez-Fornes et al., *supra*). In some embodiments, an endonuclease domain comprises a meganuclease, or a functional fragment thereof, with a sequence tolerant catalytic domain, e.g., I-TevI recognizing the minimal motif CNNNG (Kleinstiver et al. PNAS 2012). In some embodiments, a target sequence tolerant

catalytic domain is fused to a DNA binding domain, e.g., to direct activity, e.g., by fusing I-TevI to: (i) zinc fingers to create Tev-ZFEs (Kleinstiver et al. PNAS 2012), (ii) other meganucleases to create MegaTevs (Wolfs et al. Nucleic Acids Res 2014), and/or (iii) Cas9 to create TevCas9 (Wolfs et al. PNAS 2016).

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

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

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

In some embodiments, the endonuclease domain is associated with the target dsDNA *in vitro* at a frequency at least about 5-fold or 10-fold higher than with a scrambled dsDNA. In some embodiments, the endonuclease domain is associated with the target dsDNA *in vitro* at a frequency at least about 5-fold or 10-fold higher than with a scrambled dsDNA, e.g., in a cell (e.g., a HEK293T cell). In some embodiments, the frequency of association between the endonuclease domain and the target DNA or scrambled DNA is measured by ChIP-seq, e.g., as

described in He and Pu (2010) *Curr. Protoc Mol Biol* Chapter 21 (incorporated by reference herein in its entirety).

In some embodiments, the endonuclease domain can catalyze the formation of a nick at a target sequence, e.g., to an increase of at least about 5-fold or 10-fold relative to a non-target sequence (e.g., relative to any other genomic sequence in the genome of the target cell). In some embodiments, the level of nick formation is determined using NickSeq, e.g., as described in Elacqua et al. (2019) *bioRxiv* doi.org/10.1101/867937 (incorporated herein by reference in its entirety).

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

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

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

In some embodiments, the endonuclease domain has a catalytic efficiency (k_{cat}/K_m) greater than about 1 x 10^8 s^{-1} M^{-1} *in vitro*. In embodiments, the endonuclease domain has a

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

Gene modifying polypeptides comprising Cas domains

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

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

("PAM") that is specific for a given Cas endonuclease and required for cleavage activity at a target site matching the spacer of the crRNA. CRISPR endonucleases identified from various prokaryotic species have unique PAM sequence requirements, e.g., as listed for exemplary Cas enzymes in Table 7; examples of PAM sequences include 5′-NGG (Streptococcus pyogenes; SEQ ID NO: 11,019), 5′-NNAGAA (Streptococcus thermophilus CRISPR1; SEQ ID NO: 11,020), 5′-NGGNG (Streptococcus thermophilus CRISPR3; SEQ ID NO: 11,021), and 5′-NNNGATT (Neisseria meningiditis; SEQ ID NO: 11,022). Some endonucleases, e.g., Cas9 endonucleases, are associated with G-rich PAM sites, e. g., 5′-NGG (SEQ ID NO: 11,023), and perform blunt-end cleaving of the target DNA at a location 3 nucleotides upstream from (5′ from) the PAM site. Another class II CRISPR system includes the type V endonuclease Cpf1, which is smaller than Cas9; examples include AsCpf1 (from Acidaminococcus sp.) and LbCpf1 (from Lachnospiraceae sp.). Cpf1-associated CRISPR arrays are processed into mature crRNAs without the requirement of a tracrRNA; in other words, a Cpf1 system, in some embodiments, comprises only Cpf1 nuclease and a crRNA to cleave a target DNA sequence. Cpf1 endonucleases, are typically associated with T-rich PAM sites, e. g., 5′-TTN. Cpf1 can also recognize a 5′-CTA PAM motif. Cpf1 typically cleaves a target DNA by introducing an offset or staggered double-strand break with a 4- or 5-nucleotide 5′ overhang, for example, cleaving a target DNA with a 5-nucleotide offset or staggered cut located 18 nucleotides downstream from (3′ from) from a PAM site on the coding strand and 23 nucleotides downstream from the PAM site on the complimentary strand; the 5-nucleotide overhang that results from such offset cleavage allows more precise genome editing by DNA insertion by homologous recombination than by insertion at blunt-end cleaved DNA. See, e.g., Zetsche et al. (2015) Cell, 163:759 – 771.

A variety of CRISPR associated (Cas) genes or proteins can be used in the technologies provided by the present disclosure and the choice of Cas protein will depend upon the particular conditions of the method. Specific examples of Cas proteins include class II systems including Cas1, Cas2, Cas3, Cas4, Cas5, Cas6, Cas7, Cas8, Cas9, Cas10, Cpf1, C2C1, or C2C3. In some embodiments, a Cas protein, e.g., a Cas9 protein, may be from any of a variety of prokaryotic species. In some embodiments a particular Cas protein, e.g., a particular Cas9 protein, is selected to recognize a particular protospacer-adjacent motif (PAM) sequence. In some embodiments, a DNA-binding domain or endonuclease domain includes a sequence targeting polypeptide, such as a Cas protein, e.g., Cas9. In certain embodiments a Cas protein, e.g., a Cas9 protein, may be

obtained from a bacteria or archaea or synthesized using known methods. In certain embodiments, a Cas protein may be from a gram-positive bacteria or a gram-negative bacteria. In certain embodiments, a Cas protein may be from a Streptococcus (e.g., a S. pyogenes, or a S. thermophilus), a Francisella (e.g., an F. novicida), a Staphylococcus (e.g., an S. aureus), an Acidaminococcus (e.g., an Acidaminococcus sp. BV3L6), a Neisseria (e.g., an N. meningitidis), a Cryptococcus, a Corynebacterium, a Haemophilus, a Eubacterium, a Pasteurella, a Prevotella, a Veillonella, or a Marinobacter.

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

Exemplary N-terminal NLS-Cas9 domain

MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSI
KKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEE
SFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIK
FRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLE
NLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIG
DQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQL
PEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQR
TFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAW
MTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNE
LTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISG
VEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLF
DDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDS
LTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVI

EMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGR
DMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKK
MKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDS
RMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGT
ALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANG
EIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRN
SDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSF
EKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYV
NFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSA
YNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITG
LYETRIDLSQLGGDGG (SEQ ID NO: 4000)

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

Exemplary C-terminal sequence comprising an NLS

AGKRTADGSEFEKRTADGSEFESPKKKAKVE (SEQ ID NO: 4001)

Exemplary benchmarking sequence

MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSI
KKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEE
SFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIK
FRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLE
NLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIG

DQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQL
PEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQR
TFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAW
MTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNE
LTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISG
VEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLF
DDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDS
LTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVI
EMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGR
DMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKK
MKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDS
RMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGT
ALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANG
EIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRN
SDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSF
EKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYV
NFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSA
YNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITG
LYETRIDLSQLGGDGGSGGSSGGSSGSETPGTSESATPESSGGSSGGSSGGTLNIEDEYRL
HETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQE
ARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTV
PNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRL
PQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLG
NLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLG
KAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTK
PFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTK
DAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVAL
NPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAG
AAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHG
EIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQA

ARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPK KKAKVE (SEQ ID NO: 4002)

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

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

Name	*Enzyme*	*Species*	*# of AAs*	*PAM*	*SEQ ID NO:*	*Mutations to alter PAM recognition*	*Mutations to make catalytically dead*
FnCas9	Cas9	*Francisella novicida*	1629	5'-NGG-3'	11,024	Wt	D11A/H969A/N995A
FnCas9 RHA	Cas9	*Francisella novicida*	1629	5'-YG-3'	11,025	E1369R/E1449H/R1556A	D11A/H969A/N995A
SaCas9	Cas9	*Staphylococcus aureus*	1053	5'-NNGRRT-3'	11,026	Wt	D10A/H557A
SaCas9 KKH	Cas9	*Staphylococcus aureus*	1053	5'-NNNRRT-3'	11,027	E782K/N968K/R1015H	D10A/H557A
SpCas9	Cas9	*Streptococcus pyogenes*	1368	5'-NGG-3'	11,028	Wt	D10A/D839A/H840A/N863A
SpCas9 VQR	Cas9	*Streptococcus pyogenes*	1368	5'-NGA-3'	11,029	D1135V/R1335Q/T1337R	D10A/D839A/H840A/N863A
AsCpf1 RR	Cpf1	*Acidaminococcus sp. BV3L6*	1307	5'-TYCV-3'	11,030	S542R/K607R	E993A
AsCpf1 RVR	Cpf1	*Acidaminococcus sp. BV3L6*	1307	5'-TATV-3'	11,031	S542R/K548V/N552R	E993A
FnCpf1	Cpf1	*Francisella novicida*	1300	5'-NTTN-3'	11,032	Wt	D917A/E1006A/D1255A
NmCas9	Cas9	*Neisseria meningitidis*	1082	5'-NNNGATT-3'	11,033	Wt	D16A/D587A/H588A/N611A

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

Variant	**Parental Host(s)**	**Protein Sequence**	**SEQ ID NO:**	**Nickase (HNH)**	**Nickase (HNH)**	**Nickase (RuvC)**
Nme2Cas9	Neisseria meningitidis	MAAFKPNPINYILGLDIGIASVGWAMVEIDEEENPIRLIDLGVRVFERAEVPK TGDSLAMARRLARSVRRLTRRRAHRLLRARRLLKREGVLQAADFDENGLIKS LPNTPWQLRAAALDRKLTPLEWSAVLLHLIKHRGYLSQRKNEGETADKELG ALLKGVANNAHALQTGDFRTPAELALNKFEKESGHIRNQRGDYSHTFSRKD LQAELILLFEKQKEFGNPHVSGGLKEGIETLLMTQRPALSGDAVQKMLGHCT FEPAEPKAAKNTYTAERFIWLTKLNNLRILEQGSERPLTDTERATLMDEPYRK SKLTYAQARKLLGLEDTAFFKGLRYGKDNAEASTLMEMKAYHAISRALEKEG LKDKKSPLNLSSELQDEIGTAFSLFKTDEDITGRLKDRVQPEILEALLKHISFDKF VQISLKALRRIVPLMEQGKRYDEACAEIYGDHYGKKNTEEKIYLPPIPADEIRN PVVLRALSQARKVINGVVRRYGSPARIHIETAREVGKSFKDRKEIEKRQEENR KDREKAAAKFREYFPNFVGEPKSKDILKLRLYEQQHGKCLYSGKEINLVRLNE KGYVEIDHALPFSRTWDDSFNNKVLVLGSENQNKGNQTPYEYFNGKDNSR EWQEFKARVETSRFPRSKKQRILLQKFDEDGFKECNLNDTRYVNRFLCQFVA DHILLTGKGKRRVFASNGQITNLLRGFWGLRKVRAENDRHHALDAVVVACS TVAMQQKITRFVRYKEMNAFDGKTIDKETGKVLHQKTHFPQPWEFFAQEV MIRVFGKPDGKPEFEEADTPEKLRTLLAEKLSSRPEAVHEYVTPLFVSRAPNR KMSGAHKDTLRSAKRFVKHNEKISVKRVWLTEIKLADLENMVNYKNGREIEL YEALKARLEAYGGNAKQAFDPKDNPFYKKGGQLVKAVRVEKTQESGVLLNK KNAYTIADNGDMVRVDVFCKVDKKGKNQYFIVPIYAWQVAENILPDIDCKG	9,001	N611A	H588A	D16A

		YRIDDSYTFCFSLHKYDLIAFQKDEKSKVEFAYYINCDSSNGRFYLAWHDKGS KEQQFRISTQNLVLIQKYQVNELGKEIRPCRLKKRPPVR				
PpnCas9	Pasteurella pneumotropica	MQNNPLNYILGLDLGIASIGWAVVEIDEESSPIRLIDVGVRTFERAEVAKTGE SLALSRRLARSSRRLIKRRAERLKKAKRLLKAEKILHSIDEKLPINVWQLRVKGL KEKLERQEWAAVLLHLSKHRGYLSQRKNEGKSDNKELGALLSGIASNHQML QSSEYRTPAEIAVKKFQVEEGHIRNQRGSYTHTFSRLDLLAEMELLFQRQAEL GNSYTSTTLLENLTALLMWQKPALAGDAILKMLGKCTFEPSEYKAAKNSYSA ERFVWLTKLNNLRILENGTERALNDNERFALLEQPYEKSKLTYAQVRAMLAL SDNAIFKGVRYLGEDKKTVESKTTLIEMKFYHQIRKTLGSAELKKEWNELKGN SDLLDEIGTAFSLYKTDDDICRYLEGKLPERVLNALLENLNFDKFIQLSLKALHQ ILPLMLQGQRYDEAVSAIYGDHYGKKSTETTRLLPTIPADEIRNPVVLRTLTQA RKVINAVVRLYGSPARIHIETARAVGKSYQDRKKLEKQQEDNRKQRESAVKK FKEMFPHFVGEPKGKDILKMRLYELQQAKCLYSGKSLELHRLLEKGYVEVDH ALPFSRTWDDSFNNKVLVLANENQNKGNLTPYEWLDGKNNSERWQHFVV RVQTSGFSYAKKQRILNHKLDEKGFIERNLNDTRYVARFLCNFIADNMLLVG KGKRNVFASNGQITALLRHRWGLQKVREQNDRHHALDAVVVACSTVAMQ QKITRFVRYNEGNVFSGERIDRETGEIIPLHFPSPWAFFKENVEIRIFSENPKLE LENRLPDYPQYNHEWVQPLFVSRMPTRKMTGQGHMETVKSAKRLNEGLS VLKVPLTQLKLSDLERMVNRDREIALYESLKARLEQFGNDPAKAFAEPFYKKG GALVKAVRLEQTQKSGVLVRDGNGVADNASMVRVDVFTKGGKYFLVPIYT WQVAKGILPNRAATQGKDENDWDIMDEMATFQFSLCQNDLIKLVTKKKTI FGYFNGLNRATSNINIKEHDLDKSKGKLGIYLEVGVKLAISLEKYQVDELGKNI RPCRPTKRQHVR	9,002	N605A	H582A	D13A
SauCas9	Staphylococcus aureus	MKRNYILGLDIGITSVGYGIIDYETRDVIDAGVRLFKEANVENNEGRRSKRGA RRLKRRRRHRIQRVKKLLFDYNLLTDHSELSGINPYEARVKGLSQKLSEEEFSA ALLHLAKRRGVHNVNEVEEDTGNELSTKEQISRNSKALEEKYVAELQLERLKK DGEVRGSINRFKTSDYVKEAKQLLKVQKAYHQLDQSFIDTYIDLLETRRTYYE GPGEGSPFGWKDIKEWYEMLMGHCTYFPEELRSVKYAYNADLYNALNDLN NLVITRDENEKLEYYEKFQIIENVFKQKKKPTLKQIAKEILVNEEDIKGYRVTST GKPEFTNLKVYHDIKDITARKEIIENAELLDQIAKILTIYQSSEDIQEELTNLNSE LTQEEIEQISNLKGYTGTHNLSLKAINLILDELWHTNDNQIAIFNRLKLVPKKV DLSQQKEIPTTLVDDFILSPVVKRSFIQSIKVINAIIKKYGLPNDIIIELAREKNSK DAQKMINEMQKRNRQTNERIEEIIRTTGKENAKYLIEKIKLHDMQEGKCLYS LEAIPLEDLLNNPFNYEVDHIIPRSVSFDNSFNNKVLVKQEENSKKGNRTPFQ YLSSSDSKISYETFKKHILNLAKGKGRISKTKKEYLLEERDINRFSVQKDFINRNL VDTRYATRGLMNLLRSYFRVNNLDVKVKSINGGFTSFLRRKWKFKKERNKG YKHHAEDALIIANADFIFKEWKKLDKAKKVMENQMFEEKQAESMPEIETEQ EYKEIFITPHQIKHIKDFKDYKYSHRVDKKPNRELINDTLYSTRKDDKGNTLIVN NLNGLYDKDNDKLKKLINKSPEKLLMYHHDPQTYQKLKLIMEQYGDEKNPL YKYYEETGNYLTKYSKKDNGPVIKKIKYYGNKLNAHLDITDDYPNSRNKVVKL SLKPYRFDVYLDNGVYKFVTVKNLDVIKKENYYEVNSKCYEEAKKLKKISNQA EFIASFYNNDLIKINGELYRVIGVNNDLLNRIEVNMIDITYREYLENMNDKRPP RIIKTIASKTQSIKKYSTDILGNLYEVKSKKHPQIIKKG	9,003	N580A	H557A	D10A
SauCas9-KKH	Staphylococcus aureus	MKRNYILGLDIGITSVGYGIIDYETRDVIDAGVRLFKEANVENNEGRRSKRGA RRLKRRRRHRIQRVKKLLFDYNLLTDHSELSGINPYEARVKGLSQKLSEEEFSA ALLHLAKRRGVHNVNEVEEDTGNELSTKEQISRNSKALEEKYVAELQLERLKK DGEVRGSINRFKTSDYVKEAKQLLKVQKAYHQLDQSFIDTYIDLLETRRTYYE GPGEGSPFGWKDIKEWYEMLMGHCTYFPEELRSVKYAYNADLYNALNDLN NLVITRDENEKLEYYEKFQIIENVFKQKKKPTLKQIAKEILVNEEDIKGYRVTST GKPEFTNLKVYHDIKDITARKEIIENAELLDQIAKILTIYQSSEDIQEELTNLNSE LTQEEIEQISNLKGYTGTHNLSLKAINLILDELWHTNDNQIAIFNRLKLVPKKV DLSQQKEIPTTLVDDFILSPVVKRSFIQSIKVINAIIKKYGLPNDIIIELAREKNSK DAQKMINEMQKRNRQTNERIEEIIRTTGKENAKYLIEKIKLHDMQEGKCLYS LEAIPLEDLLNNPFNYEVDHIIPRSVSFDNSFNNKVLVKQEENSKKGNRTPFQ YLSSSDSKISYETFKKHILNLAKGKGRISKTKKEYLLEERDINRFSVQKDFINRNL VDTRYATRGLMNLLRSYFRVNNLDVKVKSINGGFTSFLRRKWKFKKERNKG YKHHAEDALIIANADFIFKEWKKLDKAKKVMENQMFEEKQAESMPEIETEQ EYKEIFITPHQIKHIKDFKDYKYSHRVDKKPNRKLINDTLYSTRKDDKGNTLIV	9,004	N580A	H557A	D10A

		NNLNGLYDKDNDKLKKLINKSPEKLLMYHHDPQTYQKLKLIMEQYGDEKNP LYKYYEETGNYLTKYSKKDNGPVIKKIKYYGNKLNAHLDITDDYPNSRNKVVK LSLKPYRFDVYLDNGVYKFVTVKNLDVIKKENYYEVNSKCYEEAKKLKKISNQ AEFIASFYKNDLIKINGELYRVIGVNNDLLNRIEVNMIDITYREYLENMNDKRP PHIIKTIASKTQSIKKYSTDILGNLYEVKSKKHPQIIKKG				
SauriCas9	Staphylococcus auricularis	MQENQQKQNYILGLDIGITSVGYGLIDSKTREVIDAGVRLFPEADSENNSNR RSKRGARRLKRRRIHRLNRVKDLLADYQMIDLNNVPKSTDPYTIRVKGLREPL TKEEFAIALLHIAKRRGLHNISVSMGDEEQDNELSTKQQLQKNAQQLQDKY VCELQLERLTNINKVRGEKNRFKTEDFVKEVKQLCETQRQYHNIDDQFIQQY IDLVSTRREYFEGPGNGSPYGWDGDLLKWYEKLMGRCTYFPEELRSVKYAYS ADLFNALNDLNNLVVTRDDNPKLEYYEKYHIIENVFKQKKNPTLKQIAKEIGV QDYDIRGYRITKSGKPQFTSFKLYHDLKNIFEQAKYLEDVEMLDEIAKILTIYQ DEISIKKALDQLPELLTESEKSQIAQLTGYTGTHRLSLKCIHIVIDELWESPENQ MEIFTRLNLKPKKVEMSEIDSIPTTLVDEFILSPVVKRAFIQSIKVINAVINRFGL PEDIIIELAREKNSKDRRKFINKLQKQNEATRKKIEQLLAKYGNTNAKYMIEKI KLHDMQEGKCLYSLEAIPLEDLLSNPTHYEVDHIIPRSVSFDNSLNNKVLVKQ SENSKKGNRTPYQYLSSNESKISYNQFKQHILNLSKAKDRISKKKRDMLLEER DINKFEVQKEFINRNLVDTRYATRELSNLLKTYFSTHDYAVKVKTINGGFTNH LRKVWDFKKHRNHGYKHHAEDALVIANADFLFKTHKALRRTDKILEQPGLE VNDTTVKVDTEEKYQELFETPKQVKNIKQFRDFKYSHRVDKKPNRQLINDTL YSTREIDGETYVVQTLKDLYAKDNEKVKKLFTERPQKILMYQHDPKTFEKLM TILNQYAEAKNPLAAYYEDKGEYVTKYAKKGNGPAIHKIKYIDKKLGSYLDVS NKYPETQNKLVKLSLKSFRFDIYKCEQGYKMVSIGYLDVLKKDNYYYIPKDKYE AEKQKKKIKESDLFVGSFYYNDLIMYEDELFRVIGVNSDINNLVELNMVDITY KDFCEVNNVTGEKRIKKTIGKRVVLIEKYTTDILGNLYKTPLPKKPQLIFKRGEL	9,005	N588A	H565A	D15A
SauriCas9-KKH	Staphylococcus auricularis	MQENQQKQNYILGLDIGITSVGYGLIDSKTREVIDAGVRLFPEADSENNSNR RSKRGARRLKRRRIHRLNRVKDLLADYQMIDLNNVPKSTDPYTIRVKGLREPL TKEEFAIALLHIAKRRGLHNISVSMGDEEQDNELSTKQQLQKNAQQLQDKY VCELQLERLTNINKVRGEKNRFKTEDFVKEVKQLCETQRQYHNIDDQFIQQY IDLVSTRREYFEGPGNGSPYGWDGDLLKWYEKLMGRCTYFPEELRSVKYAYS ADLFNALNDLNNLVVTRDDNPKLEYYEKYHIIENVFKQKKNPTLKQIAKEIGV QDYDIRGYRITKSGKPQFTSFKLYHDLKNIFEQAKYLEDVEMLDEIAKILTIYQ DEISIKKALDQLPELLTESEKSQIAQLTGYTGTHRLSLKCIHIVIDELWESPENQ MEIFTRLNLKPKKVEMSEIDSIPTTLVDEFILSPVVKRAFIQSIKVINAVINRFGL PEDIIIELAREKNSKDRRKFINKLQKQNEATRKKIEQLLAKYGNTNAKYMIEKI KLHDMQEGKCLYSLEAIPLEDLLSNPTHYEVDHIIPRSVSFDNSLNNKVLVKQ SENSKKGNRTPYQYLSSNESKISYNQFKQHILNLSKAKDRISKKKRDMLLEER DINKFEVQKEFINRNLVDTRYATRELSNLLKTYFSTHDYAVKVKTINGGFTNH LRKVWDFKKHRNHGYKHHAEDALVIANADFLFKTHKALRRTDKILEQPGLE VNDTTVKVDTEEKYQELFETPKQVKNIKQFRDFKYSHRVDKKPNRKLINDTL YSTREIDGETYVVQTLKDLYAKDNEKVKKLFTERPQKILMYQHDPKTFEKLM TILNQYAEAKNPLAAYYEDKGEYVTKYAKKGNGPAIHKIKYIDKKLGSYLDVS NKYPETQNKLVKLSLKSFRFDIYKCEQGYKMVSIGYLDVLKKDNYYYIPKDKYE AEKQKKKIKESDLFVGSFYKNDLIMYEDELFRVIGVNSDINNLVELNMVDITY KDFCEVNNVTGEKHIKKTIGKRVVLIEKYTTDILGNLYKTPLPKKPQLIFKRGEL	9,006	N588A	H565A	D15A
ScaCas9-Sc++	Streptococcus canis	MEKKYSIGLDIGTNSVGWAVITDDYKVPSKKFKVLGNTNRKSIKKNLMGALL FDSGETAEATRLKRTARRRYTRRKNRIRYLQEIFANEMAKLDDSFFQRLEESF LVEEDKKNERHPIFGNLADEVAYHRNYPTIYHLRKKLADSPEKADLRLIYLALA HIIKFRGHFLIEGKLNAENSDVAKLFYQLIQTYNQLFEESPLDEIEVDAKGILSA RLSKSKRLEKLIAVFPNEKKNGLFGNIIALALGLTPNFKSNFDLTEDAKLQLSKD TYDDDLDELLGQIGDQYADLFSAAKNLSDAILLSDILRSNSEVTKAPLSASMV KRYDEHHQDLALLKTLVRQQFPEKYAEIFKDDTKNGYAGYVGADKKLRKRS GKLATEEEFYKFIKPILEKMDGAEELLAKLNREDLLRKQRTFDNGSIPHQIHLK ELHAILRRQEEFYPFLKENREKIEKILTFRIPYYVGPLARGNSRFAWLTRKSEEA ITPWNFEEVVDKGASAQSFIERMTNFDEQLPNKKVLPKHSLLYEYFTVYNEL TKVKYVTERMRKPEFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDS VEIIGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIE ERLKTYAHLFDDKVMKQLKRRHYTGWGRLSRKMINGIRDKQSGKTILDFLKS	9,007	N872A	H849A	D10A

		DGFSNRNFMQLIHDDSLTFKEEIEKAQVSGQGDSLHEQIADLAGSPAIKKGIL QTVKIVDELVKVMGHKPENIVIEMARENQTTTKGLQQSRERKKRIEEGIKELE SQILKENPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVP QSFIKDDSIDNKVLTRSVENRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQ RKFDNLTKAERGGLSEADKAGFIKRQLVETRQITKHVARILDSRMNTKRDKN DKPIREVKVITLKSKLVSDFRKDFQLYKVRDINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKRFFYSNIMNFFKTEVKL ANGEIRKRPLIETNGETGEVVWNKEKDFATVRKVLAMPQVNIVKKTEVQTG GFSKESILSKRESAKLIPRKKGWDTRKYGGFGSPTVAYSILVVAKVEKGKAKKL KSVKVLVGITIMEKGSYEKDPIGFLEAKGYKDIKKELIFKLPKYSLFELENGRRR MLASAKELQKANELVLPQHLVRLLYYTQNISATTGSNNLGYIEQHREEFKEIF EKIIDFSEKYILKNKVNSNLKSSFDEQFAVSDSILLSNSFVSLLKYTSFGASGGFT FLDLDVKQGRLRYQTVTEVLDATLIYQSITGLYETRTDLSQLGGD	9,008	N863A	H840A	D10A
SpyCas9	Streptococcus pyogenes	MDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLF DSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFL VEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAH MIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLS KDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSAS MIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEF YKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQ EDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFE EVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTE GMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVED RFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYA HLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANR NFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKV VDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQ ILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSF LKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKF DNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLI REVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPK LESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEI RKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKE LLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASA GELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEII EQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAF KYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGD	9,008	N863A	H840A	D10A
SpyCas9-NG	Streptococcus pyogenes	MDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLF DSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFL VEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAH MIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLS KDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSAS MIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEF YKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQ EDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFE EVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTE GMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVED RFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYA HLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANR NFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKV VDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQ ILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSF LKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKF DNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLI REVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPK LESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEI	9,009	N863A	H840A	D10A

		RKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES IRPKRNSDKLIARKKDWDPKKYGGFVSPTVAYSVLVVAKVEKGKSKKLKSVKE LLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASA RFLQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEII EQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPRAF KYFDTTIDRKVYRSTKEVLDATLIHQSITGLYETRIDLSQLGGD				
SpyCas9-SpRY	Streptococcus pyogenes	MDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLF DSGETAERTRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFL VEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAH MIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLS KDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSAS MIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEF YKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQ EDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFE EVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTE GMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVED RFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYA HLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANR NFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKV VDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQ ILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSF LKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKF DNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLI REVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPK LESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEI RKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES IRPKRNSDKLIARKKDWDPKKYGGFLWPTVAYSVLVVAKVEKGKSKKLKSVK ELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLAS AKQLQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDE IIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTRLGAPRAF KYFDTTIDPKQYRSTKEVLDATLIHQSITGLYETRIDLSQLGGD	9,010	N863A	H840A	D10A
St1Cas9	Streptococcus thermophilus	MSDLVLGLDIGIGSVGVGILNKVTGEIIHKNSRIFPAAQAENNLVRRTNRQG RRLARRKKHRRVRLNRLFEESGLITDFTKISINLNPYQLRVKGLTDELSNEELFI ALKNMVKHRGISYLDDASDDGNSSVGDYAQIVKENSKQLETKTPGQIQLER YQTYGQLRGDFTVEKDGKKHRLINVFPTSAYRSEALRILQTQQEFNPQITDEF INRYLEILTGKRKYYHGPGNEKSRTDYGRYRTSGETLDNIFGILIGKCTFYPDEF RAAKASYTAQEFNLLNDLNNLTVPTETKKLSKEQKNQIINYVKNEKAMGPAK LFKYIAKLLSCDVADIKGYRIDKSGKAEIHTFEAYRKMKTLETLDIEQMDRETL DKLAYVLTLNTEREGIQEALEHEFADGSFSQKQVDELVQFRKANSSIFGKGW HNFSVKLMMELIPELYETSEEQMTILTRLGKQKTTSSSNKTKYIDEKLLTEEIY NPVVAKSVRQAIKIVNAAIKEYGDFDNIVIEMARETNEDDEKKAIQKIQKAN KDEKDAAMLKAANQYNGKAELPHSVFHGHKQLATKIRLWHQQGERCLYT GKTISIHDLINNSNQFEVDHILPLSITFDDSLANKVLVYATANQEKGQRTPYQ ALDSMDDAWSFRELKAFVRESKTLSNKKKEYLLTEEDISKFDVRKKFIERNLV DTRYASRVVLNALQEHFRAHKIDTKVSVVRGQFTSQLRRHWGIEKTRDTYH HHAVDALIIAASSQLNLWKKQKNTLVSYSEDQLLDIETGELISDDEYKESVFK APYQHFVDTLKSKEFEDSILFSYQVDSKFNRKISDATIYATRQAKVGKDKADE TYVLGKIKDIYTQDGYDAFMKIYKKDKSKFLMYRHDPQTFEKVIEPILENYPN KQINEKGKEVPCNPFLKYKEEHGYIRKYSKKGNGPEIKSLKYYDSKLGNHIDIT PKDSNNKVVLQSVSPWRADVYFNKTTGKYEILGLKYADLQFEKGTGTYKISQ EKYNDIKKKEGVDSDSEFKFTLYKNDLLLVKDTETKEQQLFRFLSRTMPKQKH YVELKPYDKQKFEGGEALIKVLGNVANSGQCKKGLGKSNISIYKVRTDVLGN QHIIKNEGDKPKLDF	9,011	N622A	H599A	D9A
BlatCas9	Brevibacillus laterosporus	MAYTMGIDVGIASCGWAIVDLERQRIIDIGVRTFEKAENPKNGEALAVPRRE ARSSRRRLRRKKHRIERLKHMFVRNGLAVDIQHLEQTLRSQNEIDVWQLRV DGLDRMLTQKEWLRVLIHLAQRRGFQSNRKTDGSSEDGQVLVNVTENDRL MEEKDYRTVAEMMVKDEKFSDHKRNKNGNYHGVVSRSSLLVEIHTLFETQ	9,012	N607A	H584A	D8A

		RQHHNSLASKDFELEYVNIWSAQRPVATKDQIEKMIGTCTFLPKEKRAPKAS WHFQYFMLLQTINHIRITNVQGTRSLNKEEIEQVVNMALTKSKVSYHDTRKI LDLSEEYQFVGLDYGKEDEKKKVESKETIIKLDDYHKLNKIFNEVELAKGETWE ADDYDTVAYALTFFKDDEDIRDYLQNKYKDSKNRLVKNLANKEYTNELIGKV STLSFRKVGHLSLKALRKIIPFLEQGMTYDKACQAAGFDFQGISKKKRSVVLP VIDQISNPVVNRALTQTRKVINALIKKYGSPETIHIETARELSKTFDERKNITKD YKENRDKNEHAKKHLSELGIINPTGLDIVKYKLWCEQQGRCMYSNQPISFER LKESGYTEVDHIIPYSRSMNDSYNNRVLVMTRENREKGNQTPFEYMGNDT QRWYEFEQRVTTNPQIKKEKRQNLLLKGFTNRRELEMLERNLNDTRYITKYL SHFISTNLEFSPSDKKKKVVNTSGRITSHLRSRWGLEKNRGQNDLHHAMDAI VIAVTSDSFIQQVTNYYKRKERRELNGDDKFPLPWKFFREEVIARLSPNPKEQ IEALPNHFYSEDELADLQPIFVSRMPKRSITGEAHQAQFRRVVGKTKEGKNIT AKKTALVDISYDKNGDFNMYGRETDPATYEAIKERYLEFGGNVKKAFSTDLH KPKKDGTKGPLIKSVRIMENKTLVHPVNKGKGVVYNSSIVRTDVFQRKEKYY LLPVYVTDVTKGKLPNKVIVAKKGYHDWIEVDDSFTFLFSLYPNDLIFIRQNPK KKISLKKRIESHSISDSKEVQEIHAYYKGVDSSTAAIEFIIHDGSYYAKGVGVQN LDCFEKYQVDILGNYFKVKGEKRLELETSDSNHKGKDVNSIKSTSR				
cCas9-v16	Staphylococcus aureus	MKRNYILGLDIGITSVGYGIIDYETRDVIDAGVRLFKEANVENNEGRRSKRGA RRLKRRRRHRIQRVKKLLFDYNLLTDHSELSGINPYEARVKGLSQKLSEEEFSA ALLHLAKRRGVHNVNEVEEDTGNELSTKEQISRNSKALEEKYVAELQLERLKK DGEVRGSINRFKTSDYVKEAKQLLKVQKAYHQLDQSFIDTYIDLLETRRTYYE GPGEGSPFGWKDIKEWYEMLMGHCTYFPEELRSVKYAYNADLYNALNDLN NLVITRDENEKLEYYEKFQIIENVFKQKKKPTLKQIAKEILVNEEDIKGYRVTST GKPEFTNLKVYHDIKDITARKEIIENAELLDQIAKILTIYQSSEDIQEELTNLNSE LTQEEIEQISNLKGYTGTHNLSLKAINLILDELWHTNDNQIAIFNRLKLVPKKV DLSQQKEIPTTLVDDFILSPVVKRSFIQSIKVINAIIKKYGLPNDIIIELAREKNSK DAQKMINEMQKRNRQTNERIEEIIRTTGKENAKYLIEKIKLHDMQEGKCLYS LEAIPLEDLLNNPFNYEVDHIIPRSVSFDNSFNNKVLVKQEENSKKGNRTPFQ YLSSSDSKISYETFKKHILNLAKGKGRISKTKKEYLLEERDINRFSVQKDFINRNL VDTRYATRGLMNLLRSYFRVNNLDVKVKSINGGFTSFLRRKWKFKKERNKG YKHHAEDALIIANADFIFKEWKKLDKAKKVMENQMFEEKQAESMPEIETEQ EYKEIFITPHQIKHIKDFKDYKYSHRVDKKPNRKLINDTLYSTRKDDKGNTLIV NNLNGLYDKDNDKLKKLINKSPEKLLMYHHDPQTYQKLKLIMEQYGDEKNP LYKYYEETGNYLTKYSKKDNGPVIKKIKYYGNKLNAHLDITDDYPNSRNKVVK LSLKPYRFDVYLDNGVYKFVTVKNLDVIKKENYYEVNSKCYEEAKKLKKISNQ AEFIASFYKNDLIKINGELYRVIGVNSDKNNLIEVNMIDITYREYLENMNDKRP PHIIKTIASKTQSIKKYSTDILGNLYEVKSKKHPQIIKKG	9,013	N580A	H557A	D10A
cCas9-v17	Staphylococcus aureus	MKRNYILGLDIGITSVGYGIIDYETRDVIDAGVRLFKEANVENNEGRRSKRGA RRLKRRRRHRIQRVKKLLFDYNLLTDHSELSGINPYEARVKGLSQKLSEEEFSA ALLHLAKRRGVHNVNEVEEDTGNELSTKEQISRNSKALEEKYVAELQLERLKK DGEVRGSINRFKTSDYVKEAKQLLKVQKAYHQLDQSFIDTYIDLLETRRTYYE GPGEGSPFGWKDIKEWYEMLMGHCTYFPEELRSVKYAYNADLYNALNDLN NLVITRDENEKLEYYEKFQIIENVFKQKKKPTLKQIAKEILVNEEDIKGYRVTST GKPEFTNLKVYHDIKDITARKEIIENAELLDQIAKILTIYQSSEDIQEELTNLNSE LTQEEIEQISNLKGYTGTHNLSLKAINLILDELWHTNDNQIAIFNRLKLVPKKV DLSQQKEIPTTLVDDFILSPVVKRSFIQSIKVINAIIKKYGLPNDIIIELAREKNSK DAQKMINEMQKRNRQTNERIEEIIRTTGKENAKYLIEKIKLHDMQEGKCLYS LEAIPLEDLLNNPFNYEVDHIIPRSVSFDNSFNNKVLVKQEENSKKGNRTPFQ YLSSSDSKISYETFKKHILNLAKGKGRISKTKKEYLLEERDINRFSVQKDFINRNL VDTRYATRGLMNLLRSYFRVNNLDVKVKSINGGFTSFLRRKWKFKKERNKG YKHHAEDALIIANADFIFKEWKKLDKAKKVMENQMFEEKQAESMPEIETEQ EYKEIFITPHQIKHIKDFKDYKYSHRVDKKPNRKLINDTLYSTRKDDKGNTLIV NNLNGLYDKDNDKLKKLINKSPEKLLMYHHDPQTYQKLKLIMEQYGDEKNP LYKYYEETGNYLTKYSKKDNGPVIKKIKYYGNKLNAHLDITDDYPNSRNKVVK LSLKPYRFDVYLDNGVYKFVTVKNLDVIKKENYYEVNSKCYEEAKKLKKISNQ AEFIASFYKNDLIKINGELYRVIGVNNSTRNIVELNMIDITYREYLENMNDKRP PHIIKTIASKTQSIKKYSTDILGNLYEVKSKKHPQIIKKG	9,014	N580A	H557A	D10A

cCas9-v21	Staphylococcus aureus	MKRNYILGLDIGITSVGYGIIDYETRDVIDAGVRLFKEANVENNEGRRSKRGA RRLKRRRRHRIQRVKKLLFDYNLLTDHSELSGINPYEARVKGLSQKLSEEEFSA ALLHLAKRRGVHNVNEVEEDTGNELSTKEQISRNSKALEEKYVAELQLERLKK DGEVRGSINRFKTSDYVKEAKQLLKVQKAYHQLDQSFIDTYIDLLETRRTYYE GPGEGSPFGWKDIKEWYEMLMGHCTYFPEELRSVKYAYNADLYNALNDLN NLVITRDENEKLEYYEKFQIIENVFKQKKKPTLKQIAKEILVNEEDIKGYRVTST GKPEFTNLKVYHDIKDITARKEIIENAELLDQIAKILTIYQSSEDIQEELTNLNSE LTQEEIEQISNLKGYTGTHNLSLKAINLILDELWHTNDNQIAIFNRLKLVPKKV DLSQQKEIPTTLVDDFILSPVVKRSFIQSIKVINAIIKKYGLPNDIIIELAREKNSK DAQKMINEMQKRNRQTNERIEEIIRTTGKENAKYLIEKIKLHDMQEGKCLYS LEAIPLEDLLNNPFNYEVDHIIPRSVSFDNSFNNKVLVKQEENSKKGNRTPFQ YLSSSDSKISYETFKKHILNLAKGKGRISKTKKEYLLEERDINRFSVQKDFINRNL VDTRYATRGLMNLLRSYFRVNNLDVKVKSINGGFTSFLRRKWKFKKERNKG YKHHAEDALIIANADFIFKEWKKLDKAKKVMENQMFEEKQAESMPEIETEQ EYKEIFITPHQIKHIKDFKDYKYSHRVDKKPNRKLINDTLYSTRKDDKGNTLIV NNLNGLYDKDNDKLKKLINKSPEKLLMYHHDPQTYQKLKLIMEQYGDEKNP LYKYYEETGNYLTKYSKKDNGPVIKKIKYYGNKLNAHLDITDDYPNSRNKVVK LSLKPYRFDVYLDNGVYKFVTVKNLDVIKKENYYEVNSKCYEEAKKLKKISNQ AEFIASFYKNDLIKINGELYRVIGVNSDDRNIIELNMIDITYREYLENMNDKRP PHIIKTIASKTQSIKKYSTDILGNLYEVKSKKHPQIIKKG	9,015	N580A	H557A	D10A
cCas9-v42	Staphylococcus aureus	MKRNYILGLDIGITSVGYGIIDYETRDVIDAGVRLFKEANVENNEGRRSKRGA RRLKRRRRHRIQRVKKLLFDYNLLTDHSELSGINPYEARVKGLSQKLSEEEFSA ALLHLAKRRGVHNVNEVEEDTGNELSTKEQISRNSKALEEKYVAELQLERLKK DGEVRGSINRFKTSDYVKEAKQLLKVQKAYHQLDQSFIDTYIDLLETRRTYYE GPGEGSPFGWKDIKEWYEMLMGHCTYFPEELRSVKYAYNADLYNALNDLN NLVITRDENEKLEYYEKFQIIENVFKQKKKPTLKQIAKEILVNEEDIKGYRVTST GKPEFTNLKVYHDIKDITARKEIIENAELLDQIAKILTIYQSSEDIQEELTNLNSE LTQEEIEQISNLKGYTGTHNLSLKAINLILDELWHTNDNQIAIFNRLKLVPKKV DLSQQKEIPTTLVDDFILSPVVKRSFIQSIKVINAIIKKYGLPNDIIIELAREKNSK DAQKMINEMQKRNRQTNERIEEIIRTTGKENAKYLIEKIKLHDMQEGKCLYS LEAIPLEDLLNNPFNYEVDHIIPRSVSFDNSFNNKVLVKQEENSKKGNRTPFQ YLSSSDSKISYETFKKHILNLAKGKGRISKTKKEYLLEERDINRFSVQKDFINRNL VDTRYATRGLMNLLRSYFRVNNLDVKVKSINGGFTSFLRRKWKFKKERNKG YKHHAEDALIIANADFIFKEWKKLDKAKKVMENQMFEEKQAESMPEIETEQ EYKEIFITPHQIKHIKDFKDYKYSHRVDKKPNRKLINDTLYSTRKDDKGNTLIV NNLNGLYDKDNDKLKKLINKSPEKLLMYHHDPQTYQKLKLIMEQYGDEKNP LYKYYEETGNYLTKYSKKDNGPVIKKIKYYGNKLNAHLDITDDYPNSRNKVVK LSLKPYRFDVYLDNGVYKFVTVKNLDVIKKENYYEVNSKCYEEAKKLKKISNQ AEFIASFYKNDLIKINGELYRVIGVNNNRLNKIELNMIDITYREYLENMNDKRP PHIIKTIASKTQSIKKYSTDILGNLYEVKSKKHPQIIKKG	9,016	N580A	H557A	D10A
CdiCas9	Corynebacterium diphtheriae	MKYHVGIDVGTFSVGLAAIEVDDAGMPIKTLSLVSHIHDSGLDPDEIKSAVT RLASSGIARRTRRLYRRKRRRLQQLDKFIQRQGWPVIELEDYSDPLYPWKVR AELAASYIADEKERGEKLSVALRHIARHRGWRNPYAKVSSLYLPDGPSDAFK AIREEIKRASGQPVPETATVGQMVTLCELGTLKLRGEGGVLSARLQQSDYAR EIQEICRMQEIGQELYRKIIDVVFAAESPKGSASSRVGKDPLQPGKNRALKAS DAFQRYRIAALIGNLRVRVDGEKRILSVEEKNLVFDHLVNLTPKKEPEWVTIA EILGIDRGQLIGTATMTDDGERAGARPPTHDTNRSIVNSRIAPLVDWWKTA SALEQHAMVKALSNAEVDDFDSPEGAKVQAFFADLDDDVHAKLDSLHLPV GRAAYSEDTLVRLTRRMLSDGVDLYTARLQEFGIEPSWTPPTPRIGEPVGNP AVDRVLKTVSRWLESATKTWGAPERVIIEHVREGFVTEKRAREMDGDMRR RAARNAKLFQEMQEKLNVQGKPSRADLWRYQSVQRQNCQCAYCGSPITF SNSEMDHIVPRAGQGSTNTRENLVAVCHRCNQSKGNTPFAIWAKNTSIEG VSVKEAVERTRHWVTDTGMRSTDFKKFTKAVVERFQRATMDEEIDARSME SVAWMANELRSRVAQHFASHGTTVRVYRGSLTAEARRASGISGKLKFFDGV GKSRLDRRHHAIDAAVIAFTSDYVAETLAVRSNLKQSQAHRQEAPQWREFT GKDAEHRAAWRVWCQKMEKLSALLTEDLRDDRVVVMSNVRLRLGNGSA HKETIGKLSKVKLSSQLSVSDIDKASSEALWCALTREPGFDPKEGLPANPERHI RVNGTHVYAGDNIGLFPVSAGSIALRGGYAELGSSFHHARVYKITSGKKPAF AMLRVYTIDLLPYRNQDLFSVELKPQTMSMRQAEKKLRDALATGNAEYLG	9,017	N597A	H573A	D8A

		WLVVDDELVVDTSKIATDQVKAVEAELGTIRRWRVDGFFSPSKLRLRPLQM SKEGIKKESAPELSKIIDRPGWLPAVNKLFSDGNVTVVRRDSLGRVRLESTAH LPVTWKVQ				
CjeCas9	Campylobacter jejuni	MARILAFDIGISSIGWAFSENDELKDCGVRIFTKVENPKTGESLALPRRLARSA RKRLARRKARLNHLKHLIANEFKLNYEDYQSFDESLAKAYKGSLISPYELRFRA LNELLSKQDFARVILHIAKRRGYDDIKNSDDKEKGAILKAIKQNEEKLANYQS VGEYLYKEYFQKFKENSKEFTNVRNKKESYERCIAQSFLKDELKLIFKKQREFG FSFSKKFEEEVLSVAFYKRALKDFSHLVGNCSFFTDEKRAPKNSPLAFMFVAL TRIINLLNNLKNTEGILYTKDDLNALLNEVLKNGTLTYKQTKKLLGLSDDYEFK GEKGTYFIEFKKYKEFIKALGEHNLSQDDLNEIAKDITLIKDEIKLKKALAKYDLN QNQIDSLSKLEFKDHLNISFKALKLVTPLMLEGKKYDEACNELNLKVAINEDK KDFLPAFNETYYKDEVTNPVVLRAIKEYRKVLNALLKKYGKVHKINIELAREVG KNHSQRAKIEKEQNENYKAKKDAELECEKLGLKINSKNILKLRLFKEQKEFCAY SGEKIKISDLQDEKMLEIDHIYPYSRSFDDSYMNKVLVFTKQNQEKLNQTPFE AFGNDSAKWQKIEVLAKNLPTKKQKRILDKNYKDKEQKNFKDRNLNDTRYI ARLVLNYTKDYLDFLPLSDDENTKLNDTQKGSKVHVEAKSGMLTSALRHTW GFSAKDRNNHLHHAIDAVIIAYANNSIVKAFSDFKKEQESNSAELYAKKISELD YKNKRKFFEPFSGFRQKVLDKIDEIFVSKPERKKPSGALHEETFRKEEEFYQSY GGKEGVLKALELGKIRKVNGKIVKNGDMFRVDIFKHKKTNKFYAVPIYTMDF ALKVLPNKAVARSKKGEIKDWILMDENYEFCFSLYKDSLILIQTKDMQEPEFV YYNAFTSSTVSLIVSKHDNKFETLSKNQKILFKNANEKEVIAKSIGIQNLKVFEK YIVSALGEVTKAEFRQREDFKK	9,018	N582A	H559A	D8A
GeoCas9	Geobacillus stearothermophilus	MRYKIGLDIGITSVGWAVMNLDIPRIEDLGVRIFDRAENPQTGESLALPRRLA RSARRRLRRRKHRLERIRRLVIREGILTKEELDKLFEEKHEIDVWQLRVEALDR KLNNDELARVLLHLAKRRGFKSNRKSERSNKENSTMLKHIEENRAILSSYRTV GEMIVKDPKFALHKRNKGENYTNTIARDDLEREIRLIFSKQREFGNMSCTEEF ENEYITIWASQRPVASKDDIEKKVGFCTFEPKEKRAPKATYTFQSFIAWEHIN KLRLISPSGARGLTDEERRLLYEQAFQKNKITYHDIRTLLHLPDDTYFKGIVYDR GESRKQNENIRFLELDAYHQIRKAVDKVYGKGKSSSFLPIDFDTFGYALTLFKD DADIHSYLRNEYEQNGKRMPNLANKVYDNELIEELLNLSFTKFGHLSLKALRS ILPYMEQGEVYSSACERAGYTFTGPKKKQKTMLLPNIPPIANPVVMRALTQA RKVVNAIIKKYGSPVSIHIELARDLSQTFDERRKTKKEQDENRKKNETAIRQL MEYGLTLNPTGHDIVKFKLWSEQNGRCAYSLQPIEIERLLEPGYVEVDHVIPY SRSLDDSYTNKVLVLTRENREKGNRIPAEYLGVGTERWQQFETFVLTNKQFS KKKRDRLLRLHYDENEETEFKNRNLNDTRYISRFFANFIREHLKFAESDDKQK VYTVNGRVTAHLRSRWEFNKNREESDLHHAVDAVIVACTTPSDIAKVTAFY QRREQNKELAKKTEPHFPQPWPHFADELRARLSKHPKESIKALNLGNYDDQ KLESLQPVFVSRMPKRSVTGAAHQETLRRYVGIDERSGKIQTVVKTKLSEIKL DASGHFPMYGKESDPRTYEAIRQRLLEHNNDPKKAFQEPLYKPKKNGEPGP VIRTVKIIDTKNQVIPLNDGKTVAYNSNIVRVDVFEKDGKYYCVPVYTMDIM KGILPNKAIEPNKPYSEWKEMTEDYTFRFSLYPNDLIRIELPREKTVKTAAGEE INVKDVFVYYKTIDSANGGLELISHDHRFSLRGVGSRTLKRFEKYQVDVLGNI YKVRGEKRVGLASSAHSKPGKTIRPLQSTRD	9,019	N605A	H582A	D8A
iSpyMacCas9	Streptococcus spp.	MDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLF DSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFL VEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAH MIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRKLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLS KDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSAS MIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEF YKFIKPILEKMDGTEELLVKLKREDLLRKQRTFDNGSIPHQIHLGELHAILRRQ EDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFE EVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTE GMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVED RFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYA HLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANR NFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKV VDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQ	9,020	N863A	H840A	D10A

		ILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSF LKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKF DNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLI REVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPK LESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEI RKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEIQTVGQNGG LFDDNPKSPLEVTPSKLVPLKKELNPKKYGGYQKPTTAYPVLLITDTKQLIPISV MNKKQFEQNPVKFLRDRGYQQVGKNDFIKLPKYTLVDIGDGIKRLWASSKEI HKGNQLVVSKKSQILLYHAHHLDSDLSNDYLQNHNQQFDVLFNEIISFSKKC KLGKEHIQKIENVYSNKKNSASIEELAESFIKLLGFTQLGATSPFNFLGVKLNQ KQYKGKKDYILPCTEGTLIRQSITGLYETRVDLSKIGEDSGGSGGSKRTADGSE FES				
NmeCas9	Neisseria meningitidis	MAAFKPNSINYILGLDIGIASVGWAMVEIDEEENPIRLIDLGVRVFERAEVPK TGDSLAMARRLARSVRRLTRRRAHRLLRTRRLLKREGVLQAANFDENGLIKS LPNTPWQLRAAALDRKLTPLEWSAVLLHLIKHRGYLSQRKNEGETADKELG ALLKGVAGNAHALQTGDFRTPAELALNKFEKESGHIRNQRSDYSHTFSRKDL QAELILLFEKQKEFGNPHVSGGLKEGIETLLMTQRPALSGDAVQKMLGHCTF EPAEPKAAKNTYTAERFIWLTKLNNLRILEQGSERPLTDTERATLMDEPYRKS KLTYAQARKLLGLEDTAFFKGLRYGKDNAEASTLMEMKAYHAISRALEKEGL KDKKSPLNLSPELQDEIGTAFSLFKTDEDITGRLKDRIQPEILEALLKHISFDKFV QISLKALRRIVPLMEQGKRYDEACAEIYGDHYGKKNTEEKIYLPPIPADEIRNP VVLRALSQARKVINGVVRRYGSPARIHIETAREVGKSFKDRKEIEKRQEENRK DREKAAAKFREYFPNFVGEPKSKDILKLRLYEQQHGKCLYSGKEINLGRLNEK GYVEIDHALPFSRTWDDSFNNKVLVLGSENQNKGNQTPYEYFNGKDNSRE WQEFKARVETSRFPRSKKQRILLQKFDEDGFKERNLNDTRYVNRFLCQFVA DRMRLTGKGKKRVFASNGQITNLLRGFWGLRKVRAENDRHHALDAVVVA CSTVAMQQKITRFVRYKEMNAFDGKTIDKETGEVLHQKTHFPQPWEFFAQ EVMIRVFGKPDGKPEFEEADTLEKLRTLLAEKLSSRPEAVHEYVTPLFVSRAP NRKMSGQGHMETVKSAKRLDEGVSVLRVPLTQLKLKDLEKMVNREREPKL YEALKARLEAHKDDPAKAFAEPFYKYDKAGNRTQQVKAVRVEQVQKTGVW VRNHNGIADNATMVRVDVFEKGDKYYLVPIYSWQVAKGILPDRAVVQGKD EEDWQLIDDSFNFKFSLHPNDLVEVITKKARMFGYFASCHRGTGNINIRIHD LDHKIGKNGILEGIGVKTALSFQKYQIDELGKEIRPCRLKKRPPVR	9,021	N611A	H588A	D16A
ScaCas9	Streptococcus canis	MEKKYSIGLDIGTNSVGWAVITDDYKVPSKKFKVLGNTNRKSIKKNLMGALL FDSGETAEATRLKRTARRRYTRRKNRIRYLQEIFANEMAKLDDSFFQRLEESF LVEEDKKNERHPIFGNLADEVAYHRNYPTIYHLRKKLADSPEKADLRLIYLALA HIIKFRGHFLIEGKLNAENSDVAKLFYQLIQTYNQLFEESPLDEIEVDAKGILSA RLSKSKRLEKLIAVFPNEKKNGLFGNIIALALGLTPNFKSNFDLTEDAKLQLSKD TYDDDLDELLGQIGDQYADLFSAAKNLSDAILLSDILRSNSEVTKAPLSASMV KRYDEHHQDLALLKTLVRQQFPEKYAEIFKDDTKNGYAGYVDGIGIKHRKRTT KLATQEEFYKFIKPILEKMDGAEELLAKLNRDDLLRKQRTFDNGSIPHQIHLKE LHAILRRQEEFYPFLKENREKIEKILTFRIPYYVGPLARGNSRFAWLTRKSEEAI TPWNFEEVVDKGASAQSFIERMTNFDEQLPNKKVLPKHSLLYEYFTVYNELT KVKYVTERMRKPEFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSV EIIGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEE RLKTYAHLFDDKVMKQLKRRHYTGWGRLSRKMINGIRDKQSGKTILDFLKS DGFSNRNFMQLIHDDSLTFKEEIEKAQVSGQGDSLHEQIADLAGSPAIKKGIL QTVKIVDELVKVMGHKPENIVIEMARENQTTTKGLQQSRERKKRIEEGIKELE SQILKENPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVP QSFIKDDSIDNKVLTRSVENRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQ RKFDNLTKAERGGLSEADKAGFIKRQLVETRQITKHVARILDSRMNTKRDKN DKPIREVKVITLKSKLVSDFRKDFQLYKVRDINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKRFFYSNIMNFFKTEVKL ANGEIRKRPLIETNGETGEVVWNKEKDFATVRKVLAMPQVNIVKKTEVQTG GFSKESILSKRESAKLIPRKKGWDTRKYGGFGSPTVAYSILVVAKVEKGKAKKL KSVKVLVGITIMEKGSYEKDPIGFLEAKGYKDIKKELIFKLPKYSLFELENGRRR MLASATELQKANELVLPQHLVRLLYYTQNISATTGSNNLGYIEQHREEFKEIF EKIIDFSEKYILKNKVNSNLKSSFDEQFAVSDSILLSNSFVSLLKYTSFGASGGFT FLDLDVKQGRLRYQTVTEVLDATLIYQSITGLYETRTDLSQLGGD	9,022	N872A	H849A	D10A

ScaCas9-HiFi-Sc++	Streptococcus canis	MEKKYSIGLDIGTNSVGWAVITDDYKVPSKKFKVLGNTNRKSIKKNLMGALL FDSGETAEATRLKRTARRRYTRRKNRIRYLQEIFANEMAKLDDSFFQRLEESF LVEEDKKNERHPIFGNLADEVAYHRNYPTIYHLRKKLADSPEKADLRLIYLALA HIIKFRGHFLIEGKLNAENSDVAKLFYQLIQTYNQLFEESPLDEIEVDAKGILSA RLSKSKRLEKLIAVFPNEKKNGLFGNIIALALGLTPNFKSNFDLTEDAKLQLSKD TYDDDLDELLGQIGDQYADLFSAAKNLSDAILLSDILRSNSEVTKAPLSASMV KRYDEHHQDLALLKTLVRQQFPEKYAEIFKDDTKNGYAGYVGADKKLRKRS GKLATEEEFYKFIKPILEKMDGAEELLAKLNRDDLLRKQRTFDNGSIPHQIHLK ELHAILRRQEEFYPFLKENREKIEKILTFRIPYYVGPLARGNSRFAWLTRKSEEA ITPWNFEEVVDKGASAQSFIERMTNFDEQLPNKKVLPKHSLLYEYFTVYNEL TKVKYVTERMRKPEFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDS VEIIGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIE ERLKTYAHLFDDKVMKQLKRRHYTGWGRLSRKMINGIRDKQSGKTILDFLKS DGFSNANFMQLIHDDSLTFKEEIEKAQVSGQGDSLHEQIADLAGSPAIKKGIL QTVKIVDELVKVMGHKPENIVIEMARENQTTTKGLQQSRERKKRIEEGIKELE SQILKENPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVP QSFIKDDSIDNKVLTRSVENRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQ RKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVARILDSRMNTKRDKN DKPIREVKVITLKSKLVSDFRKDFQLYKVRDINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKRFFYSNIMNFFKTEVKL ANGEIRKRPLIETNGETGEVVWNKEKDFATVRKVLAMPQVNIVKKTEVQTG GFSKESILSKRESAKLIPRKKGWDTRKYGGFGSPTVAYSILVVAKVEKGKAKKL KSVKVLVGITIMEKGSYEKDPIGFLEAKGYKDIKKELIFKLPKYSLFELENGRRR MLASAKELQKANELVLPQHLVRLLYYTQNISATTGSNNLGYIEQHREEFKEIF EKIIDFSEKYILKNKVNSNLKSSFDEQFAVSDSILLSNSFVSLLKYTSFGASGGFT FLDLDVKQGRLRYQTVTEVLDATLIYQSITGLYETRTDLSQLGGD	9,023	N872A	H849A	D10A
SpyCas9-3var-NRRH	Streptococcus pyogenes	MDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLF DSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFL VEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAH MIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLS KDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSAS MVKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEE FYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGIIPHQIHLGELHAILRRQ GDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFE EVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTE GMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVED RFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYA HLFDDKVMKQLKRLRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRN FMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVV DELVKVMGGHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQI LKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSF LKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKF DNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLI REVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPK LESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEI RKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKGNSDKLIARKKDWDPKKYGGFNSPTAAYSVLVVAKVEKGKSKKLKSVK ELLGITIMERSSFEKNPIGFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLAS AGVLHKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDE IIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGVPAA FKYFDTTIDKKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGD	9,024	N863A	H840A	D10A
SpyCas9-3var-NRTH	Streptococcus pyogenes	MDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLF DSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFL VEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAH MIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLS KDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSAS MVKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEE	9,025	N863A	H840A	D10A

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

		VDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQ ILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSF LKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKF DNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLI REVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPK LESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEI RKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKE LLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASA GELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEII EQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAF KYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGD				
SpyCas9-QQR1	Streptococcus pyogenes	MDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLF DSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFL VEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAH MIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLS KDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSAS MIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEF YKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQ EDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFE EVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTE GMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVED RFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYA HLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANR NFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKV VDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQ ILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSF LKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKF DNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLI REVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPK LESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEI RKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKE LLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASA RELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEII EQISEFSKRVILADAQLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAF KYFDTTFKQKQYRSTKEVLDATLIHQSITGLYETRIDLSQLGGD	9,028	N863A	H840A	D10A
SpyCas9-SpG	Streptococcus pyogenes	MDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLF DSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFL VEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAH MIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLS KDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSAS MIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEF YKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQ EDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFE EVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTE GMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVED RFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYA HLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANR NFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKV VDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQ ILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSF LKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKF DNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLI REVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPK LESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEI RKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES	9,029	N863A	H840A	D10A

		ILPKRNSDKLIARKKDWDPKKYGGFLWPTVAYSVLVVAKVEKGKSKKLKSVK ELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLAS AKQLQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDE IIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAA FKYFDTTIDRKQYRSTKEVLDATLIHQSITGLYETRIDLSQLGGD				
SpyCas9-VQR	Streptococcus pyogenes	MDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLF DSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFL VEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAH MIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLS KDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSAS MIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEF YKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQ EDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFE EVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTE GMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVED RFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYA HLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANR NFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKV VDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQ ILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSF LKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKF DNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLI REVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPK LESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEI RKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFVSPTVAYSVLVVAKVEKGKSKKLKSVKE LLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASA GELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEII EQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAF KYFDTTIDRKQYRSTKEVLDATLIHQSITGLYETRIDLSQLGGD	9,030	N863A	H840A	D10A
SpyCas9-VRER	Streptococcus pyogenes	MDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLF DSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFL VEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAH MIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLS KDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSAS MIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEF YKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQ EDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFE EVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTE GMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVED RFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYA HLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANR NFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKV VDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQ ILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSF LKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKF DNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLI REVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPK LESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEI RKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFVSPTVAYSVLVVAKVEKGKSKKLKSVKE LLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASA RELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEII EQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAF KYFDTTIDRKEYRSTKEVLDATLIHQSITGLYETRIDLSQLGGD	9,031	N863A	H840A	D10A

SpyCas9-xCas	Streptococcus pyogenes	MDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLF DSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFL VEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAH MIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDTKLQLS KDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSAS MIKLYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEF YKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGIIPHQIHLGELHAILRRQE DFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEK VVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTE GMRKPAFLSGDQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVED RFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYA HLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANR NFIQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVV DELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQI LKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSF LKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKF DNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLI REVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPK LESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEI RKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKE LLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASA GVLQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEII EQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAF KYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGD	9,032	N863A	H840A	D10A
SpyCas9-xCas-NG	Streptococcus pyogenes	MDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLF DSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFL VEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAH MIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDTKLQLS KDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSAS MIKLYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEF YKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGIIPHQIHLGELHAILRRQE DFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEK VVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTE GMRKPAFLSGDQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVED RFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYA HLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANR NFIQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVV DELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQI LKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSF LKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKF DNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLI REVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPK LESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEI RKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES IRPKRNSDKLIARKKDWDPKKYGGFVSPTVAYSVLVVAKVEKGKSKKLKSVKE LLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASA RFLQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEII EQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPRAF KYFDTTIDRKVYRSTKEVLDATLIHQSITGLYETRIDLSQLGGD	9,033	N863A	H840A	D10A
St1Cas9-CNRZ1066	Streptococcus thermophilus	MSDLVLGLDIGIGSVGVGILNKVTGEIIHKNSRIFPAAQAENNLVRRTNRQG RRLARRKKHRRVRLNRLFEESGLITDFTKISINLNPYQLRVKGLTDELSNEELFI ALKNMVKHRGISYLDDASDDGNSSVGDYAQIVKENSKQLETKTPGQIQLER YQTYGQLRGDFTVEKDGKKHRLINVFPTSAYRSEALRILQTQQEFNPQITDEF INRYLEILTGKRKYYHGPGNEKSRTDYGRYRTSGETLDNIFGILIGKCTFYPDEF RAAKASYTAQEFNLLNDLNNLTVPTETKKLSKEQKNQIINYVKNEKAMGPAK LFKYIAKLLSCDVADIKGYRIDKSGKAEIHTFEAYRKMKTLETLDIEQMDRETL	9,034	N622A	H599A	D9A

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

St1Cas9-TH1477	Streptococcus thermophilus	MSDLVLGLDIGIGSVGVGILNKVTGEIIHKNSRIFPAAQAENNLVRRTNRQG RRLARRKKHRRVRLNRLFEESGLITDFTKISINLNPYQLRVKGLTDELSNEELFI ALKNMVKHRGISYLDDASDDGNSSVGDYAQIVKENSKQLETKTPGQIQLER YQTYGQLRGDFTVEKDGKKHRLINVFPTSAYRSEALRILQTQQEFNPQITDEF INRYLEILTGKRKYYHGPGNEKSRTDYGRYRTSGETLDNIFGILIGKCTFYPDEF RAAKASYTAQEFNLLNDLNNLTVPTETKKLSKEQKNQIINYVKNEKAMGPAK LFKYIAKLLSCDVADIKGYRIDKSGKAEIHTFEAYRKMKTLETLDIEQMDRETL DKLAYVLTLNTEREGIQEALEHEFADGSFSQKQVDELVQFRKANSSIFGKGW HNFSVKLMMELIPELYETSEEQMTILTRLGKQKTTSSSNKTKYIDEKLLTEEIY NPVVAKSVRQAIKIVNAAIKEYGDFDNIVIEMARETNEDDEKKAIQKIQKAN KDEKDAAMLKAANQYNGKAELPHSVFHGHKQLATKIRLWHQQGERCLYT GKTISIHDLINNSNQFEVDHILPLSITFDDSLANKVLVYATANQEKGQRTPYQ ALDSMDDAWSFRELKAFVRESKTLSNKKKEYLLTEEDISKFDVRKKFIERNLV DTRYASRVVLNALQEHFRAHKIDTKVSVVRGQFTSQLRRHWGIEKTRDTYH HHAVDALIIAASSQLNLWKKQKNTLVSYSEDQLLDIETGELISDDEYKESVFK APYQHFVDTLKSKEFEDSILFSYQVDSKFNRKISDATIYATRQAKVGKDKADE TYVLGKIKDIYTQDGYDAFMKIYKKDKSKFLMYRHDPQTFEKVIEPILENYPN KQINEKGKEVPCNPFLKYKEEHGYIRKYSKKGNGPEIKSLKYYDSKLGNHIDIT PKDSNNKVVLQSLKPWRTDVYFNKNTGKYEILGLKYSDMQFEKGTGKYSISK EQYENIKVREGVDENSEFKFTLYKNDLLLLKDSENGEQILLRFTSRNDTSKHYV ELKPYNRQKFEGSEYLIKSLGTVVKGGRCIKGLGKSNISIYKVRTDVLGNQHIIK NEGDKPKLDF	9,037	N622A	H599A	D9A
sRGN3.1	Staphylococcus spp.	MNQKFILGLDIGITSVGYGLIDYETKNIIDAGVRLFPEANVENNEGRRSKRGS RRLKRRRIHRLERVKLLLTEYDLINKEQIPTSNNPYQIRVKGLSEILSKDELAIAL LHLAKRRGIHNVDVAADKEETASDSLSTKDQINKNAKFLESRYVCELQKERLE NEGHVRGVENRFLTKDIVREAKKIIDTQMQYYPEIDETFKEKYISLVETRREYF EGPGQGSPFGWNGDLKKWYEMLMGHCTYFPQELRSVKYAYSADLFNALN DLNNLIIQRDNSEKLEYHEKYHIIENVFKQKKKPTLKQIAKEIGVNPEDIKGYRI TKSGTPEFTSFKLFHDLKKVVKDHAILDDIDLLNQIAEILTIYQDKDSIVAELGQ LEYLMSEADKQSISELTGYTGTHSLSLKCMNMIIDELWHSSMNQMEVFTYL NMRPKKYELKGYQRIPTDMIDDAILSPVVKRTFIQSINVINKVIEKYGIPEDIIIE LARENNSDDRKKFINNLQKKNEATRKRINEIIGQTGNQNAKRIVEKIRLHDQ QEGKCLYSLESIPLEDLLNNPNHYEVDHIIPRSVSFDNSYHNKVLVKQSENSK KSNLTPYQYFNSGKSKLSYNQFKQHILNLSKSQDRISKKKKEYLLEERDINKFE VQKEFINRNLVDTRYATRELTNYLKAYFSANNMNVKVKTINGSFTDYLRKV WKFKKERNHGYKHHAEDALIIANADFLFKENKKLKAVNSVLEKPEIETKQLDI QVDSEDNYSEMFIIPKQVQDIKDFRNFKYSHRVDKKPNRQLINDTLYSTRKK DNSTYIVQTIKDIYAKDNTTLKKQFDKSPEKFLMYQHDPRTFEKLEVIMKQYA NEKNPLAKYHEETGEYLTKYSKKNNGPIVKSLKYIGNKLGSHLDVTHQFKSST KKLVKLSIKNYRFDVYLTEKGYKFVTIAYLNVFKKDNYYYIPKDKYQELKEKKKI KDTDQFIASFYKNDLIKLNGDLYKIIGVNSDDRNIIELDYYDIKYKDYCEINNIK GEPRIKKTIGKKTESIEKFTTDVLGNLYLHSTEKAPQLIFKRGL	9,038	N585A	H562A	D10A
sRGN3.3	Staphylococcus spp.	MNQKFILGLDIGITSVGYGLIDYETKNIIDAGVRLFPEANVENNEGRRSKRGS RRLKRRRIHRLERVKLLLTEYDLINKEQIPTSNNPYQIRVKGLSEILSKDELAIAL LHLAKRRGIHNVDVAADKEETASDSLSTKDQINKNAKFLESRYVCELQKERLE NEGHVRGVENRFLTKDIVREAKKIIDTQMQYYPEIDETFKEKYISLVETRREYF EGPGQGSPFGWNGDLKKWYEMLMGHCTYFPQELRSVKYAYSADLFNALN DLNNLIIQRDNSEKLEYHEKYHIIENVFKQKKKPTLKQIAKEIGVNPEDIKGYRI TKSGTPEFTSFKLFHDLKKVVKDHAILDDIDLLNQIAEILTIYQDKDSIVAELGQ LEYLMSEADKQSISELTGYTGTHSLSLKCMNMIIDELWHSSMNQMEVFTYL NMRPKKYELKGYQRIPTDMIDDAILSPVVKRTFIQSINVINKVIEKYGIPEDIIIE LARENNSDDRKKFINNLQKKNEATRKRINEIIGQTGNQNAKRIVEKIRLHDQ QEGKCLYSLESIPLEDLLNNPNHYEVDHIIPRSVSFDNSYHNKVLVKQSENSK KSNLTPYQYFNSGKSKLSYNQFKQHILNLSKSQDRISKKKKEYLLEERDINKFE VQKEFINRNLVDTRYATRELTSYLKAYFSANNMDVKVKTINGSFTNHLRKV WRFDKYRNHGYKHHAEDALIIANADFLFKENKKLQNTNKILEKPTIENNTKK VTVEKEEDYNNVFETPKLVEDIKQYRDYKFSHRVDKKPNRQLINDTLYSTRM KDEHDYIVQTITDIYGKDNTNLKKQFNKNPEKFLMYQNDPKTFEKLSIIMKQ YSDEKNPLAKYYEETGEYLTKYSKKNNGPIVKKIKLLGNKVGNHLDVTNKYEN	9,039	N585A	H562A	D10A

		STKKLVKLSIKNYRFDVYLTEKGYKFVTIAYLNVFKKDNYYYIPKDKYQELKEKK KIKDTDQFIASFYKNDLIKLNGDLYKIIGVNSDDRNIIELDYYDIKYKDYCEINNI KGEPRIKKTIGKKTESIEKFTTDVLGNLYLHSTEKAPQLIFKRGL				

In some embodiments, a Cas protein requires a protospacer adjacent motif (PAM) to be present in or adjacent to a target DNA sequence for the Cas protein to bind and/or function. In some embodiments, the PAM is or comprises, from 5′ to 3′, NGG (SEQ ID NO: 11,024), YG (SEQ ID NO: 11,025), NNGRRT (SEQ ID NO: 11,026), NNNRRT (SEQ ID NO: 11,027), NGA (SEQ ID NO: 11,029), TYCV (SEQ ID NO: 11,030), TATV (SEQ ID NO: 11,031), NTTN (SEQ ID NO: 11,032), or NNNGATT (SEQ ID NO: 11,033), where N stands for any nucleotide, Y stands for C or T, R stands for A or G, and V stands for A or C or G.In some embodiments, a Cas protein is a protein listed in Table 7 or 8. In some embodiments, a Cas protein comprises one or more mutations altering its PAM. In some embodiments, a Cas protein comprises E1369R, E1449H, and R1556A mutations or analogous substitutions to the amino acids corresponding to said positions. In some embodiments, a Cas protein comprises E782K, N968K, and R1015H mutations or analogous substitutions to the amino acids corresponding to said positions. In some embodiments, a Cas protein comprises D1135V, R1335Q, and T1337R mutations or analogous substitutions to the amino acids corresponding to said positions. In some embodiments, a Cas protein comprises S542R and K607R mutations or analogous substitutions to the amino acids corresponding to said positions. In some embodiments, a Cas protein comprises S542R, K548V, and N552R mutations or analogous substitutions to the amino acids corresponding to said positions. Exemplary advances in the engineering of Cas enzymes to recognize altered PAM sequences are reviewed in Collias et al Nature Communications 12:555 (2021), incorporated herein by reference in its entirety.

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

In some embodiments, the Cas protein is modified to deactivate or partially deactivate the nuclease, e.g., nuclease-deficient Cas9. Whereas wild-type Cas9 generates double-strand breaks (DSBs) at specific DNA sequences targeted by a gRNA, a number of CRISPR endonucleases having modified functionalities are available, for example: a “nickase” version of Cas9 that has been partially deactivated generates only a single-strand break; a catalytically inactive Cas9

("dCas9") does not cut target DNA. In some embodiments, dCas9 binding to a DNA sequence may interfere with transcription at that site by steric hindrance. In some embodiments, dCas9 binding to an anchor sequence may interfere with (e.g., decrease or prevent) genomic complex (e.g., ASMC) formation and/or maintenance. In some embodiments, a DNA-binding domain comprises a catalytically inactive Cas9, e.g., dCas9. Many catalytically inactive Cas9 proteins are known in the art. In some embodiments, dCas9 comprises mutations in each endonuclease domain of the Cas protein, e.g., D10A and H840A or N863A mutations. In some embodiments, a catalytically inactive or partially inactive CRISPR/Cas domain comprises a Cas protein comprising one or more mutations, e.g., one or more of the mutations listed in Table 7. In some embodiments, a Cas protein described on a given row of Table 7 comprises one, two, three, or all of the mutations listed in the same row of Table 7. In some embodiments, a Cas protein, e.g., not described in Table 7, comprises one, two, three, or all of the mutations listed in a row of Table 7 or a corresponding mutation at a corresponding site in that Cas protein.

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

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

dCas9, comprises a D10 mutation (e.g., a D10A mutation) and a H557 mutation (e.g., a H557A mutation) or analogous substitutions to the amino acids corresponding to said positions.

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

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

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

In some embodiments, a catalytically inactive Cas9 protein, e.g., dCas9, or partially deactivated Cas9 protein comprises a D16 mutation (e.g., a D16A mutation) or an analogous substitution to the amino acid corresponding to said position. In some embodiments, a catalytically inactive Cas9 protein, e.g., dCas9, or partially deactivated Cas9 protein comprises a

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

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

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

selected from L1111R, G1218R, E1219F, D1332A, D1332S, D1332T, D1332V, D1332L, D1332K, D1332R, T1337L, T1337I, T1337V, T1337F, T1337S, T1337N, T1337K, T1337R, T1337H, T1337Q, and T1337M, or corresponding amino acid substitutions thereto.

In some embodiments, the endonuclease domain or DNA binding domain comprises a Cas domain, e.g., a Cas9 domain. In embodiments, the endonuclease domain or DNA binding domain comprises a nuclease-active Cas domain, a Cas nickase (nCas) domain, or a nuclease-inactive Cas (dCas) domain. In embodiments, the endonuclease domain or DNA binding domain comprises a nuclease-active Cas9 domain, a Cas9 nickase (nCas9) domain, or a nuclease-inactive Cas9 (dCas9) domain. In some embodiments, the endonuclease domain or DNA binding domain comprises a Cas9 domain of Cas9 (e.g., dCas9 and nCas9), Cas12a/Cpfl, Cas12b/C2cl, Cas12c/C2c3, Cas12d/CasY, Cas12e/CasX, Cas12g, Cas12h, or Cas12i. In some embodiments, the endonuclease domain or DNA binding domain comprises a Cas9 (e.g., dCas9 and nCas9), Cas12a/Cpfl, Cas12b/C2cl, Cas12c/C2c3, Cas12d/CasY, Cas12e/CasX, Cas12g, Cas12h, or Cas12i. In some embodiments, the endonuclease domain or DNA binding domain comprises an S. pyogenes or an S. thermophilus Cas9, or a functional fragment thereof. In some embodiments, the endonuclease domain or DNA binding domain comprises a Cas9 sequence, e.g., as described in Chylinski, Rhun, and Charpentier (2013) RNA Biology 10:5, 726-737; incorporated herein by reference. In some embodiments, the endonuclease domain or DNA binding domain comprises the HNH nuclease subdomain and/or the RuvC1 subdomain of a Cas, e.g., Cas9, e.g., as described herein, or a variant thereof. In some embodiments, the endonuclease domain or DNA binding domain comprises Cas12a/Cpfl, Cas12b/C2cl, Cas12c/C2c3, Cas12d/CasY, Cas12e/CasX, Cas12g, Cas12h, or Cas12i. In some embodiments, the endonuclease domain or DNA binding domain comprises a Cas polypeptide (e.g., enzyme), or a functional fragment thereof. In embodiments, the Cas polypeptide (e.g., enzyme) is selected from Cas1, Cas1B, Cas2, Cas3, Cas4, Cas5, Cas5d, Cas5t, Cas5h, Cas5a, Cas6, Cas7, Cas8, Cas8a, Cas8b, Cas8c, Cas9 (e.g., Csn1 or Csx12), Cas10, Cas10d, Cas12a/Cpfl, Cas12b/C2cl, Cas12c/C2c3, Cas12d/CasY, Cas12e/CasX, Cas12g, Cas12h, Cas12i, Csy1 , Csy2, Csy3, Csy4, Cse1, Cse2, Cse3, Cse4, Cse5e, Csc1, Csc2, Csa5, Csn1, Csn2, Csm1, Csm2, Csm3, Csm4, Csm5, Csm6, Cmr1, Cmr3, Cmr4, Cmr5, Cmr6, Csb1, Csb2, Csb3, Csx17, Csx14, Csx10, Csx16, CsaX, Csx3, Csx1, Csx1S, Csx11, Csf1, Csf2, CsO, Csf4, Csd1, Csd2, Cst1, Cst2, Csh1, Csh2, Csa1, Csa2, Csa3, Csa4, Csa5, Type II Cas effector proteins, Type V Cas effector proteins,

Type VI Cas effector proteins, CARF, DinG, Cpf1, Cas12b/C2c1, Cas12c/C2c3, Cas12b/C2c1, Cas12c/C2c3, SpCas9(K855A), eSpCas9(1.1), SpCas9-HF1, hyper accurate Cas9 variant (HypaCas9), homologues thereof, modified or engineered versions thereof, and/or functional fragments thereof. In embodiments, the Cas9 comprises one or more substitutions, e.g., selected from H840A, D10A, P475A, W476A, N477A, D1125A, W1126A, and D1127A. In embodiments, the Cas9 comprises one or more mutations at positions selected from: D10, G12, G17, E762, H840, N854, N863, H982, H983, A984, D986, and/or A987, e.g., one or more substitutions selected from D10A, G12A, G17A, E762A, H840A, N854A, N863A, H982A, H983A, A984A, and/or D986A. In some embodiments, the endonuclease domain or DNA binding domain comprises a Cas (e.g., Cas9) sequence from Corynebacterium ulcerans, Corynebacterium diphtheria, Spiroplasma syrphidicola, Prevotella intermedia, Spiroplasma taiwanense, Streptococcus iniae, Belliella baltica, Psychroflexus torquis, Streptococcus thermophilus, Listeria innocua, Campylobacter jejuni, Neisseria meningitidis, Streptococcus pyogenes, or Staphylococcus aureus, or a fragment or variant thereof.

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

In some embodiments, the endonuclease domain or DNA binding domain comprises spCas9, spCas9-VRQR(SEQ ID NO: 5019), spCas9- VRER(SEQ ID NO: 5020), xCas9 (sp), saCas9, saCas9-KKH, spCas9-MQKSER(SEQ ID NO: 5021), spCas9-LRKIQK(SEQ ID NO: 5022), or spCas9- LRVSQL(SEQ ID NO: 5023).

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

Cas9 nickase (H840A):

DKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEA
TRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGN
IVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDV
DKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLI

ALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAIL
LSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAG
YIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAI
LRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVV
DKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLS
GEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKII
KDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWG
RLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSL
HEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRE
RMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDV
DAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRK
FDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVI
TLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYK
VYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWD
KGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGG
FDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKK
DLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPED
NEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHL
FTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGD (SEQ
ID NO: 11,001)

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

SMDKKYSIGLAIGTNSVGWAVITDDYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGET
AEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPI
FGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDN
SDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLF
GNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLS
DAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNG
YAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGE
LHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFE
EVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKP
AFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDL

LKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYT
GWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQ
GDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQK
NSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLS
DYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLI
TQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIR
EVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVY
GDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETG
EIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPK
KYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYK
EVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKG
SPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAE
NIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGD
(SEQ ID NO: 5007)

TAL Effectors and Zinc Finger Nucleases

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

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

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

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

Table 9 – RVDs and Nucleic Acid Base Specificity

Target	Possible RVD Amino Acid Combinations												
A	NI	NN	CI	HI	KI								
G	NN	GN	SN	VN	LN	DN	QN	EN	HN	RH	NK	AN	FN
C	HD	RD	KD	ND	AD								
T	NG	HG	VG	IG	EG	MG	YG	AA	EP	VA	QG	KG	RG

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

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

repeats, may be removed or added in order to suit a specific target sequence. In an embodiment, the TAL effector molecule of the present invention comprises between 6.5 and 33.5 TAL effector domains, e.g., repeats. In an embodiment, TAL effector molecule of the present invention comprises between 8 and 33.5 TAL effector domains, e.g., repeats, e.g., between 10 and 25 TAL effector domains, e.g., repeats, e.g., between 10 and 14 TAL effector domains, e.g., repeats.

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

In addition to the TAL effector domains, the TAL effector molecule of the present invention may comprise additional sequences derived from a naturally occurring TAL effector. The length of the C-terminal and/or N-terminal sequence(s) included on each side of the TAL effector domain portion of the TAL effector molecule can vary and be selected by one skilled in the art, for example based on the studies of Zhang et al. (2011). Zhang et al., have characterized a number of C-terminal and N-terminal truncation mutants in Hax3 derived TAL-effector based proteins and have identified key elements, which contribute to optimal binding to the target sequence and thus activation of transcription. Generally, it was found that transcriptional activity is inversely correlated with the length of N-terminus. Regarding the C-terminus, an important element for DNA binding residues within the first 68 amino acids of the Hax 3 sequence was identified. Accordingly, in some embodiments, the first 68 amino acids on the C-terminal side of the TAL effector domains of the naturally occurring TAL effector is included in

the TAL effector molecule. Accordingly, in an embodiment, a TAL effector molecule comprises 1) one or more TAL effector domains derived from a naturally occurring TAL effector; 2) at least 70, 80, 90, 100, 110, 120, 130, 140, 150, 170, 180, 190, 200, 220, 230, 240, 250, 260, 270, 280 or more amino acids from the naturally occurring TAL effector on the N-terminal side of the TAL effector domains; and/or 3) at least 68, 80, 90, 100, 110, 120, 130, 140, 150, 170, 180, 190, 200, 220, 230, 240, 250, 260 or more amino acids from the naturally occurring TAL effector on the C-terminal side of the TAL effector domains.

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

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

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

Exemplary selection methods, including phage display and two-hybrid systems, are disclosed in U.S. Pat. Nos. 5,789,538; 5,925,523; 6,007,988; 6,013,453; 6,410,248; 6,140,466;

6,200,759; and 6,242,568; as well as International Patent Publication Nos. WO 98/37186; WO 98/53057; WO 00/27878; and WO 01/88197 and GB 2,338,237. In addition, enhancement of binding specificity for zinc finger proteins has been described, for example, in International Patent Publication No. WO 02/077227.

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

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

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

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

proteins). In some embodiments, the Zn finger molecule comprises at least three Zn finger proteins. In some embodiments, the Zn finger molecule comprises four, five or six fingers. In some embodiments, the Zn finger molecule comprises 8, 9, 10, 11 or 12 fingers. In some embodiments, a Zn finger molecule comprising three Zn finger proteins recognizes a target DNA sequence comprising 9 or 10 nucleotides. In some embodiments, a Zn finger molecule comprising four Zn finger proteins recognizes a target DNA sequence comprising 12 to 14 nucleotides. In some embodiments, a Zn finger molecule comprising six Zn finger proteins recognizes a target DNA sequence comprising 18 to 21 nucleotides.

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

Linkers

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

Table 10 Exemplary linker sequences

Amino Acid Sequence	SEQ ID NO
GGS	5101
GGSGGS	5102
GGSGGSGGS	5103
GGSGGSGGSGGS	5104
GGSGGSGGSGGSGGS	5105
GGSGGSGGSGGSGGSGGS	5106
GGGGS	5107
GGGGSGGGGS	5108
GGGGSGGGGSGGGGS	5109
GGGGSGGGGSGGGGSGGGGS	5110
GGGGSGGGGSGGGGSGGGGSGGGGS	5111
GGGGSGGGGSGGGGSGGGGSGGGGSGGGGS	5112
GGG	5113
GGGG	5114
GGGGG	5115
GGGGGG	5116
GGGGGGG	5117
GGGGGGGG	5118
GSS	5119
GSSGSS	5120
GSSGSSGSS	5121
GSSGSSGSSGSS	5122
GSSGSSGSSGSSGSS	5123
GSSGSSGSSGSSGSSGSS	5124
EAAAK	5125
EAAAKEAAAK	5126
EAAAKEAAAKEAAAK	5127
EAAAKEAAAKEAAAKEAAAK	5128
EAAAKEAAAKEAAAKEAAAKEAAAK	5129
EAAAKEAAAKEAAAKEAAAKEAAAKEAAAK	5130
PAP	5131
PAPAP	5132
PAPAPAP	5133
PAPAPAPAP	5134
PAPAPAPAPAP	5135
PAPAPAPAPAPAP	5136

Amino Acid Sequence	SEQ ID NO
GGSGGG	5137
GGGGGS	5138
GGSGSS	5139
GSSGGS	5140
GGSEAAAK	5141
EAAAKGGS	5142
GGSPAP	5143
PAPGGS	5144
GGGGSS	5145
GSSGGG	5146
GGGEAAAK	5147
EAAAKGGG	5148
GGGPAP	5149
PAPGGG	5150
GSSEAAAK	5151
EAAAKGSS	5152
GSSPAP	5153
PAPGSS	5154
EAAAKPAP	5155
PAPEAAAK	5156
GGSGGGGSS	5157
GGSGSSGGG	5158
GGGGGSGSS	5159
GGGGSSGGS	5160
GSSGGSGGG	5161
GSSGGGGGS	5162
GGSGGGEAAAK	5163
GGSEAAAKGGG	5164
GGGGGSEAAAK	5165
GGGEAAAKGGS	5166
EAAAKGGSGGG	5167
EAAAKGGGGGS	5168
GGSGGGPAP	5169
GGSPAPGGG	5170
GGGGGSPAP	5171
GGGPAPGGS	5172
PAPGGSGGG	5173
PAPGGGGGS	5174

Amino Acid Sequence	SEQ ID NO
GGSGSSEAAAK	5175
GGSEAAAKGSS	5176
GSSGGSEAAAK	5177
GSSEAAAKGGS	5178
EAAAKGGSGSS	5179
EAAAKGSSGGS	5180
GGSGSSPAP	5181
GGSPAPGSS	5182
GSSGGSPAP	5183
GSSPAPGGS	5184
PAPGGSGSS	5185
PAPGSSGGS	5186
GGSEAAAKPAP	5187
GGSPAPEAAAK	5188
EAAAKGGSPAP	5189
EAAAKPAPGGS	5190
PAPGGSEAAAK	5191
PAPEAAAKGGS	5192
GGGGSSEAAAK	5193
GGGEAAAKGSS	5194
GSSGGGEAAAK	5195
GSSEAAAKGGG	5196
EAAAKGGGGSS	5197
EAAAKGSSGGG	5198
GGGGSSPAP	5199
GGGPAPGSS	5200
GSSGGGPAP	5201
GSSPAPGGG	5202
PAPGGGGSS	5203
PAPGSSGGG	5204
GGGEAAAKPAP	5205
GGGPAPEAAAK	5206
EAAAKGGGPAP	5207
EAAAKPAPGGG	5208
PAPGGGEAAAK	5209
PAPEAAAKGGG	5210
GSSEAAAKPAP	5211
GSSPAPEAAAK	5212

Amino Acid Sequence	SEQ ID NO
EAAAKGSSPAP	5213
EAAAKPAPGSS	5214
PAPGSSEAAAK	5215
PAPEAAAKGSS	5216
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	5217
GGGGSEAAAKGGGGS	5218
EAAAKGGGGSEAAAK	5219
SGSETPGTSESATPES	5220
GSAGSAAGSGEF	5221
SGGSSGGSSGSETPGTSESATPESSGGSSGGSS	5222

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

Gene modifying polypeptide selection by pooled screening

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

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

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

A gene modifying polypeptide candidate may comprise 1) a Cas-nuclease, for example a wild-type Cas nuclease, e.g., a wild-type Cas9 nuclease, a mutant Cas nuclease, e.g., a Cas nickase, for example, a Cas9 nickase such as a Cas9 N863A nickase, or a Cas nuclease selected from **Table 7 or Table 8**, 2) a peptide linker, e.g., a sequence from **Table D or Table 10,** that may exhibit varying degrees of length, flexibility, hydrophobicity, and/or secondary structure; and 3) a reverse

transcriptase (RT), e.g. an RT domain from **Table D or Table 6**. A gene modifying polypeptide candidate library comprises: a plurality of different gene modifying polypeptide candidates that differ from each other with respect to one, two or all three of the Cas nuclease, peptide linker or RT domain components, or a plurality of nucleic acid expression vectors that encode such gene modifying polypeptide candidates.

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

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

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

may be removed by a full media change the next day and virus-containing media may be harvested 48 hours after. Lentiviral media may be concentrated using Lenti-X Concentrator (TaKaRa Biosciences) and 5 mL lentiviral aliquots may be made and stored at -80°C. Lentiviral titering is performed by enumerating colony forming units post-selection, e.g., post Puromycin selection.

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

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

In a particular embodiment, to ascertain whether genome editing occurs, BFP- or GFP-expressing mammalian cells, e.g., HEK293T or U2OS cells, may be infected with gene modifying library candidates and then transfected or electroporated with tgRNA plasmid or RNA, e.g., by electroporation of 250,000 cells/well with 200 ng of a tgRNA plasmid designed to convert BFP-to-GFP or GFP-to-BFP, at a cell count ensuring >250x-1000x coverage per library candidate. In such an embodiment, the genome-editing capacity of the various constructs in this assay may be

assessed by sorting the cells by Fluorescence-Activated Cell Sorting (FACS) for expression of the color-converted fluorescent protein (FP) at 4-10 days post-electroporation. Cells are sorted and harvested as distinct populations of unedited cells (exhibiting original florescence protein signal), edited cells (exhibiting converted fluorescence protein signal), and imperfect edit (exhibiting no florescence protein signal) cells. A sample of unsorted cells may also be harvested as the input population to determine candidate enrichment during analysis.

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

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

In some embodiments, multiple tgRNAs may be used to screen the gene modifying candidate library. In particular embodiments, a plurality of tgRNAs may be utilized to optimize template/Cas-linker-RT fusion pairs, e.g., for gene editing of particular target genes, for example, gene targets for the treatment of disease. In specific embodiments, a pooled approach to screening gene modifying candidates may be performed using a multiplicity of different tgRNAs in an arrayed format.

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

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

Sequences of exemplary Cas9-linker-RT fusions

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

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

Exemplary Gene Modifying Polypeptides

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

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

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

Table T1. Selection of exemplary gene modifying polypeptides

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

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

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

Table T2. Selection of exemplary gene modifying polypeptides

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

2338	GGSPAPEAAAK	15,429	MLVCB_P08361_3mutA
2527	GGSPAPEAAAK	15,430	MLVFF_P26809_3mutA
141	EAAAKGGSPAP	15,431	PERV_Q4VFZ2_3mut
341	EAAAKGGSPAP	15,432	PERV_Q4VFZ2_3mut
2315	EAAAKPAPGGS	15,433	MLVCB_P08361_3mutA
3080	EAAAKPAPGGS	15,434	MLVMS_P03355_3mutA_WS
2688	GGGGSSEAAAK	15,435	MLVMS_P03355_PLV919
2885	GGGGSSEAAAK	15,436	MLVMS_P03355_PLV919
2810	GSSGGGEAAAK	15,437	MLVMS_P03355_3mutA_WS
3057	GSSGGGEAAAK	15,438	MLVMS_P03355_3mutA_WS
1861	GSSEAAAKGGG	15,439	MLVAV_P03356_3mutA
3056	GSSGGGPAP	15,440	MLVMS_P03355_3mutA_WS
1038	GSSPAPGGG	15,441	XMRV6_A1Z651_3mutA
2308	PAPGGGGSS	15,442	MLVCB_P08361_3mutA
1672	GGGEAAAKPAP	15,443	KORV_Q9TTC1-Pro_3mutA
2526	GGGEAAAKPAP	15,444	MLVFF_P26809_3mutA
1938	GGGPAPEAAAK	15,445	BAEVM_P10272_3mutA
2641	GSSEAAAKPAP	15,446	MLVMS_P03355_PLV919
2891	GSSEAAAKPAP	15,447	MLVMS_P03355_PLV919
1225	GSSPAPEAAAK	15,448	FLV_P10273_3mutA
2839	GSSPAPEAAAK	15,449	MLVMS_P03355_3mutA_WS
3127	GSSPAPEAAAK	15,450	MLVMS_P03355_3mutA_WS
2798	PAPGSSEAAAK	15,451	MLVMS_P03355_3mutA_WS
3091	PAPGSSEAAAK	15,452	MLVMS_P03355_3mutA_WS
1372	AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	15,453	AVIRE_P03360_3mutA
1197	AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	15,454	FLV_P10273_3mutA
2611	AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	15,455	MLVMS_P03355_PLV919
2784	AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	15,456	MLVMS_P03355_3mutA_WS
480	AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	15,457	SFV1_P23074_2mutA
647	AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	15,458	SFV3L_P27401_2mutA

1006	AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	15,459	XMRV6_A1Z651_3mutA
2518	SGSETPGTSESATPES	15,460	MLVFF_P26809_3mutA

Subsequences of Exemplary Gene Modifying Polypeptides

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

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

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

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

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

In certain embodiments, the DNA binding domain comprises a DNA binding domain of a gene modifying polypeptide of any one of SEQ ID NOs: 1-7743, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto. In certain embodiments, the DNA binding domain comprises a DNA binding domain of a gene modifying polypeptide as listed in any of Tables A1, T1, or T2, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto. In certain embodiments, the DNA binding domain comprises a Cas domain (e.g., as listed in Table 8). In certain embodiments, the DNA binding domain comprises the amino acid sequence of a SpyCas9 polypeptide (e.g., as listed in Table 8, e.g., a Cas9 N863A polypeptide), or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto. In certain embodiments, the DNA binding domain comprises the amino acid sequence:

DKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLK
RTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYH
EKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYN
QLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFD
LAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASM
IKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDG
TEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIP
YYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSL
LYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDS
VEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAH
LFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFK
EDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQT
TQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRL
SDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKF
DNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSK
LVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKS
EQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM
PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGK
SKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASA
GELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVI

LADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDA TLIHQSITGLYETRIDLSQLGGD (SEQ ID NO: 11,096),
or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto.

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

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

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

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

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

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

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

Linkers and RT domains

In some embodiments, the gene modifying polypeptide comprises a linker (e.g., as described herein) and an RT domain (e.g., as described herein). In certain embodiments, the

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

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

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

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

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

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

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

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

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

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

RT Families and Mutants

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

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

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

In certain embodiments, a gene modifying polypeptide comprises comprises the amino acid sequence of an RT domain sequence from an AVIRE RT domain. In embodiments, the amino acid sequence of an RT domain sequence comprises one or more point mutations as listed in column 2 of Table M1, or a point mutation corresponding thereto. In embodiments, the amino acid sequence of an RT domain sequence comprises one or more point mutations as listed in column 4 of Table M1 (Gen2 AVIRE), or a point mutation corresponding thereto. In embodiments, the amino acid sequence of an RT domain sequence comprises one or more point mutations at an amino acid position of the RT domain as listed in columns 3 and 4 of Table M2, or an amino acid position corresponding thereto. In certain embodiments, the RT domain comprises an IENSSP (e.g., at the C-terminus).

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

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

E302K	E302K		
		T306K	T306K
F309N	Y309N		
W313F	W313F	W313F	W313F
T330P	G330P	T330P	G330P
L435G	T436G		
N454K	N455K		
D524G	D526G		
E562Q	E564Q		
D583N	D585N		
H594Q	H596Q		
L603W	L605W	L603W	L605W
D653N	D655N		
L671P	L673P		
		IENSSP at C-term	

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

WT residue & position			
MLVMS aa	**MLVMS position # ***	**AVIRE aa**	**AVIRE position # ***
H	8	Y	8
P	51	Q	51
S	67	T	67
E	69	E	69
T	197	T	197
D	200	D	200
H	204	N	204
E	302	E	302
T	306	T	306
F	309	Y	309
W	313	W	313
T	330	G	330
L	435	T	436
N	454	N	455
D	524	D	526
E	562	E	564
D	583	D	585

H	594	H	596
L	603	L	605
D	653	D	655
L	671	S	673

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

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

In embodiments, the RT domain comprises the amino acid sequence of an RT domain of a BAEVM RT (e.g., an BAEVM_P10272 sequence, e.g., SEQ ID NO: 8004), or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto. In some embodiments, the RT domain comprises the amino acid sequence of a BAEVM RT further

comprising one, two, three, four, or five mutations selected from the group consisting of D198N, E328P, L602W, T304K, and W311F, or a corresponding position in a homologous RT domain. In some embodiments, the RT domain comprises the amino acid sequence of a BAEVM RT further comprising one, two, or three mutations selected from the group consisting of D198N, E328P, and L602W, or a corresponding position in a homologous RT domain.

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

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

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

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

In embodiments, the RT domain comprises the amino acid sequence of an RT domain of a KORV RT (e.g., an KORV_Q9TTC1 sequence, e.g., SEQ ID NO: 8047), or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto. In some embodiments, the RT domain comprises the amino acid sequence of a GALV RT further comprising one, two, three, four, five, or six mutations selected from the group consisting of

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

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

In embodiments, the RT domain comprises the amino acid sequence of an RT domain of a MLVBM RT (e.g., an MLVBM_Q7SVK7 sequence, e.g., SEQ ID NO: 8056), or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto. In some embodiments, the RT domain comprises the amino acid sequence of a MLVBM RT further comprising one, two, three, four, or five mutations selected from the group consisting of D199N, T329P, L602W, T305K, and W312F, or a corresponding position in a homologous RT domain. In some embodiments, the RT domain comprises the amino acid sequence of a MLVBM RT further comprising one, two, and three mutations selected from the group consisting of D200N, T330P, and L603W, or a corresponding position in a homologous RT domain.

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

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

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

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

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

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

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

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

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

In certain embodiments, the RT domain of a gene modifying polypeptide comprises the amino acid sequence of an RT domain of an AVIRE RT, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto. In embodiments, the RT domain comprises the amino acid sequence of an RT domain comprised in a sequence listed in column 1 of Table A5, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto. In some embodiments, the gene modifying polypeptide further comprises a linker having at least 99% or 100% identity to SEQ ID NO: 5217 or SEQ ID NO:11,041.

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

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

AVIRE SEQ ID NOs:	MLVMS SEQ ID NOs:				
1	2704	3007	3038	2638	2930
2	2706	3007	3038	2639	2930
3	2708	3008	3039	2639	2931
4	2709	3008	3039	2640	2931
5	2709	3009	3040	2640	2932
6	2710	3010	3040	2641	2932
7	2957	3010	3041	2641	2933
9	2957	3011	3041	2642	2933
10	2958	3012	3042	2642	2934
12	2959	3012	3042	2643	2934
13	2960	3013	3043	2643	2935
14	2962	3013	3043	2644	2935
6076	6042	3014	3044	2644	2936
6143	6068	3014	3044	2645	2936
6200	6097	3015	3045	2645	2937
6254	6136	3015	3045	2646	2937
6274	6156	3016	3046	2646	2938
6315	6215	3016	3046	2647	2938
6328	6216	3017	3047	2647	2939
6337	6301	3018	3047	2648	2939
6403	6352	3018	3048	2648	2940
6420	6365	3019	3048	2649	2940
6440	6411	3019	3049	2649	2941
6513	6436	3020	3049	2650	2941
6552	6458	3020	3050	2650	2942
6613	6459	3021	3051	2651	2942

6671	6524	3021	3051	2651	2943
6822	6562	3022	3052	2652	2943
6840	6563	3023	3052	2652	2944
6884	6699	3023	3053	2653	2945
6907	6865	3024	3053	2653	2945
6970	7022	3024	3054	2654	2946
7025	7037	3025	3054	2655	2946
7052	7088	3025	3055	2655	2947
7078	7116	3026	3055	2656	2947
7243	7175	3026	3056	2656	2948
7253	7200	3027	3056	2657	2948
7318	7206	3027	3057	2657	2949
7379	7277	3028	3057	2658	2949
7486	7294	3028	3058	2658	2950
7524	7330	3029	3058	2659	2950
7668	7411	3030	3059	2659	2951
7680	7455	3030	3059	2660	2951
7720	7477	3031	3060	2660	2952
1137	7511	3031	3060	2661	2952
1138	7538	3032	3061	2661	2953
1139	7559	3032	3061	2662	2953
1140	7560	3033	3062	2662	2954
1141	7593	3033	3062	2663	2954
1142	7594	3034	3063	2663	2955
1143	7607	3034	3063	2664	2955
1144	7623	6025	3064	2664	6485
1145	7638	6041	3064	2665	6486
1146	7717	6043	3065	2665	6504
1147	7731	6098	3065	2666	6505
1148	7732	6099	3066	2666	6595
1149	2711	6180	3066	2667	6596
1150	2711	6182	3067	2667	6751
1151	2712	6237	3067	2668	6752
1152	2712	6238	3068	2668	6777
1153	2713	6311	3068	2669	6778
1154	2713	6312	3069	2669	7172
1155	2714	6578	3069	2670	7174
1156	2714	6579	3070	2670	7313
1157	2715	6663	3070	2671	7314
1158	2715	6664	3071	2671	
1159	2716	6708	3071	2672	

1160	2716	6709	3072	2672	
1161	2717	6809	3072	2673	
1162	2717	6831	3073	2673	
1163	2718	6832	3073	2674	
1164	2718	6864	3074	2674	
1165	2719	6866	3074	2675	
1166	2719	7089	3075	2675	
1167	2720	7157	3075	2676	
6015	2720	7159	3076	2676	
6029	2721	7173	3076	2677	
6045	2721	7176	3077	2677	
6077	2722	7293	3077	2678	
6129	2722	7295	3078	2678	
6144	2723	7343	3078	2679	
6164	2723	7393	3079	2680	
6201	2724	7394	3079	2680	
6227	2724	7425	3080	2681	
6244	2725	7426	3080	2681	
6250	2725	7444	3081	2682	
6264	2726	7445	3081	2682	
6289	2726	7476	3082	2683	
6304	2727	7478	3082	2683	
6316	2727	7496	3083	2684	
6384	2728	7497	3083	2684	
6421	2728	7537	3084	2685	
6441	2729	7539	3084	2685	
6492	2729	2780	3085	2686	
6514	2730	2780	3085	2686	
6530	2730	2781	3086	2687	
6569	2731	2781	3086	2687	
6584	2731	2782	3087	2688	
6621	2732	2782	3087	2688	
6651	2732	2783	3088	2689	
6659	2733	2783	3088	2689	
6683	2734	2784	3089	2690	
6703	2734	2784	3089	2690	
6727	2735	2785	3090	2691	
6732	2735	2785	3090	2692	
6745	2736	2786	3091	2692	
6755	2736	2786	3091	2693	
6784	2737	2787	3092	2693	

6817	2737	2787	3092	2694	
6823	2738	2788	3093	2694	
6841	2739	2788	3093	2695	
6871	2740	2789	3094	2695	
6885	2740	2789	3095	2696	
6898	2741	2790	3095	2696	
6908	2741	2790	3096	2697	
6933	2742	2791	3096	2697	
6971	2742	2791	3097	2698	
7009	2743	2792	3097	2698	
7018	2743	2792	3098	2699	
7045	2744	2793	3098	2699	
7053	2744	2793	3099	2700	
7068	2745	2794	3099	2700	
7079	2745	2794	3100	2701	
7096	2746	2795	3100	2701	
7104	2746	2795	3101	2702	
7122	2747	2796	3101	2702	
7151	2747	2796	3102	2703	
7163	2748	2797	3102	2703	
7181	2748	2797	3103	2862	
7244	2749	2798	3103	2862	
7273	2750	2798	3104	2863	
7319	2750	2799	3104	2863	
7336	2751	2799	3105	2864	
7380	2751	2800	3105	2864	
7402	2752	2800	3106	2865	
7462	2752	2801	3106	2865	
7487	2753	2801	3107	2866	
7525	2753	2802	3107	2866	
7569	2754	2802	3108	2867	
7626	2754	2803	3108	2867	
7689	2755	2803	3109	2868	
7707	2755	2804	3109	2868	
7721	2756	2804	3110	2869	
1371	2756	2805	3110	2869	
1372	2757	2805	3111	2870	
1373	2758	2806	3111	2870	
1374	2758	2806	3112	2871	
1375	2759	2807	3112	2871	
1376	2759	2807	3113	2872	

1377	2760	2808	3113	2872	
1378	2760	2808	3114	2873	
1379	2761	2809	3114	2873	
1380	2761	2809	3115	2874	
1381	2762	2810	3115	2874	
1382	2762	2810	3116	2875	
1383	2763	2811	3116	2875	
1384	2763	2811	3117	2876	
1385	2764	2812	3117	2876	
1386	2764	2812	3118	2877	
1387	2765	2813	3118	2877	
1388	2765	2813	3119	2878	
1389	2766	2814	3119	2878	
1390	2766	2814	3120	2879	
1391	2767	2815	3120	2879	
1392	2767	2815	3121	2880	
1393	2768	2816	3121	2880	
1394	2768	2816	3122	2881	
1395	2769	2817	3122	2881	
1396	2769	2817	3123	2882	
1397	2770	2818	3123	2882	
1398	2770	2818	3124	2883	
1399	2771	2819	3124	2883	
1400	2771	2819	3125	2884	
1401	2772	2820	3125	2884	
1402	2773	2820	3126	2885	
1403	2773	2821	3126	2885	
1404	2774	2821	3127	2886	
1405	2774	2822	3127	2886	
1406	2775	2822	3128	2887	
1407	2775	2823	3128	2887	
1408	2776	2823	3129	2888	
1409	2776	2824	3129	2888	
1410	2777	2824	3130	2889	
1411	2777	2825	3130	2889	
1412	2778	2825	3131	2890	
1413	2779	2826	3131	2890	
1414	2779	2826	3132	2891	
1415	2965	2827	3133	2891	
1416	2965	2827	3133	2892	
1417	2966	2828	3134	2893	

1418	2966	2828	3134	2893	
1419	2967	2829	3135	2894	
1420	2968	2829	3135	2894	
1421	2968	2830	3136	2895	
1422	2969	2830	3136	2895	
1423	2969	2831	6181	2896	
1424	2970	2831	6183	2896	
1425	2970	2832	6284	2897	
1426	2971	2832	6285	2897	
1427	2971	2833	6760	2898	
1428	2972	2833	6761	2898	
1429	2972	2834	7036	2899	
1430	2973	2834	7038	2899	
1431	2974	2835	7158	2900	
1432	2974	2835	7160	2900	
1433	2975	2836	2610	2901	
1434	2976	2836	2610	2901	
1435	2976	2837	2611	2902	
1436	2977	2837	2611	2902	
1437	2977	2838	2612	2903	
1439	2978	2838	2612	2903	
1440	2978	2839	2613	2904	
1441	2979	2839	2613	2904	
1442	2979	2840	2614	2905	
1443	2980	2840	2614	2905	
1444	2980	2841	2615	2906	
1445	2981	2841	2615	2906	
1446	2981	2842	2616	2907	
1447	2982	2842	2616	2907	
6001	2982	2843	2617	2908	
6030	2983	2843	2617	2908	
6078	2983	2844	2618	2909	
6108	2984	2844	2618	2909	
6130	2985	2845	2619	2910	
6165	2985	2845	2619	2910	
6265	2986	2846	2620	2911	
6275	2987	2846	2620	2911	
6305	2987	2847	2621	2912	
6329	2988	2847	2621	2912	
6370	2988	2848	2622	2913	
6385	2989	2848	2622	2913	

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

Systems

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

(e.g., a gRNA that binds to a polypeptide that induces a nick, e.g., in the opposite strand of the target DNA bound by the gene modifying polypeptide).

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

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

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

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

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

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

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

In certain embodiments, the gene modifying polypeptide comprises the linker of an amino acid sequence selected from SEQ ID NOs: 1-7743, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto. In certain embodiments, the gene modifying polypeptide comprises a sequence encoding the linker of a polypeptide having an amino acid sequence selected from SEQ ID NOs: 6001-7743, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto. In certain embodiments, the gene modifying polypeptide comprises a sequence encoding the linker of a

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

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

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

SEQ ID NO:	Amino Acid Sequence
34	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSPAPGGLDDEYRLYSPLVKPDQNIQF HCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
35	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSPAPGGLDDEYRLYSPLVKPDQNIQF

	WLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDI HPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDL LLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPL TKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTL GQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYV VEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRL AIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFESPKKKAKVE
35	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
36	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI

	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAA AKEAAAKEAAAKAGGLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPV QSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQG FKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIP APTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVA YLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHD CHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHG AIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAK VE
36	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAA AKEAAAKEAAAKAGGLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPV QSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQG FKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIP APTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVA YLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHD CHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHG AIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAK VE
37	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK

	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKGGLDDEYRLYSPLVKPDQ NIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKR VQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQY VDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFCRLFIPGFATLAAP LYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDAD KLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDG SSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRLAI PKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
38	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGSSPAPGGLDDEYRLYSPLVKPDQNIQFWL EQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHP TVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLL AGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPLTK PKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQ NITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVE GKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRLAI IHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
39	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD

	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAAKGGLDDEYR LYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRP VQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRI QHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFCRLF IPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIA AVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLT GEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRL ILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
40	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
40	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK

	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGGEAAAKGGLDDEYRLYSPLVKPDQNIQF
	WLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDI
	HPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDL
	LLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPL
	TKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTL
	GQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYV
	VEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRL
	AIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
41	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGGEAAAKGGLDDEYRLYSPLVKPDQNIQ
	FWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQD
	IHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDD
	LLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFCRLFIPGFATLAAPLYP
	LTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLT
	LGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSY
	VVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKR
	LAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
41	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL

	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSSGSSGSSGGLDDEYRLYSPLVKPDQNIQ FWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQD VVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKR LAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
43	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSSPAPGGLDDEYRLYSPLVKPDQNIQFWL EQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHP TVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLL AGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPLTK PKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQ NITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVE GKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRLAI IHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
47	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH

	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGSSPAPGGLDDEYRLYSPLVKPDQNIQFWLEQF
	PQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVP
	NPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQFLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGA
	TKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPLTKPKG
	EFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQTH
	VIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKR
	MAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRLAIIHC
	PGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
48	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGGLDDEYRLYSPLVKPDQNIQFWLE
	QFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPT
	VPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQFLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLA
	GATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPLTKP
	KGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQN
	ITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEG
	KRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRLAII
	HCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
49	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER

	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSEAAAKPAPGGLDDEYRLYSPLVKPDQNIQF WLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVPRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDI HPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQY LLAGATKQDCLEGTKALLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFCRLFIPGFATLAAP KLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDG SSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHL PKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
51	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGGGGSGGGGSGGGGSGGLDDEYRLYSPLVKPDQ NIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKR VQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQY VDDLLLAGATKQDCLEGTKALLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFCRLFIPGFATLAAP LYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDAD KLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDG SSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHL PKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
62	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL

	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPGGLDDEYRLYSPLVKPDQNIQF WLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDI HPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDL LLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPL TKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTL GQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYV VEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRL AIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
65	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGEAAAKGGSGGLDDEYRLYSPLVKPDQNIQF WLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDI HPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDL LLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPL TKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTL GQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYV VEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRL AIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
83	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA

	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGSSGGSGGLDDEYRLYSPLVKPDQNIQF
	WLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDI
	HPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDL
	LLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPL
	TKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTL
	GQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYV
	VEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRL
	AIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
90	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGSGSETPGTSESATPESGGLDDEYRLYSPLVKPD
	PLYPLITKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDA
	QNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNK
	DKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTD
	RVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQ
	GSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALH
	YVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFCRLFIPGFATLAA
	LPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
97	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT

	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILLRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGSEAAAKGGTLQLDDEYRLYSPLVK PDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREV NKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFDEALHRDLANFRIQHPQVTL LQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATL AAPLYPLTKEKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVK DADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWF TDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGLLTSAGREIKNKEEILSLLEA LHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
112	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILLRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGPAPGGTLQLDDEYRLYSPLVKPDQN IQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRV QDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFDEALHRDLANFRIQHPQVTLLQYV DDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPL YPLTKEKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADK LTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGS SYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGLLTSAGREIKNKEEILSLLEALHLP KRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE

113	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGSGSSGSGSSGGTLQLDDEYRLYSP LVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDL REVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQ VTLLQYVDDLLLAGATKQDCLEGTKALLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGF ATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAI LVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVL TWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSL LEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFESPKKKAKVE
113	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGSGSSGSGSSGGTLQLDDEYRLYSP LVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDL REVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQ VTLLQYVDDLLLAGATKQDCLEGTKALLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGF ATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAI LVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVL

	TWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSL LEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
117	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAAKEAAAKGGT LQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRK PGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALH RDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLG TAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGW REIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
117	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAAKEAAAKGGT LQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRK PGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALH RDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLG TAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGW

	PVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRK
	DLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSININIYTDSRYAFATAHVHGAIYKQRGWLTSAG
	REIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
121	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSSEAAAKGGTLQLDDEYRLYSPLVKPDQN
	IQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRV
	QDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYV
	DDLLLAGATKQDCLEGTKALLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPL
	YPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADK
	LTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTGEVLTWFTDGS
	SYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSININIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLP
	KRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
121	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSSEAAAKGGTLQLDDEYRLYSPLVKPDQN
	IQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRV
	QDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYV
	DDLLLAGATKQDCLEGTKALLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPL

	YPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADK LTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGS SYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLP KRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFESPKKKAKVE
122	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGSGSETPGTSESATPESGGTLQLDDEYRLYSPLV KPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLRE VNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVT LLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFAT LAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILV KDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTW FTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLE ALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFESPKKKAKVE
123	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGSSGGTLQLDDEYRLYSPLVKPDQNIQFWL EQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHP TVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLL

	AGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTK PKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQ NITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVE GKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRLAI IHCPGHQKADPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
124	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGGTLQLDDEYRLYSPLVKPDQNIQF WLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDI
126	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGGTLQLDDEYRLYSPLVKPDQNIQF WLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDI

	HPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDL LLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPL TKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTL GQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYV VEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRL AIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
127	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGGEAAAKGGTLQLDDEYRLYSPLVKPDQN
133	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSEAAAKGGGGGTLQLDDEYRLYSPLVKPDQN

	IQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRV QDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYV DDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPL YPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADK LTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGS SYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLP KRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFESPKKKAKVE
138	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
139	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI

	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGSSEAAAKGGTLQLDDEYRLYSPLVKPDQN
	IQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRV
	QDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYV
	DDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPL
	YPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADK
	LTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGS
	SYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLP
	KRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
140	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGSGGSSGSETPGTSESATPESSGGSSGGSS
	GGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLP
	VRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNE
	ALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVRE
	FLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVA
	SGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETG
	VRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLT
	SAGREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
141	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY

	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSPAPGGTLQLDDEYRLYSPLVKPDQN IQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRV QDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYV DDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPL YPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADK LTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGS SYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLP KRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
142	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD REVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQ VTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGF ATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAI LVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVL TWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSL LEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
142	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV

	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGSGGSGGSGGTLQLDDEYRLYSP LVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDL REVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQ VTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGF ATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAI LVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLEETGVRKDLTDIPLTGEVL TWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSININIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSL LEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
144	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGSGGSGGTLQLDDEYRLYSPLVKPDQNIQ FWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQD IHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDD LLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYP LTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLT LGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSY VVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSININIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKR LAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
147	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK

	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGTLQLDDEYRLYSPLVKPDQNIQFWLE QFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPT VPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLA GATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKP KGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQN ITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEG KRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRLAII HCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
151	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGTLQLDDEYRLYSPLVKPDQNIQFWLE QFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPT VPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLA GATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKP KGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQN ITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEG KRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRLAII HCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
156	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD

	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKALEAEAAAKEAA AKEAAAKEAAAKAGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGIL VPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRL PQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVV QIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRR PVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPV THDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAH VHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKK AKVE
156	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKALEAEAAAKEAA AKEAAAKEAAAKAGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGIL VPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRL PQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVV QIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRR PVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPV THDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAH VHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKK AKVE
157	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH

	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	RVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQ
	YVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPL
	PLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADK
	DKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTD
	QNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNK
	RLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
164	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSPAPEAAAKGGTLQLDDEYRLYSPLVKPDQN
	IQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRV
	QDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYV
	DDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPL
	YPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADK
	LTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGS
	SYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSININYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLP
	KRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
168	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER

	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKPAPGGSGGTLQLDDEYRLYSPLVKPDQN IQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRV QDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYV DDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPL YPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADK LTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGS SYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLP KRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
173	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKPAPGGSGGTLQLDDEYRLYSPLVKPDQNIQ FWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQD IHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDD LLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYP LTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLT LGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSY VVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKR LAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
190	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL

	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKALEAEAAAKEAA
	AKEAAAKEAAAKAGGLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPV
	QSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQG
	FKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIP
	APTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVA
	YLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHD
	CHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHG
	AIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAK
	VE
190	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKALEAEAAAKEAA
	AKEAAAKEAAAKAGGLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPV
	QSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQG
	FKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIP
	APTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVA
	YLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHD
	CHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHG
	AIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAK
	VE

191	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV PDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREV NKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTL LQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFCRLFIPGFATL AAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVK DADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWF TDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEA LHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFESPKKKAKVE
192	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGSGGSGSGGSGGLDDEYRLYSPLVK WLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDI HPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDL LLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPL TKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTL GQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYV

	VEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRL AIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
193	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAAKEAAAKGGL DDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGT NDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDL ANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAG FCRLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVC LKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLT DIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREI KNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
195	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSPAPGGLDDEYRLYSPLVKPDQNIQF WLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDI HPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDL LLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPL TKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTL

	GQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYV VEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRL AIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
195	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSPAPGGLDDEYRLYSPLVKPDQNIQF WLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDI HPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDL LLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPL TKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTL GQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYV VEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRL AIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
196	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGSGSETPGTSESATPESGGLDDEYRLYSPLVKPD QNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNK RVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQ YVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFCRLFIPGFATLAA

	PLYPLTKPKGEFSWAPEHQKAFDAIKKALSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDA
	DKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTD
	GSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALH
	LPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
199	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGGEAAAKGGLDDEYRLYSPLVKPDQNIQF
	WLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDI
	HPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDL
	LLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPL
	TKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTL
	GQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYV
	VEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRL
	AIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
199	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGGEAAAKGGLDDEYRLYSPLVKPDQNIQF
	WLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDI
	HPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDL

	LLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPL TKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTL GQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYV VEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRL AIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFESPKKKAKVE
202	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSSPAPGGLDDEYRLYSPLVKPDQNIQFWL EQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHP

	TVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLL AGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPLTK PKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQ NITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVE GKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRLAI IHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
208	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGSSGGSGGLDDEYRLYSPLVKPDQNIQFWLEQF
212	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGSSGGSGGLDDEYRLYSPLVKPDQNIQFWLEQF

	PQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVP NPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGA TKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPLTKPKG EFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNIT VIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKR MAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSININIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRLAIIHC PGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
213	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
216	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI

	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSGGGGSGGGGSGGLDDEYRLYSPLVKPDQ
	NIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKR
	VQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQY
	VDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFCRLFIPGFATLAAP
	LYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDAD
	KLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDG
	SSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHL
	PKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
217	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGSEAAAKGGLDDEYRLYSPLVKPDQNIQF
	WLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDI
	HPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDL
	LLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPL
	TKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTL
	GQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYV
	VEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRL
	AIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFESPKKKAKVE
219	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY

	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGGLDDEYRLYSPLVKPDQNIQFWLE QFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPT VPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLA GATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPLTKP KGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQN ITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEG KRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRLAII HCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
223	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSPAPGGLDDEYRLYSPLVKPDQNIQFWLEQF PQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVP NPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGA TKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPLTKPKG EFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNIT VIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKR MAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRLAIIHC PGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
224	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV

	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKPAPGSSGGLDDEYRLYSPLVKPDQNIQF WLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDI HPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDL LLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPL TKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTL GQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYV VEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSININIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRL AIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
225	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGSSEAAAKGGLDDEYRLYSPLVKPDQNIQF WLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDI HPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDL LLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPL TKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTL GQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYV VEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSININIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRL AIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
228	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK

	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGSSGSSGGSSGGLDDEYRLYSPLVKPDQNIQ
	FWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQD
	IHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDD
	LLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFCRLFIPGFATLAAPLYP
	LTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFFLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLT
	LGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSY
	VVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKR
	LAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
228	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGSSGSSGGLDDEYRLYSPLVKPDQNIQ
	FWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQD
	IHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDD
	LLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFCRLFIPGFATLAAPLYP
	LTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFFLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLT
	LGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSY
	VVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKR
	LAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
229	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD

	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGEAAAKGGSGGLDDEYRLYSPLVKPDQNIQF WLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDI HPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDL LLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPL TKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTL GQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYV VEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEIKLSLLEALHLPKRL AIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFESPKKKAKVE
232	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAAKGGLDDEYR LYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRP VQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRI QHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFCRLF IPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIA AVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLT GEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEE ILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFESPKKKAKVE
235	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK

	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGSGGSGGLDDEYRLYSPLVKPDQNIQFWLEQF
	PQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVP
	NPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGA
	TKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPLTKPKG
	EFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNIT
	VIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKR
	MAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRLAIIHC
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	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
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	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSEAAAKPAPGGLDDEYRLYSPLVKPDQNIQF
	WLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDI
	HPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDL
	LLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPL
	TKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTL
	GQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYV
	VEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRL
	AIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
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	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL

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	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
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	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGSGGLDDEYRLYSPLVKPDQNIQFWLEQF
	PQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVP
	NPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGA
	TKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPLTKPKG
	EFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNIT
	VIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKR
	MAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRLAIIHC
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	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
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	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
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	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSEAAAKGGSGGLDDEYRLYSPLVKPDQNIQF
	WLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDI
	HPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDL
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	TKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTL
	GQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYV
	VEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRL
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	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
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	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
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	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
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	IQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHP
	QDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFDEALHRDLANFRIQHPQVTLLQYV
	DDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPL
	YPLTKEKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADK
	LTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGS
	SYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSININYTDSRYAFATAHVHGAIYKQRGLLTSAGREIKNKEEILSLLEALHLP
	KRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
278	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGPAPGGTLQLDDEYRLYSPLVKPDQN
	IQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRV
	QDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFDEALHRDLANFRIQHPQVTLLQYV
	DDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPL
	YPLTKEKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADK
	LTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGS
	SYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSININYTDSRYAFATAHVHGAIYKQRGLLTSAGREIKNKEEILSLLEALHLP
	KRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
279	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER

	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKGGTLQLDDEYRLYSPLVK PDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREV NKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFDEALHRDLANFRIQHPQVTL LQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATL AAPLYPLTKEKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVK DADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWF TDGSSYVVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGLLTSAGREIKNKEEILSLLEA LHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
280	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKGGTLQLDDEYRLYSPLVK PDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREV NKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFDEALHRDLANFRIQHPQVTL LQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATL AAPLYPLTKEKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVK DADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWF TDGSSYVVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGLLTSAGREIKNKEEILSLLEA LHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE REIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
298	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL

	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKGGTLQLDDEYRLYSPLVK PDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREV NKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTL LQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATL AAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVK DADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWF TDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEA LHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
299	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSGGGGTLQLDDEYRLYSPLVKPDQN IQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRV QDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYV DDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPL YPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADK LTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGS SYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLP KRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
300	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA

	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKALEAEAAAKEAA AKEAAAKEAAAKAGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGIL VPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRL PQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVV QIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRR PVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPV THDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAH VHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKK AKVE
300	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKALEAEAAAKEAA AKEAAAKEAAAKAGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGIL VPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRL PQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVV QIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRR PVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPV THDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAH VHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKK AKVE

302	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV IQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRV QDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYV DDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPL YPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADK LTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGS SYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLP KRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
303	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSPAPEAAAKGGTLQLDDEYRLYSPLVKPDQN ALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVRE FLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVA SGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETG

	VRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLT SAGREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
304	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKPAPGSSGGTLQLDDEYRLYSPLVKPDQN IQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRV QDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYV DDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPL YPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADK LTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGS SYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLP KRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
305	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGGEAAAKGGTLQLDDEYRLYSPLVKPDQN IQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRV QDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYV DDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPL YPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADK

	LTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGS SYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLP KRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
306	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGGTLQLDDEYRLYSPLVKPDQNIQF WLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDI HPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDL LLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPL TKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTL GQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYV VEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRL AIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
307	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSSPAPGGTLQLDDEYRLYSPLVKPDQNIQ FWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQD IHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDD LLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYP

	LTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLT LGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSY VVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKR LAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
308	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGTLQLDDEYRLYSPLVKPDQNIQFWLE QFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPT VPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLA GATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKP KGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQN ITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEG KRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRLAII HCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
309	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPAPAPGGTLQLDDEYRLYSPLVKPD QNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNK RVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQ

	YVDDLLLAGATKQDCLEGTKALLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAA PLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDA DKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTD GSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALH LPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFESPKKKAKVE
311	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAAKEAAAKGGT LQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRK
313	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAAKEAAAKGGT LQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRK

	PGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALH RDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLG TAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGW PVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRK DLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSININYTDSRYAFATAHVHGAIYKQRGWLTSAG REIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFESPKKKAKVE
313	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAAKEAAAKGGT LQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRK PGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALH RDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLG TAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGW PVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRK DLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSININYTDSRYAFATAHVHGAIYKQRGWLTSAG REIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFESPKKKAKVE
314	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGPAPGSSGGTLQLDDEYRLYSPLVKPDQNIQ

	FWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQD IHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDD LLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYP LTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLT LGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSY VVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKR LAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFESPKKKAKVE
316	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
316	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI

	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGSGGGSGGSGGTLQLDDEYRLYSP
	LVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDL
	REVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQ
	VTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGF
	ATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAI
	LVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVL
	TWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSL
	LEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
317	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGGEAAAKGGTLQLDDEYRLYSPLVKPDQN
	IQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRV
	QDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYV
	DDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPL
	YPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADK
	LTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGS
	SYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLP
	KRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
317	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY

	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGGEAAAKGGTLQLDDEYRLYSPLVKPDQN IQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRV QDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYV DDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPL YPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADK LTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGS SYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLP KRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
318	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSSEAAAKGGTLQLDDEYRLYSPLVKPDQN IQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRV QDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYV DDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPL YPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADK LTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGS SYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLP KRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
318	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV

	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSSEAAAKGGTLQLDDEYRLYSPLVKPDQN IQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRV QDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYV DDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPL YPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADK LTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLEETGVRKDLTDIPLTGEVLTWFTDGS SYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLP KRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
319	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPEAAAKGGGGGTLQLDDEYRLYSPLVKPDQN IQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRV QDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYV DDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPL YPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADK LTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLEETGVRKDLTDIPLTGEVLTWFTDGS SYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLP KRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
320	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK

	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSGSSGGTLQLDDEYRLYSPLVKPDQNIQ
	FWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQD
	IHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDD
	LLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYP
	LTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFFLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLT
	LGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSY
	VVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKR
	LAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
320	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVVTLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSGSSGGTLQLDDEYRLYSPLVKPDQNIQ
	FWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQD
	IHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDD
	LLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYP
	LTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFFLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLT
	LGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSY
	VVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKR
	LAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
321	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD

	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGSEAAAKGGTLQLDDEYRLYSPLVKPDQN IQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRV QDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQFLAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYV DDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPL YPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADK LTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGS SYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLP KRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFESPKKKAKVE
322	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
324	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK

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	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGEAAAKPAPGGTLQLDDEYRLYSPLVKPDQN
	IQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRV
	QDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYV
	DDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPL
	YPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADK
	LTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGS
	SYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLP
	KRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
328	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
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	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
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	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGSGSETPGTSESATPESGGTLQLDDEYRLYSPLV
	KPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLRE
	VNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVT
	LLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFAT
	LAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILV
	KDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTW
	FTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLE
	ALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
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	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL

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	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
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	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGGGTLQLDDEYRLYSPLVKPDQNIQFWL
	EQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHP
	TVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLL
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	NITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVE
	EQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHP
	GKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRLAI
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	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
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	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
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	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
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	FWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQD
	IHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDD
	LLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYP
	LTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLT
	LGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSY
	VVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKR
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	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH

	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSPAPGGTLQLDDEYRLYSPLVKPDQN IQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRV QDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYV DDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPL YPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADK LTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGS SYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSININIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLP KRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
346	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGPAPEAAAKGGTLQLDDEYRLYSPLVKPDQN IQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRV QDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYV DDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPL YPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADK LTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGS SYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSININIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLP KRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
352	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER

	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSEAAAKGGGGGTLQLDDEYRLYSPLVKPDQN IQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRV QDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYV DDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPL YPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADK LTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGS SYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLP KRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
352	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSEAAAKGGGGGTLQLDDEYRLYSPLVKPDQN IQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRV QDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYV DDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPL YPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADK LTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGS SYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLP KRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
358	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL

	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKPAPGGGGTLQLDDEYRLYSPLVKPDQN
	IQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRV
	QDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYV
	YPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADK
	LTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGS
	SYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLP
	KRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
363	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGSSEAAAKGGTLQLDDEYRLYSPLVKPDQN
	IQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRV
	QDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYV
	DDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLYGYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	YPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADK
	LTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGS
	SYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLP
	KRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
365	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA

	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSEAAAKGGGGTLQLDDEYRLYSPLVKPDQN IQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRV QDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYV DDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPL YPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADK LTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGS SYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSININIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLP KRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
384	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGGGTLQLDDEYRLYSPLVKPDQNIQ FWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQD IHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDD LLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYP LTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLT LGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSY VVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSININIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKR LAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
386	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT

	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILLRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGSSGGTLQLDDEYRLYSPLVKPDQNIQFWL EQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHP TVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLL AGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTK PKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQ NITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAFPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVE GKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRLAI IHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
392	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILLRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGSSGGTLQLDDEYRLYSPLVKPDQNIQFWLE QFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPT VPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLA GATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKP KGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQN ITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEG KRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRLAII HCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE

396	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGSGSSGSGSSGGTLQLDDEYRLYSP LVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDL REVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQ VTLLQYVDDLLLAGATKQDCLEGTKALLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGF ATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAI LVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVL TWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSL LEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFESPKKKAKVE
396	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGSGSSGSGSSGGTLQLDDEYRLYSP LVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDL REVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQ VTLLQYVDDLLLAGATKQDCLEGTKALLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGF ATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAI LVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVL

	TWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSL
	LEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
480	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKALEAEAAAKEAA
	AKEAAAKEAAAKAGGMDPLQLLQPLEAEIKGTKLKAHWNSGATITCVPEAFLEDERPIQTMLIKTIHGEKQQDVYYLTFKVQGRKVEAEVLASPYDYILLN
	PSDVPWLMKKPLQLTVLVPLHEYQERLLQQTALPKEQKELLQKLFLKYDALWQHWENQVGHRRIKPHNIATGTLAPRPQKQYPINPKAKPSIQIVIDDLLK
	QGVLIQQNSTMNTPVYPVPKPDGKWRMVLDYREVNKTIPLIAAQNQHSAGILSSIYRGKYKTTLDLTNGFWAHPITPESYWLTAFTWQGKQYCWTRLPQGF
	LNSPALFNADVVDLLKEIPNVQAYVDDIYISHDDPQEHLEQLEKIFSILLNAGYVVSLKKSEIAQREVEFLGFNITKEGRGLTDTFKQKLLNITPPKDLKQ
	LQSILGKLNFARNFIPNYSELVKPLYTIVAPANGKFISWTEDNSNQLQHIISVLNQADNLEERNPETRLIIKVNSSPSAGYIRYYNEGSKRPIMYVNYIFS
	KAEAKFTQTEKLLTTMHKGLIKAMDLAMGQEILVYSPIVSMTKIQRTPLPERKALPVRWITWMTYLEDPRIQFHYDKSLPELQQIPNVTEDVIAKTKHPSE
	FAMVFYTDGSAIKHPDVNKSHSAGMGIAQVQFIPEYKIVHQWSIPLGDHTAQLAEIAAVEFACKKALKISGPVLIVTDSFYVAESANKELPYWKSNGFLNN
	KKKPLRHVSKWKSIAECLQLKPDIIIMHEKGHQQPMTTLHTEGNNLADKLATQGSYVVHAGKRTADGSEFEKRTADGSEFESPKKKAKVE
550	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAAKEAAAKGGI
	PWLMKKPLQLTTLVPLQEYEERLLKQTMLTGSYKEKLQSLFLKYDALWQHWENQVGHRRIKPHHIATGTVNPRPQKQYPINPKAKASIQTVTVINDLLKQGVL
	IQQNSIMNTPVYPVPKPDGKWRMVLDYREVNKTIPLIAAQNQHSAGILSSIFRGKYKTTLDLSNGFWAHSITPESYWLTAFTWLGQQYCWTRLPQGFLNSP
	ALFNADVVDLLKEVPNVQVYVDDIYISHDDPREHLEQLEKVFSLLLNAGYVVSLKKSEIAQHEVEFLGFNITKEGRGLTETFKQKLLNITPPRDLKQLQSI

	LGKLNFARNFIPNFSELVKPLYNIIATAPGKYITWTTDNSQQLQNIISMLNSAENLEERNPEVRLIMKVNTSPSAGYIRFYNEFAKRPIMYLNYVYTKAEV KFTNTEKLLTTIHKGLIKALDLGMGQEILVYSPIVSMTKIQKTPLPERKALPIRWITWMSYLEDPRIQFHYDKTLPELQQVPTVTDDIIAKIKHPSEFSMV FYTDGSAIKHPNVNKSHNAGMGIAQVQFKPEFTVINTWSIPLGDHTAQLAEVAAVEFACKKALKIDGPVLIVTDSFYVAESVNKELPYWQSNGFFNNKKKP LKHVSKWKSIADCIQLKPDIIIIHEKGHQPTASTFHTEGNNLADKLATQGSYVVNAGKRTADGSEFEKRTADGSEFESPKKKAKVE
590	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAAKGGM DPLQLLQPLEAEIKGTKLKAHWNSGATITCVPQAFLSEEVPIKNIWIKTIHGEKEQPVYYLTFKIQGRKVEAEVISSPYDYIILVS
591	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKEAAAKEAAAKEAA AKEAAAKEAAAKAGGMDPLQLLQPLEAEIKGTKLKAHWNSGATITCVPQAFLEEEVPIKNIWIKTIHGEKEQPVYYLTFKIQGRKVEAEVISSPYDYIILVS

	PSDIPWLMKKPLQLTTLVPLQEYEERLLKQTMLTGSYKEKLQSLFLKYDALWQHWENQVGHRRIKPHHIATGTVNPRPQKQYPINPKAKASIQTVINDLLK
	QGVLIQQNSIMNTPVYPVPKPDGKWRMVLDYREVNKTIPLIAAQNQHSAGILSSIFRGKYKTTLDLSNGFWAHSITPESYWLTAFTWLGQQYCWTRLPQGF
	LNSPALFNADVVDLLKEVPNVQVYVDDIYISHDDPREHLEQLEKVFSLLLNAGYVVSLKKSEIAQHEVEFLGFNITKEGRGLTETFKQKLLNITPPRDLKQ
	LQSILGLLNFARNFIPNFSELVKPLYNIIATAPGKYITWTTDNSQQLQNIISMLNSAENLEERNPEVRLIMKVNTSPSAGYIRFYNEFAKRPIMYLNYVYT
	KAEVKFTNTEKLLTTIHKGLIKALDLGMGQEILVYSPIVSMTKIQKTPLPERKALPIRWITWMSYLEDPRIQFHYDKTLPELQQVPTVTDDIIAKIKHPSE
	FSMVFYTDGSAIKHPNVNKSHNAGMGIAQVQFKPEFTVINTWSIPLGDHTAQLAEVAAVEFACKKALKIDGPVLIVTDSFYVAESVNKELPYWQSNGFFNN
	KKKPLKHVSKWKSIADCIQLKPDIIIIHEKGHQPTASTFHTEGNNLADKLATQGSYVVNAGKRTADGSEFESPKKKAKVE
647	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKALEAEAAAAKEAA
	AKEAAAKEAAAKAGGMDPLQLLQPLEAEIKGTKLKAHWNSGATITCVPQAFLEEEVPIKNIWIKTIHGEKEQPVYYLTFKIQGRKVEAEVISSPYDYIILVS
	PSDIPWLMKKPLQLTTLVPLQEYEERLLKQTMLTGSYKEKLQSLFLKYDALWQHWENQVGHRRIKPHHIATGTVNPRPQKQYPINPKAKASIQTVINDLLK
	QGVLIQQNSIMNTPVYPVPKPDGKWRMVLDYREVNKTIPLIAAQNQHSAGILSSIFRGKYKTTLDLSNGFWAHSITPESYWLTAFTWLGQQYCWTRLPQGF
	LNSPALFNADVVDLLKEVPNVQVYVDDIYISHDDPREHLEQLEKVFSLLLNAGYVVSLKKSEIAQHEVEFLGFNITKEGRGLTETFKQKLLNITPPRDLKQ
	LQSILGKLNFARNFIPNFSELVKPLYNIIATAPGKYITWTTDNSQQLQNIISMLNSAENLEERNPEVRLIMKVNTSPSAGYIRFYNEFAKRPIMYLNYVYT
	KAEVKFTNTEKLLTTIHKGLIKALDLGMGQEILVYSPIVSMTKIQKTPLPERKALPIRWITWMSYLEDPRIQFHYDKTLPELQQVPTVTDDIIAKIKHPSE
	FSMVFYTDGSAIKHPNVNKSHNAGMGIAQVQFKPEFTVINTWSIPLGDHTAQLAEVAAVEFACKKALKIDGPVLIVTDSFYVAESVNKELPYWQSNGFFNN
	KKKPLKHVSKWKSIADCIQLKPDIIIIHEKGHQPTASTFHTEGNNLADKLATQGSYVVNAGKRTADGSEFESPKKKAKVE
715	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
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	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY

	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKALEAEAAAKEAA AKEAAAKEAAAKAGGMDLLKPLTVERKGVKIKGYWNSQADITCVPKDLLQGEEPVRQQNVTTIHGTQEGDVYYVNLKIDGRRINTEVIGTTLDYAIITPGD VPWILKKPLELTIKLDLEEQQGTLLNNSILSKKGKEELKQLFEKYSALWQSWENQVGHRRIRPHKIATGTVKPTPQKQYHINPKAKPDIQIVINDLLKQGV LIQKESTMNTPVYPVPKPNGRWRMVLDYRAVNKVTPLIAVQNQHSYGILGSLFKGRYKTTIDLSNGFWAHPIVPEDYWITAFTWQGKQYCWTVLPQGFLNS PGLFTGDVVDLLQGIPNVEVYVDDVYISHDSEKEHLEYLDILLFNRLKEAGYIISLKKSNIANSIVDFLGFQITNEGRGLTDTFKEKLENITAPTTLKQLQS ILGLLNFARNFIPDFTELIAPLYALIPKSTKNYVFPWQIEHSTTLETLITKLNGAEYLQGRKGDKTLIMKVNASYTTGYIRYYNEGEKKPISYVSIVFSKTE LKFTELEKLLTTVHKGLLKALDLSMGQNIHVYSPIVSMQNIQKTPQTAKKALASRWLSWLSYLEDPRIRFFYDPQMPALKDLPAVDTGKDNKKHPSNFQHI FYTDGSAITSPTKEGHLNAGMGIVYFINKDGNLQKQQEWSISLGNHTAQFAEIAAFEFALKKCLPLGGNILVVTDSNYVAKAYNEELDVWASNGFVNNRKK PLKHISKWKSVADLKRLRPDVVVTHEPGHQKLDSSPHAYGNNLADQLATQASFKVHAGKRTADGSEFEKRTADGSEFESPKKKAKVE
800	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSEAAAKGGVLNLEEEYRLHEKPVPSSID PSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMSKEARERGIRPHIQRFLDLGVLVPCQSPWNTPLLPVKKPGTNDYRPVQDLREINKRVQ DIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLADFRALNPQVVLLQYVD DLLVAAPTYRDCKEGTQKLLQELSKIGYRVSAKKAQLCQKEVTYLGYLLKEGKRWLTPARKATVMKIPPPTTPRQVREFLGTAGFCRLWIPGFASLAAPLY PLTKPSIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAVAAVALLLKDADKL TLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVHRCSEILAEETGTRRDLKDQPLPGVPAWYTDGSSF IAEGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDINIYTDSRYAFATAHIHGAIYKQRGWLTSAGKDIKNKEEILALLEAIHLPKR VAIIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
801	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK

	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKALEAEAAAKEAA AKEAAAKEAAAKAGGVLNLEEEYRLHEKPVPSSIDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMSKEARE GIRPHIQRFLDLGVLV PCQSPWNTPLLPVKKPGTNDYRPVQDLREINKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLP QGFKNSPTLFNEALHRDLAPFRALNPQVVLLQYVDDLLVAAPTYRDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLLKEGKRWLTPARKATVMK IPPPTTPRQVREFLGTAGFCRLWIPGFASLAAPLYPLTKPSIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRP VAYLSKKLDPVASGWPTCLKAVAAVALLLKDADKLTLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPV HRCSEILAEETGTRRDLKDQPLPGVPAWYTDGSSFIAEGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDINIYTDSRYAFATAHIHGAIYKQRGWLTSAGKDIKNKEEILALLEAIHLPKRVA GAIYKQRGWLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKPAGKRTADGSEFESPKKKAKVE PKKKAKVE
804	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
805	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK

	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGGGGVLNLEEEYRLHEKPVPSSIDPSWLQ
	LFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMSKEARAGIRPHIQRFLDLGVLVPCQSPWNTPLLPVKKPGTNDYRPVQDLREINKRVQDIHPT
	VPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLAPFRALNPQVVLLQYVDDLLVA
	APTYRDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLLKEGKRWLTPARKATVMKIPPPTTPRQVREFLGTAGFCRLWIPGFASLAAPLYPLTKP
	SIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAVAAVALLLK
	VTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVHRCSEILAEETGTRRDLKDQPLPGVPAWYT
	RRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDINIYTDSRYAFATAHIHGAIYKQRGWLTSAGKDIKNKEEILALLEAIHLPKRVAIIH
	CPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
806	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGSGSETPGTSESATPESGGVLNLEEEYRLHEKPV
	PSSIDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMSKEAREGIRPHIQRFLDLGVLVPCQSPWNTPLLPVKKPGTNDYRPVQDLREI
	NKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLAPFRALNPQVVL
	LQYVDDLLVAAPTYRDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLLKEGKRWLTPARKATVMKIPPPTTPRQVREFLGTAGFCRLWIPGFASL
	AAPLYPLTKPSIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAVAAVALLLK
	DADKLTLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVHRCSEILAEETGTRRDLKDQPLPGVPAWYT
	DGSSFIAEGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDINIYTDSRYAFATAHIHGAIYKQRGWLTSAGKDIKNKEEILALLEAI
	HLPKRVAIIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
818	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL

	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGSGSGSGSGSGSGGVLNLEEEYRLHEK
	PVPSSIDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMSKEAREGIRPHIQRFLDLGVLVPCQSPWNTPLLPVKKPGTNDYRPVQDLR
	EINKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLAPFRALNPQV
	VLLQYVDDLLVAAPTYRDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLLKEGKRWLTPARKATVMKIPPPTTPRQVREFLGTAGFCRLWIPGFAS
	SLAAPLYPLTKPSIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAVAAVALLLKDADKLTLG
	LKDADKLTLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVHRCSEILAEETGTRRDLKDQPLPGVPAWYTDGSSFIAE
	YTDGSSFIAEGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDININIYTDSRYAFATAHIHGAIYKQRGWLTSAGKDIKNKEEILALLE
	AIHLPKRVAIIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
819	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPEAAAKGGVLNLEEEYRLHEKPVPSSIDPSW
	LQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMSKEAREGIRPHIQRFLDLGVLVPCQSPWNTPLLPVKKPGTNDYRPVQDLREINKRVQDIH
	PTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLAPFRALNPQVVLLQYVDDLL
	VAAPTYRDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLLKEGKRWLTPARKATVMKIPPPTTPRQVREFLGTAGFCRLWIPGFASLAAPLYPLT
	KPSIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAVAAVALLLKDADKLTLG
	QNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVHRCSEILAEETGTRRDLKDQPLPGVPAWYTDGSSFIAE
	GKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDININIYTDSRYAFATAHIHGAIYKQRGWLTSAGKDIKNKEEILALLEAIHLPKRVAI
	IHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
871	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
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	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH

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	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
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	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
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	IASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVHRCSEILAEETGTRRDLKDQPLPGVPAWYTDGSSFIAEGKRRA
	GAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDINIYTDSRYAFATAHIHGAIYKQRGWLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPG
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	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGSGSSGGVLNLEEEYRLHEKPVPSSIDPS
	WLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMSKEARE GIRPHIQRFLDLGVLVPCQSPWNTPLLPVKKPGTNDYRPVQDLREINKRVQDI
	HPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLAPFRALNPQVVLLQYVDDL
	LVAAPTYRDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLLKEGKRWLTPARKATVMKIPPPTTPRQVREFLGKAGFCRLFIPGFASLAAPLYPL
	TKPSIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAVAAVALLLKDADKLTL
	GQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVHRCSEILAEETGTRRDLKDQPLPGVPAWYTDGSSFIA
	EGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDINIYTDSRYAFATAHIHGAIYKQRGWLTSAGKDIKNKEEILALLEAIHLPKRVA
	IIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKPAGKRTADGSEFESPKKKAKVE
882	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILLRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGSGSSGGVLNLEEEYRLHEKPVPSSIDPSWLQ
	LFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMSKEAREGIRPHIQRFLDLGVLVPCQSPWNTPLLPVKKPGTNDYRPVQDLREINKRVQDIHPT
	VPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLAPFRALNPQVVLLQYVDDLLVA
	APTYRDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLLKEGKRWLTPARKATVMKIPPPTTPRQVREFLGKAGFCRLFIPGFASLAAPLYPLTKP
	SIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAVAAVALLLKDADKLTLGQN
	VTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVHRCSEILAEETGTRRDLKDQPLPGVPAWYTDGSSFIAEGK
	RRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDINIYTDSRYAFATAHIHGAIYKQRGWLTSAGKDIKNKEEILALLEAIHLPKRVAIIH
	CPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKPAGKRTADGSEFESPKKKAKVE

883	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSEAAAKGGVLNLEEEYRLHEKPVPSSIDPSW LQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMSKEARERGIRPHIQRFLDLGVLVPCQSPWNTPLLPVKKPGTNDYRPVQDLREINKRVQDIH PTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLAPFRALNPQVVLLQYVDDLL VAAPTYRDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLLKEGKRWLTPARKATVMKIPPPTTPRQVREFLGKAGFCRLFIPGFASLAAPLYPLT KPSIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAVAAVALLLKDADKLTLG QNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVHRCSEILAEETGTRRDLKDQPLPGVPAWYTDGSSFIAE GKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDINIYTDSRYAFATAHIHGAIYKQRGWLTSAGKDIKNKEEILALLEAIHLPKRVAI IHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
884	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSPAPGGVLNLEEEYRLHEKPVPSSIDPSWLQ LFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMSKEARERGIRPHIQRFLDLGVLVPCQSPWNTPLLPVKKPGTNDYRPVQDLREINKRVQDIHPT VPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLAPFRALNPQVVLLQYVDDLLVA APTYRDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLLKEGKRWLTPARKATVMKIPPPTTPRQVREFLGKAGFCRLFIPGFASLAAPLYPLTKP SIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAVAAVALLLKDADKLTLGQN VTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVHRCSEILAEETGTRRDLKDQPLPGVPAWYTDGSSFIAEGK

	RRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDINIYTDSRYAFATAHIHGAIYKQRGWLTSAGKDIKNKEEILALLEAIHLPKRVAIIH CPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
890	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPAPAPGGVLNLEEEYRLHEKPVPSS IDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMSKEARAGEIGRPHIQRFLDLGVLVPCQSPWNTPLLPVKKPGTNDYRPVQDLREINKR VQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLAPFRALNPQVVLLQY VDDLLVAAPTYRDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLLKEGKRWLTPARKATVMKIPPPTTPRQVREFLGKAGFCRLFIPGFASLAAP LYPLTKPSIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAVAAVALLLKDAD KLTLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVHRCSEILAEETGTRRDLKDQPLPGVPAWYTDGS SFIAEGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDINIYTDSRYAFATAHIHGAIYKQRGWLTSAGKDIKNKEEILALLEAIHLP KRVAIIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
898	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSPAPEAAAKGGVLNLEEEYRLHEKPVPSSID PSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMSKEARAGEIGRPHIQRFLDLGVLVPCQSPWNTPLLPVKKPGTNDYRPVQDLREINKRVQ DIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLAPFRALNPQVVLLQYVD DLLVAAPTYRDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLLKEGKRWLTPARKATVMKIPPPTTPRQVREFLGKAGFCRLFIPGFASLAAPLY PLTKPSIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAVAAVALLLKDADKL

	TLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVHRCSEILAEETGTRRDLKDQPLPGVPAWYTDGSSF
	IAEGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDININYTDSRYAFATAHIHGAIYKQRGWLTSAGKDIKNKEEILALLEAIHLPKR
	VAIIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
900	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGSEAAAKGGGVLNLEEEYRLHEKPVP
	SSIDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMSKEARAEGIRPHIQRFLDLGVLVPCQSPWNTPLLPVKKPGTNDYRPVQDLREIN
	KRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLAPFRALNPQVVLL
	QYVDDLLVAAPTYRDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLLKEGKRWLTPARKATVMKIPPPTTPRQVREFLGKAGFCRLFIPGFASLA
	APLYPLTKPSIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAVAAVALLLKD
	ADKLTLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVHRCSEILAEETGTRRDLKDQPLPGVPAWYTD
	GSSFIAEGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDININYTDSRYAFATAHIHGAIYKQRGWLTSAGKDIKNKEEILALLEAIH
	LPKRVAIIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
901	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGEAAAKGGGSGGVLNLEEEYRLHEKPVPSSID
	PSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMSKEARAEGIRPHIQRFLDLGVLVPCQSPWNTPLLPVKKPGTNDYRPVQDLREINKRVQ
	DIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLAPFRALNPQVVLLQYVD
	DLLVAAPTYRDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLLKEGKRWLTPARKATVMKIPPPTTPRQVREFLGKAGFCRLFIPGFASLAAPLY

	PLTKPSIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAVAAVALLLKDADKL
	TLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVHRCSEILAEETGTRRDLKDQPLPGVPAWYTDGSSF
	IAEGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDININIYTDSRYAFATAHIHGAIYKQRGWLTSAGKDIKNKEEILALLEAIHLPKR
	VAIIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
912	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSEAAAKPAPGGVLNLEEEYRLHEKPVPSSID
	PSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMSKEARAEGIRPHIQRFLDLGVLVPCQSPWNTPLLPVKKPGTNDYRPVQDLREINKRVQ
	DIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLAPFRALNPQVVLLQYVD
	DLLVAAPTYRDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLLKEGKRWLTPARKATVMKIPPPTTPRQVREFLGKAGFCRLFIPGFASLAAPLY
	PLTKPSIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAVAAVALLLKDADKL
	TLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVHRCSEILAEETGTRRDLKDQPLPGVPAWYTDGSSF
	IAEGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDININIYTDSRYAFATAHIHGAIYKQRGWLTSAGKDIKNKEEILALLEAIHLPKR
	VAIIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
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	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGSEAAAKGGVLNLEEEYRLHEKPVPSSID
	PSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMSKEARAEGIRPHIQRFLDLGVLVPCQSPWNTPLLPVKKPGTNDYRPVQDLREINKRVQ
	DIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLAPFRALNPQVVLLQYVD

	DLLVAAPTYRDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLLKEGKRWLTPARKATVMKIPPPTTPRQVREFLGKAGFCRLFIPGFASLAAPLY PLTKPSIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAVAAVALLLKDADKL TLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVHRCSEILAEETGTRRDLKDQPLPGVPAWYTDGSSF IAEGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDININIYTDSRYAFATAHIHGAIYKQRGWLTSAGKDIKNKEEILALLEAIHLPKR VAIIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKPAGKRTADGSEFESPKKKAKVE
929	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGSGSGSGGVLNLEEEYRLHEKPVPSSIDPS WLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMSKEAREGIRPHIQRFLDLGVLVPCQSPWNTPLLPVKKPGTNDYRPVQDLREINKRVQDI HPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLAPFRALNPQVVLLQYVDDL LVAAPTYRDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLLKEGKRWLTPARKATVMKIPPPTTPRQVREFLGKAGFCRLFIPGFASLAAPLYPL TKPSIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAVAAVALLLKDADKLTL GQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVHRCSEILAEETGTRRDLKDQPLPGVPAWYTDGSSFIA EGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDININIYTDSRYAFATAHIHGAIYKQRGWLTSAGKDIKNKEEILALLEAIHLPKRVA IIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKPAGKRTADGSEFESPKKKAKVE
933	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKGGVLNLEEEYRLHEKPVP SSIDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMSKEAREGIRPHIQRFLDLGVLVPCQSPWNTPLLPVKKPGTNDYRPVQDLREIN

	KRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLAPFRALNPQVVLL QYVDDLLVAAPTYRDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLLKEGKRWLTPARKATVMKIPPPTTPRQVREFLGKAGFCRLFIPGFASLA APLYPLTKPSIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAVAAVALLLKD ADKLTLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVHRCSEILAEETGTRRDLKDQPLPGVPAWYTD GSSFIAEGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDINIYTDSRYAFATAHIHGAIYKQRGWLTSAGKDIKNKEEILALLEAIH LPKRVAIIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
958	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGGSGGSGGSGGTLNIEDEYRLHET SKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQD LREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHP DLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPG FAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIA VLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDLTDQPIPDAD YTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIKNKNEILA LLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
960	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGSSPAPGGTLNIEDEYRLHETSKEPDVP

	LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY VDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAP LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDLTDQPIPDADYTWYTDG SSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIKNKNEILALLKALFL PKRLSIIHCPGHQKGNSAEARGNRMADQAARE AAMKAVLETSTLLAGKRTADGSEFESPKKKAKVE
961	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
963	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI

	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGPAPGGTLNIEDEYRLHETSKEPDVP
	LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR
	VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY
	VDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAP
	LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG
	KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDLTDQPIPDADYTWYTDG
	SSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIKNKNEILALLKALFL
	PKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFESPKKKAKVE
964	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGGSGGSGGSGGTLNIEDEYRLHETSKE
	PDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLRE
	VNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLI
	LLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAE
	MAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLT
	KDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDLTDQPIPDADYTW
	YTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIKNKNEILALLK
	ALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFESPKKKAKVE
966	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY

	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSEAAAKGGTLNIEDEYRLHETSKEPDVPLGS TWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVED IHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDD LLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYP LTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLT MGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDLTDQPIPDADYTWYTDGSSF LQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIKNKNEILALLKALFLPKR LSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
967	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGSSEAAAKGGTLNIEDEYRLHETSKEPDVP LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY VDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAP LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDLTDQPIPDADYTWYTDG SSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIKNKNEILALLKALFL PKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
978	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV

	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPGGTLNIEDEYRLHETSKEPDVPLG
	STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE
	DIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVD
	DLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLY
	PLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKL
	TMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDLTDQPIPDADYTWYTDGSS
	FLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIKNKNEILALLKALFLPK
	RLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
987	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
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	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSPAPGGSGGTLNIEDEYRLHETSKEPDVPLG
	STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE
	DIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVD
	DLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLY
	PLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKL
	TMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDLTDQPIPDADYTWYTDGSS
	FLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIKNKNEILALLKALFLPK
	RLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
100 6	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK

	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKALEAEAAAKEAA AKEAAAKEAAAKAGGTLNIEDEYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGI LVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTR LPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWR RPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKE APHDCLEILAETHGTRPDLTDQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIKNKNEILALLKALFL HVHGEIYRRRGWLTSEGREIKNKNEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAARAAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE ESPKKKAKVE
1007	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK	
1008	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK

	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKGGTLNIEDEYRLH
	ETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPV
	QDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQ
	HPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFI
	PGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAA
	IAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDLTDQPIPDADYTWYTDGSSFLQE
	ADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIKNKNEI
	LALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1009	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGTLNIEDEYRLHETSKEPDVPLGSTWL
	SDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHP
	TVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLL
	AATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTK
	PGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQ
	PLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDLTDQPIPDADYTWYTDGSSFLQE
	GQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIKNKNEIILALLKALFLPKRLSI
	IHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1011	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL

	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGTLNIEDEYRLHETSKEPDVPLGSTWLSD
	FPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTV
	RRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIKNKNEILALLKALFLPKRLSIIH
	CPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFESPKKKAKVE
1012	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
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	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGSSGGGGGTLNIEDEYRLHETSKEPDVP
	LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR
	VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY
	VDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP
	LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG
	KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDLTDQPIPDADYTWYTDG
	SSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIKNKNEILALLKALFL
	PKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1015	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
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	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH

	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSPAPGGTLNIEDEYRLHETSKEPDVPLG
	STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE
	DIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVD
	DLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLY
	PLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKL
	TMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDLTDQPIPDADYTWYTDGSS
	FLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIKNKNEILALLKALFLPK
	RLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
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	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGSSGGTLNIEDEYRLHETSKEPDVPLGSTW
	LSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIH
	PTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLL
	LAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLT
	KPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMG
	QPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDLTDQPIPDADYTWYTDGSSFLQ
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1017	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER

	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSPAPGGTLNIEDEYRLHETSKEPDVPLGSTW LSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIH PTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLL LAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLT KPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMG QPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDLTDQPIPDADYTWYTDGSSFLQ EGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIKNKNEILALLKALFLPKRLS IIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1018	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSPAPGGTLNIEDEYRLHETSKEPDVP LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY VDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDLTDQPIPDADYTWYTDG SSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIKNKNEILALLKALFL PKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1019	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL

	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKVVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGGSGGSGGTLNIEDEYRLHETSKEPDV
	PLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNK
	RVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILL
	YVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAA
	PLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDA
	GKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDLTDQPIPDADYTWYTD
	GSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIKNKNEILALLKALF
	LPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFESPKKKAKVE
1020	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKVVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIILKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPAPAPGGTLNIEDEYRLHETSKEPD VPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVN KRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILL QYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMA APLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKD AGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDLTDQPIPDADYTWYT DGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIKNKNEILALLKAL FLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFESPKKKAKVE
1021	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA

	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGT
	LNIEDEYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVK
	KPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEAL
	HRDLADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFL
	GKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAG
	WPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTR
	PDLTDQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSE
	GREIKNKNEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1022	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGSGGGGTLNIEDEYRLHETSKEPDVPLG
	STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE
	DIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVD
	DLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLY
	PLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKL
	TMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDLTDQPIPDADYTWYTDGSS
	FLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIKNKNEILALLKALFLPK
	RLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE

1023	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSGGTLNIEDEYRLHETSKEPDVPLGS TWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVED IHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDD LLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYP LTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLT MGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDLTDQPIPDADYTWYTDGSSF LQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIKNKNEILALLKALFLPKR LSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFESPKKKAKVE
1025	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGPAPGGSGGTLNIEDEYRLHETSKEPDVPLG STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE DIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVD DLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLY PLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKL TMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDLTDQPIPDADYTWYTDGSS

	FLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIKNKNEILALLKALFLPK RLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
10209	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAAKGGTLNIED EYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTN DYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGF CRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCL RMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDLTD QPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIK NKNEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
10303	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGSSGGGGTLNIEDEYRLHETSKEPDVPLG STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE DIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVD DLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLY PLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKL

	TMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDLTDQPIPDADYTWYTDGSS FLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIKNKNEILALLKALFLPK RLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1034	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGSEAAAKGGTLNIEDEYRLHETSKEPDVP LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY VDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDLTDQPIPDADYTWYTDG SSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIKNKNEILALLKALFL PKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1037	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGSEAAAKGGTLNIEDEYRLHETSKE PDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLRE VNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLI LLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAE

	MAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLT KDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDLTDQPIPDADYTW YTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIKNKNEILALLK ALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAARE AAMKAVLETSTLLAGKRTADGSEFESPKKKAKVE
1038	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSPAPGGGGTLNIEDEYRLHETSKEPDVPLG STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE DIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVD DLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLY PLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKL TMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDLTDQPIPDADYTWYTDGSS FLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIKNKNEILALLKALFLPK RLSIIHCPGHQKGNSAEARGNRMADQAARE AAMKAVLETSTLLAGKRTADGSEFESPKKKAKVE
1039	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGSSPAPGGTLNIEDEYRLHETSKEPDVP LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY

	VDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP
	LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG
	KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDLTDQPIPDADYTWYTDG
	SSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIKNKNEILALLKALFL
	PKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFESPKKKAKVE
1043	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGEAAAKGGTLNIEDEYRLHETSKEPDVPLGS
	TWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVED
1043	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGEAAAKGGTLNIEDEYRLHETSKEPDVPLGS
	TWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVED

	IHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDD
	LLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYP
	LTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLT
	MGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDLTDQPIPDADYTWYTDGSSF
	LQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIKNKNEILALLKALFLPKR
	LSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKPTADGSEFESPKKKAKVE
1046	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGSSGGTLNIEDEYRLHETSKEPDVPLGSTW
	IHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDD
	LLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYP
	LTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLT
	MGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDLTDQPIPDADYTWYTDGSSF
	LQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIKNKNEILALLKALFLPKR
	LSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKPTADGSEFESPKKKAKVE
1047	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGSSGGTLNIEDEYRLHETSKEPDVPLGSTW

	LSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIH PTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLL LAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLT KPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMG QPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDLTDQPIPDADYTWYTDGSSFLQ EGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIKNKNEIILALLKALFLPKRLS IIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFESPKKKAKVE
1049	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
1052	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI

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	LNIEDEYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVK
	KPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEAL
	HRDLADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFL
	GKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAG
	WPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTR
	PDLTDQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSE
	GREIKNKNEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1056	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGSSGGTLNIEDEYRLHETSKEPDVP
	LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR
	VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY
	VDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP
	LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG
	KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDLTDQPIPDADYTWYTDG
	SSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIKNKNEILALLKALFL
	PKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1059	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY

	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGSSEAAAKGGTLNIEDEYRLHETSKEPDVP LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY VDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDLTDQPIPDADYTWYTDG SSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIKNKNEILALLKALFL PKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFESPKKKAKVE
1060	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGSSEAAAKGGTLNIEDEYRLHETSKEPDVP LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY VDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDLTDQPIPDADYTWYTDG SSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIKNKNEILALLKALFL PKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFESPKKKAKVE
1061	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV

	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGSPAPGGTLNIEDEYRLHETSKEPDVPLG STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE DIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVD DLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLY PLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKL TMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDLTDQPIPDADYTWYTDGSS FLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIKNKNEILALLKALFLPK RLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFESPKKKAKVE
107 6	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGPAPEAAAKGGTLNIEDEYRLHETSKEPDVP LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY VDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDLTDQPIPDADYTWYTDG SSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIKNKNEILALLKALFL PKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFESPKKKAKVE
108 3	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK

	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSEAAAKGGTLNIEDEYRLHETSKEPDVPLGS TWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVED IHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDD LLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYP LTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLT MGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDLTDQPIPDADYTWYTDGSSF LQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIKNKNEILALLKALFLPKR LSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFFEKRTADGSEFESPKKKAKVE
109 3	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKALEAEAAAKEAA AKEAAAKEAAAKAGGVPWILKKPLELTIKLDLEEQQGTLLNNSILSKKGKEELKQLFEKYSALWQSWENQVGHRRIRPHKIATGTVKPTPQKQYHINPKAK PDIQIVINDLLKQGVLIQKESTMNTPVYPVPKPNGRWRMVLDYRAVNKVTPLIAVQNQHSYGILGSLFKGRYKTTIDLSNGFWAHPIVPEDYWITAFTWQG KQYCWTVLPQGFLNSPGLFNGDVVDLLQGIPNVEVYVDDVYISHDSEKEHLEYLDILFNRLKEAGYIISLKKSNIANSIVDFLGFQITNEGRGLTDTFKEK LENITAPTTLKQLQSILGLLNFARNFIPDFTELIAPLYALIPKSPKNYVVPWQIEHSTTLETLITKLNGAEYLQGRKGDKTLIMKVNASYTTGYIRYYNEGE KKPISYVSIVFSKTELKFTELEKLLTVHKGLLKALDLSMGQNIHVYSPIVSMQNIQKTPQTAKKALASRWLSWLSYLEDPRIRFFYDPQMPALKDLPAVD TGKDNKKHPSNFQHIFYTDGSAITSPTKEGHLNAGMGIVYFINKDGNLQKQQEWSISLGNHTAQFAEIAAFEFALKKCLPLGGNILVVTDSNYVAKAYNEE LDVWASNGFVNNRKKPLKHISKWKSVADLKRLRPDVVVTHEPGHQKLDSSPHAYGNNLADQLATQASFKVHAGKRTADGSEFEKRTADGSEFESPKKKAKV E
111 5	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK

	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKALEAEAAAKEAA AKEAAAKEAAAKAGGMDLLKPLTVERKGVKIKGYWNSQADITCVPKDLLQGEEPVRQQNVTTIHGTQEGDVYYVNLKIDGRRINTEVIGTTLDYAIITPGD VPWILKKPLELTIKLDLEEQQGTLLNNSILSKKGKEELKQLFEKYSALWQSWENQVGHRRIRPHKIATGTVKPTPQKQYHINPKAKPDIQIVINDLLKQGV LIQKESTMNTPVYPVPKPNGRWRMVLDYRAVNKVTPLIAVQNQHSYGILGSLFKGRYKTTIDLSNGFWAHPIVPEDYWITAFTWQGKQYCWTVLPQGFLNS PGLFNGDVVDLLQGIPNVEVYVDDVYISHDSEKEHLEYLDILLFNRLKEAGYIISLKKSNIANSIVDFLGFQITNEGRGLTDTFKEKLENITAPTTLKQLQS ILGLLNFARNFIPDFTELIAPLYALIPKSPKNYVPWQIEHSTTLETLITKLNGAEYLQGRKGDKTLIMKVNASYTTGYIRYYNEGEKKPISYVSIVFSKTE LKFTELEKLLTTVHKGLLKALDLSMGQNIHVYSPIVSMQNIQKTPQTAKKALASRWLSWLSYLEDPRIRFFYDPQMPALKDLPAVDTGKDNKKHPSNFQHI FYTDGSAITSPTKEGHLNAGMGIVYFINKDGNLQKQEWSISLGNHTAQFAEIAAFEFALKKCLPLGGNILVVTDSNYVAKAYNEELDVWASNGFVNNRKK PLKHISKWKSVADLKRLRPDVVVTHEPGHQKLDSSPHAYGNNLADQLATQASFKVHAGKRTADGSEFEKRTADGSEFESPKKKAKVE
113 7	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKGGTAPLEEEYRLF LEAPIQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGTSEYRMV QDLREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEEGESGQLTWTRLPQGFKNSPTLFNEALNRDLQGFRLD HPSVSLLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAILQIPVPKTKRQVREFLGTIGYCRLWI PGFAELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSKRLDPVAAGWPRCLRAIA AAALLTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTSTRPDLTDQPL AQAEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALELEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWLTAGGKAIKNAP EILALLTAVWLPKRVAVMHCKGHQKDDAPTSTGNRRADEVARERVAIRPLSTQATISAGKRTADGSEFEKRTADGSEFESPKKKAKVE
116 8	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH

	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSPAPGGTLQLEEEYRLFEPESTQKQEMD
	IWLKNFPQAWAETGGMGTAHCQAPVLIQLKATATPISIRQYPMPHEAYQGIKPHIRRMLDQGILKPCQSPWNTPLLPVKKPGTEDYRPVQDLREVNKRVED
	IHPTVPNPYNLLSTLPPSHPWYTVLDLKDAFFCLRLHSESQLLFAFEWRDPEIGLSGQLTWTRLPQGFKNSPTLFNEALHSDLADFRVRYPALVLLQYVDD
	LLLAAATRTECLEGTKALLETLGNKGYRASAKKAQICLQEVTYLGYSLKDGQRWLTKARKEAILSIPVPKNSRQVREFLGTAGYCRLWIPGFAELAAPLYP
	LTRPGTLFQWGTEQQLAFEDIKKALLSSPALGLPDITKPFELFIDENSGFAKGVLVQKLGPWKRPVAYLSKKLDTVASGWPPCLRMVAAIAILVKDAGKLT
	LGQPLTILTSHPVEALVRQPPNKWLSNARMTHYQAMLLDAERVHFGPTVSLNPATLLPLPSGGNHHDCLQILAETHGTRPDLTDQPLPDADLTWYTDGSSF
	IRNGEREAGAAVTTESEVIWAAPLPPGTSAQRAELIALTQALKMAEGKKLTVYTDSRYAFATTHVHGEIYRRRGWLTSEGKEIKNKNEILALLEALFLPKR
	LSIIHCPGHQKGDSPQAKGNRLADDTAKKAATETHSSLTVLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
117 1	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAAKEAAAKGGT
	LQLEEEYRLFEPESTQKQEMDIWLKNFPQAWAETGGMGTAHCQAPVLIQLKATATPISIRQYPMPHEAYQGIKPHIRRMLDQGILKPCQSPWNTPLLPVKK
	PGTEDYRPVQDLREVNKRVEDIHPTVPNPYNLLSTLPPSHPWYTVLDLKDAFFCLRLHSESQLLFAFEWRDPEIGLSGQLTWTRLPQGFKNSPTLFNEALH
	SDLADFRVRYPALVLLQYVDDLLLAAATRTECLEGTKALLETLGNKGYRASAKKAQICLQEVTYLGYSLKDGQRWLTKARKEAILSIPVPKNSRQVREFLG
	TAGYCRLWIPGFAELAAPLYPLTRPGTLFQWGTEQQLAFEDIKKALLSSPALGLPDITKPFELFIDENSGFAKGVLVQKLGPWKRPVAYLSKKLDTVASGW
	PPCLRMVAAIAILVKDAGKLTLGQPLTILTSHPVEALVRQPPNKWLSNARMTHYQAMLLDAERVHFGPTVSLNPATLLPLPSGGNHHDCLQILAETHGTRP
	DLTDQPLPDADLTWYTDGSSFIRNGEREAGAAVTTESEVIWAAPLPPGTSAQRAELIALTQALKMAEGKKLTVYTDSRYAFATTHVHGEIYRRRGWLTSEG
	KEIKNKNEILALLEALFLPKRLSIIHCPGHQKGDSPQAKGNRLADDTAKKAATETHSSLTVLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
119 7	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER

	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKALEAEAAAAKEAA AKEAAAKEAAAKAGGTLQLEEEYRLFEPESTQKQEMDIWLKNFPQAWAETGGMGTAHCQAPVLIQLKATATPISIRQYPMPHEAYQGIKPHIRRMLDQGILKPCQSPWNTPLLPVKKPGTEDYRPVQ KPCQSPWNTPLLPVKKPGTEDYRPVQDLREVNKRVEDIHPTVPNPYNLLSTLPPSHPWYTVLDLKDAFFCLRLHSESQLLFAFEWRDPEIGLSGQLTWTRLPQGFKNSPTLFNEALHSDLADFRVRY PQGFKNSPTLFNEALHSDLADFRVRYPALVLLQYVDDLLLAAATRTECLEGTKALLETLGNKGYRASAKKAQICLQEVTYLGYSLKDGQRWLTKARKEAIL SIPVPKNSRQVREFLGKAGYCRLFIPGFAELAAPLYPLTRPGTLFQWGTEQQLAFEDIKKALLSSPALGLPDITKPFELFIDENSGFAKGVLVQKLGPWKR PVAYLSKKLDTVASGWPPCLRMVAAIAILVKDAGKLTLGQPLTILTSHPVEALVRQPPNKWLSNARMTHYQAMLLDAERVHFGPTVSLNPATLLPLPSGGN HHDCLQILAETHGTRPDLTDQPLPDADLTWYTDGSSFIRNGEREAGAAVTTESEVIWAAPLPPGTSAQRAELIALTQALKMAEGKKLTVYTDSRYAFATTH VHGEIYRRRGWLTSEGKEIKNKNEILALLEALFLPKRLSIIHCPGHQKGDSPQAKGNRLADDTAKKAATETHSSLTVLPAGKRTADGSEFEKRTADGSEFE SPKKKAKVE
1198	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKGGTLQLEEEYRLF EPESTQKQEMDIWLKNFPQAWAETGGMGTAHCQAPVLIQLKATATPISIRQYPMPHEAYQGIKPHIRRMLDQGILKPCQSPWNTPLLPVKKPGTEDYRPVQ DLREVNKRVEDIHPTVPNPYNLLSTLPPSHPWYTVLDLKDAFFCLRLHSESQLLFAFEWRDPEIGLSGQLTWTRLPQGFKNSPTLFNEALHSDLADFRVRY PALVLLQYVDDLLLAAATRTECLEGTKALLETLGNKGYRASAKKAQICLQEVTYLGYSLKDGQRWLTKARKEAILSIPVPKNSRQVREFLGKAGYCRLFIP GFAELAAPLYPLTRPGTLFQWGTEQQLAFEDIKKALLSSPALGLPDITKPFELFIDENSGFAKGVLVQKLGPWKRPVAYLSKKLDTVASGWPPCLRMVAAI AILVKDAGKLTLGQPLTILTSHPVEALVRQPPNKWLSNARMTHYQAMLLDAERVHFGPTVSLNPATLLPLPSGGNHHDCLQILAETHGTRPDLTDQPLPDA DLTWYTDGSSFIRNGEREAGAAVTTESEVIWAAPLPPGTSAQRAELIALTQALKMAEGKKLTVYTDSRYAFATTHVHGEIYRRRGWLTSEGKEIKNKNEIIL ALLEALFLPKRLSIIHCPGHQKGDSPQAKGNRLADDTAKKAATETHSSLTVLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1202	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA

	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGGGSGGGGSGGGGSGGTLQLEE
	EYRLFEPESTQKQEMDIWLKNFPQAWAETGGMGTAHCQAPVLIQLKATATPISIRQYPMPHEAYQGIKPHIRRMLDQGILKPCQSPWNTPLLPVKKPGTED
	YRPVQDLREVNKRVEDIHPTVPNPYNLLSTLPPSHPWYTVLDLKDAFFCLRLHSESQLLFAFEWRDPEIGLSGQLTWTRLPQGFKNSPTLFNEALHSDLAD
	FRVRYPALVLLQYVDDLLLAAATRTECLEGTKALLETLGNKGYRASAKKAQICLQEVTYLGYSLKDGQRWLTKARKEAILSIPVPKNSRQVREFLGKAGYC
	RLFIPGFAELAAPLYPLTRPGTLFQWGTEQQLAFEDIKKALLSSPALGLPDITKPFELFIDENSGFAKGVLVQKLGPWKRPVAYLSKKLDTVASGWPPCLR
	MVAAIAILVKDAGKLTLGQPLTILTSHPVEALVRQPPNKWLSNARMTHYQAMLLDAERVHFGPTVSLNPATLLPLPSGGNHHDCLQILAETHGTRPDLTDQ
	PLPDADLTWYTDGSSFIRNGEREAGAAVTTESEVIWAAPLPPGTSAQRAELIALTQALKMAEGKKLTVYTDSRYAFATTHVHGEIYRRRGWLTSEGKEIKN
	KNEILALLEALFLPKRLSIIHCPGHQKGDSPQAKGNRLADDTAKKAATETHSSLTVLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1203	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGEAAAKGGGGSGGTLQLEEEYRLFEPEST
	QKQEMDIWLKNFPQAWAETGGMGTAHCQAPVLIQLKATATPISIRQYPMPHEAYQGIKPHIRRMLDQGILKPCQSPWNTPLLPVKKPGTEDYRPVQDLREV
	NKRVEDIHPTVPNPYNLLSTLPPSHPWYTVLDLKDAFFCLRLHSESQLLFAFEWRDPEIGLSGQLTWTRLPQGFKNSPTLFNEALHSDLADFRVRYPALVL
	LQYVDDLLLAAATRTECLEGTKALLETLGNKGYRASAKKAQICLQEVTYLGYSLKDGQRWLTKARKEAILSIPVPKNSRQVREFLGKAGYCRLFIPGFAEL
	AAPLYPLTRPGTLFQWGTEQQLAFEDIKKALLSSPALGLPDITKPFELFIDENSGFAKGVLVQKLGPWKRPVAYLSKKLDTVASGWPPCLRMVAAIAILVK
	DAGKLTLGQPLTILTSHPVEALVRQPPNKWLSNARMTHYQAMLLDAERVHFGPTVSLNPATLLPLPSGGNHHDCLQILAETHGTRPDLTDQPLPDADLTWY
	TDGSSFIRNGEREAGAAVTTESEVIWAAPLPPGTSAQRAELIALTQALKMAEGKKLTVYTDSRYAFATTHVHGEIYRRRGWLTSEGKEIKNKNEILALLEA
	LFLPKRLSIIHCPGHQKGDSPQAKGNRLADDTAKKAATETHSSLTVLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE

1210	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV EDIHPTVPNPYNLLSTLPPSHPWYTVLDLKDAFFCLRLHSESQLLFAFEWRDPEIGLSGQLTWTRLPQGFKNSPTLFNEALHSDLADFRVRYPALVLLQYV DDLLLAAATRTECLEGTKALLETLGNKGYRASAKKAQICLQEVTYLGYSLKDGQRWLTKARKEAILSIPVPKNSRQVREFLGKAGYCRLFIPGFAELAAPL YPLTRPGTLFQWGTEQQLAFEDIKKALLSSPALGLPDITKPFELFIDENSGFAKGVLVQKLGPWKRPVAYLSKKLDTVASGWPPCLRMVAAIAILVKDAGK LTLGQPLTILTSHPVEALVRQPPNKWLSNARMTHYQAMLLDAERVHFGPTVSLNPATLLPLPSGGNHHDCLQILAETHGTRPDLTDQPLPDADLTWYTDGS SFIRNGEREAGAAVTTESEVIWAAPLPPGTSAQRAELIALTQALKMAEGKKLTVYTDSRYAFATTHVHGEIYRRRGWLTSEGKEIKNKNEILALLEALFLP KRLSIIHCPGHQKGDSPQAKGNRLADDTAKKAATETHSSLTVLPAGKRTADGSEFESPKKKAKVE
1216	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAKGSSGGGGTLQLEEEYRLFEPESTQKQE IWLKNFPQAWAETGGMGTAHCQAPVLIQLKATATPISIRQYPMPHEAYQGIKPHIRRMLDQGILKPCQSPWNTPLLPVKKPGTEDYRPVQDLREVNKRVED IHPTVPNPYNLLSTLPPSHPWYTVLDLKDAFFCLRLHSESQLLFAFEWRDPEIGLSGQLTWTRLPQGFKNSPTLFNEALHSDLADFRVRYPALVLLQYVDD LLLAAATRTECLEGTKALLETLGNKGYRASAKKAQICLQEVTYLGYSLKDGQRWLTKARKEAILSIPVPKNSRQVREFLGKAGYCRLFIPGFAELAAPLYP LTRPGTLFQWGTEQQLAFEDIKKALLSSPALGLPDITKPFELFIDENSGFAKGVLVQKLGPWKRPVAYLSKKLDTVASGWPPCLRMVAAIAILVKDAGKLT LGQPLTILTSHPVEALVRQPPNKWLSNARMTHYQAMLLDAERVHFGPTVSLNPATLLPLPSGGNHHDCLQILAETHGTRPDLTDQPLPDADLTWYTDGSSF

	IRNGEREAGAAVTTESEVIWAAPLPPGTSAQRAELIALTQALKMAEGKKLTVYTDSRYAFATTHVHGEIYRRRGWLTSEGKEIKNKNEILALLEALFLPKR
	LSIIHCPGHQKGDSPQAKGNRLADDTAKKAATETHSSLTVLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
12119	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPAPGGTLQLEEEYRLFEPESTQK
	QEMDIWLKNFPQAWAETGGMGTAHCQAPVLIQLKATATPISIRQYPMPHEAYQGIKPHIRRMLDQGILKPCQSPWNTPLLPVKKPGTEDYRPVQDLREVNK
	RVEDIHPTVPNPYNLLSTLPPSHPWYTVLDLKDAFFCLRLHSESQLLFAFEWRDPEIGLSGQLTWTRLPQGFKNSPTLFNEALHSDLADFRVRYPALVLLQ
	YVDDLLLAAATRTECLEGTKALLETLGNKGYRASAKKAQICLQEVTYLGYSLKDGQRWLTKARKEAILSIPVPKNSRQVREFLGKAGYCRLFIPGFAELAAPL
	PLYPLTRPGTLFQWGTEQQLAFEDIKKALLSSPALGLPDITKPFELFIDENSGFAKGVLVQKLGPWKRPVAYLSKKLDTVASGWPPCLRMVAAIAILVKDA
	GKLTLGQPLTILTSHPVEALVRQPPNKWLSNARMTHYQAMLLDAERVHFGPTVSLNPATLLPLPSGGNHHDCLQILAETHGTRPDLTDQPLPDADLTWYTD
	GSSFIRNGEREAGAAVTTESEVIWAAPLPPGTSAQRAELIALTQALKMAEGKKLTVYTDSRYAFATTHVHGEIYRRRGWLTSEGKEIKNKNEILALLEALF
	LPKRLSIIHCPGHQKGDSPQAKGNRLADDTAKKAATETHSSLTVLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
12225	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGSSPAPEAAAKGGTLQLEEEYRLFEPESTQKQE
	MDIWLKNFPQAWAETGGMGTAHCQAPVLIQLKATATPISIRQYPMPHEAYQGIKPHIRRMLDQGILKPCQSPWNTPLLPVKKPGTEDYRPVQDLREVNKRV
	EDIHPTVPNPYNLLSTLPPSHPWYTVLDLKDAFFCLRLHSESQLLFAFEWRDPEIGLSGQLTWTRLPQGFKNSPTLFNEALHSDLADFRVRYPALVLLQYV
	DDLLLAAATRTECLEGTKALLETLGNKGYRASAKKAQICLQEVTYLGYSLKDGQRWLTKARKEAILSIPVPKNSRQVREFLGKAGYCRLFIPGFAELAAPL
	YPLTRPGTLFQWGTEQQLAFEDIKKALLSSPALGLPDITKPFELFIDENSGFAKGVLVQKLGPWKRPVAYLSKKLDTVASGWPPCLRMVAAIAILVKDAGK

	LTLGQPLTILTSHPVEALVRQPPNKWLSNARMTHYQAMLLDAERVHFGPTVSLNPATLLPLPSGGNHHDCLQILAETHGTRPDLTDQPLPDADLTWYTDGS SFIRNGEREAGAAVTTESEVIWAAPLPPGTSAQRAELIALTQALKMAEGKKLTVYTDSRYAFATTHVHGEIYRRRGWLTSEGKEIKNKNEILALLEALFLP KRLSIIHCPGHQKGDSPQAKGNRLADDTAKKAATETHSSLTVLPAGKRTADGSEFESPKKKAKVE
1235	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGGSGGTLQLEEEYRLFEPESTQKQE MDIWLKNFPQAWAETGGMGTAHCQAPVLIQLKATATPISIRQYPMPHEAYQGIKPHIRRMLDQGILKPCQSPWNTPLLPVKKPGTEDYRPVQDLREVNKRV EDIHPTVPNPYNLLSTLPPSHPWYTVLDLKDAFFCLRLHSESQLLFAFEWRDPEIGLSGQLTWTRLPQGFKNSPTLFNEALHSDLADFRVRYPALVLLQYV DDLLLAAATRTECLEGTKALLETLGNKGYRASAKKAQICLQEVTYLGYSLKDGQRWLTKARKEAILSIPVPKNSRQVREFLGKAGYCRLFIPGFAELAAPL YPLTRPGTLFQWGTEQQLAFEDIKKALLSSPALGLPDITKPFELFIDENSGFAKGVLVQKLGPWKRPVAYLSKKLDTVASGWPPCLRMVAAIAILVKDAGK LTLGQPLTILTSHPVEALVRQPPNKWLSNARMTHYQAMLLDAERVHFGPTVSLNPATLLPLPSGGNHHDCLQILAETHGTRPDLTDQPLPDADLTWYTDGS SFIRNGEREAGAAVTTESEVIWAAPLPPGTSAQRAELIALTQALKMAEGKKLTVYTDSRYAFATTHVHGEIYRRRGWLTSEGKEIKNKNEILALLEALFLP KRLSIIHCPGHQKGDSPQAKGNRLADDTAKKAATETHSSLTVLPAGKRTADGSEFESPKKKAKVE
1242	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGSSGGSEAAAKGGTLQLEEEYRLFEPESTQKQE MDIWLKNFPQAWAETGGMGTAHCQAPVLIQLKATATPISIRQYPMPHEAYQGIKPHIRRMLDQGILKPCQSPWNTPLLPVKKPGTEDYRPVQDLREVNKRV EDIHPTVPNPYNLLSTLPPSHPWYTVLDLKDAFFCLRLHSESQLLFAFEWRDPEIGLSGQLTWTRLPQGFKNSPTLFNEALHSDLADFRVRYPALVLLQYV DDLLLAAATRTECLEGTKALLETLGNKGYRASAKKAQICLQEVTYLGYSLKDGQRWLTKARKEAILSIPVPKNSRQVREFLGKAGYCRLFIPGFAELAAPL

	YPLTRPGTLFQWGTEQQLAFEDIKKALLSSPALGLPDITKPFELFIDENSGFAKGVLVQKLGPWKRPVAYLSKKLDTVASGWPPCLRMVAAIAILVKDAGK LTLGQPLTILTSHPVEALVRQPPNKWLSNARMTHYQAMLLDAERVHFGPTVSLNPATLLPLPSGGNHHDCLQILAETHGTRPDLTDQPLPDADLTWYTDGS SFIRNGEREAGAAVTTESEVIWAAPLPPGTSAQRAELIALTQALKMAEGKKLTVYTDSRYAFATTHVHGEIYRRRGWLTSEGKEIKNKNEILALLEALFLP KRLSIIHCPGHQKGDSPQAKGNRLADDTAKKAATETHSSLTVLPAGKRTADGSEFESPKKKAKVE
126 2	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGEAAAKPAPGGTLQLEEEYRLFFEPESTQKQE MDIWLKNFPQAWAETGGMGTAHCQAPVLIQLKATATPISIRQYPMPHEAYQGIKPHIRRMLDQGILKPCQSPWNTPLLPVKKPGTEDYRPVQDLREVNKRV EDIHPTVPNPYNLLSTLPPSHPWYTVLDLKDAFFCLRLHSESQLLFAFEWRDPEIGLSGQLTWTRLPQGFKNSPTLFNEALHSDLADFRVRYPALVLLQYV DDLLLAAATRTECLEGTKALLETLGNKGYRASAKKAQICLQEVTYLGYSLKDGQRWLTKARKEAILSIPVPKNSRQVREFLGKAGYCRLFIPGFAELAAPL YPLTRPGTLFQWGTEQQLAFEDIKKALLSSPALGLPDITKPFELFIDENSGFAKGVLVQKLGPWKRPVAYLSKKLDTVASGWPPCLRMVAAIAILVKDAGK LTLGQPLTILTSHPVEALVRQPPNKWLSNARMTHYQAMLLDAERVHFGPTVSLNPATLLPLPSGGNHHDCLQILAETHGTRPDLTDQPLPDADLTWYTDGS SFIRNGEREAGAAVTTESEVIWAAPLPPGTSAQRAELIALTQALKMAEGKKLTVYTDSRYAFATTHVHGEIYRRRGWLTSEGKEIKNKNEILALLEALFLP KRLSIIHCPGHQKGDSPQAKGNRLADDTAKKAATETHSSLTVLPAGKRTADGSEFESPKKKAKVE
137 1	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGSEAAAKGGTAPLEEEYRLFLEAPIQNVT LLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGTSEYRMVQDLREVNKR VETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEEGESGQLTWTRLPQGFKNSPTLFNEALNRDLQGFRLDHPSVSLLQY

	VDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAILQIPVPKTKRQVREFLGKIGYCRLFIPGFAELAQP LYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSKRLDPVAAGWPRCLRAIAAAALLTREA SKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTSTRPDLTDQPLAQAEATLFT DGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWLTAGGKAIKNAPEILALLTAV WLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFESPKKKAKVE
1372	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKALEAEAAAKEAA AKEAAAKEAAAKAGGTAPLEEEYRLFLEAPIQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYPITLEAKRSLRETIRKFRAAGI LRPVHSPWNTPLLPVRKSGTSEYRMVQDLREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEEGESGQLTWTR LPQGFKNSPTLFNEALNRDLQGFRLDHPSVSLLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAI LQIPVPKTKRQVREFLGKIGYCRLFIPGFAELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPW KRPVAYLSKRLDPVAAGWPRCLRAIAAAALLTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDD TLPIHHCLDTLDSLTSTRPDLTDQPLAQAEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFA TLHVHGMIYRERGWLTAGGKAIKNAPEILALLTAVWLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFEKRTADGS EFESPKKKAKVE
1373	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKALEAEAAAKEAA

	APLEEEYRLFLEAPIQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVR
	KSGTSEYRMVQDLREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEEGESGQLTWTRLPQGFKNSPTLFNEAL
	NRDLQGFRLDHPSVSLLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAILQIPVPKTKRQVREFL
	GKIGYCRLFIPGFAELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSKRLDPVAA
	GWPRCLRAIAAAALLTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTS
	TRPDLTDQPLAQAEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWLT
	AGGKAIKNAPEILALLTAVWLPKRVAVMHCKGHQKDDAPTSTGNRRADEVARAVIRPLSTQATISAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1374	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGGGSGGGGSGGGGSGGTAPLEEEYRLF
	LEAPIQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGTSEYRMV
	QDLREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEEGESGQLTWTRLPQGFKNSPTLFNEALNRDLQGFRLD
	HPSVSLLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAILQIPVPKTKRQVREFLGKIGYCRLFI
	PGFAELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSKRLDPVAAGWPRCLRAIA
	AAALLTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTSTRPDLTDQPL
	AQAEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWLTAGGKAIKNAP
	EILALLTAVWLPKRVAVMHCKGHQKDDAPTSTGNRRADEVARAVIRPLSTQATISAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1375	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI

	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSPAPGGTAPLEEEYRLFLEAPIQNVTLLEQW
	KREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGTSEYRMVQDLREVNKRVETIH
	PTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEEGESGQLTWTRLPQGFKNSPTLFNEALNRDLQGFRLDHPSVSLLQYVDDLL
	IAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAILQIPVPKTKRQVREFLGKIGYCRLFIPGFAELAQPLYAAT
	RPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSKRLDPVAAGWPRCLRAIAAAALLTREASKLTF
	GQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTSTRPDLTDQPLAQAEATLFTDGSSY
	IRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWLTAGGKAIKNAPEILALLTAVWLPKR
	VAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1376	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
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	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
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	IQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGTSEYRMVQDLR
	EVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEEGESGQLTWTRLPQGFKNSPTLFNEALNRDLQGFRLDHPSV
	SLLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAILQIPVPKTKRQVREFLGKIGYCRLFIPGFA
	ELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSKRLDPVAAGWPRCLRAIAAAAL
	LTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTSTRPDLTDQPLAQAE
	ATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWLTAGGKAIKNAPEILA
	LLTAVWLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1377	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM
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	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY

	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPEAAAKGGSGGTAPLEEEYRLFLEAPIQNVT LLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGTSEYRMVQDLREVNKR VETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEEGESGQLTWTRLPQGFKNSPTLFNEALNRDLQGFRLDHPSVSLLQY VDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAILQIPVPKTKRQVREFLGKIGYCRLFIPGFAELAQP LYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSKRLDPVAAGWPRCLRAIAAAALLTREA SKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTSTRPDLTDQPLAQAEATLFT DGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWLTAGGKAIKNAPEILALLTAV WLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1380	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGTAPLEEEYRLFLEAPIQNVTLLEQWK REIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGTSEYRMVQDLREVNKRVETIHP TVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEEGESGQLTWTRLPQGFKNSPTLFNEALNRDLQGFRLDHPSVSLLQYVDDLLI AADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAILQIPVPKTKRQVREFLGKIGYCRLFIPGFAELAQPLYAATR PGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSKRLDPVAAGWPRCLRAIAAAALLTREASKLTFG QDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTSTRPDLTDQPLAQAEATLFTDGSSYI RDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWLTAGGKAIKNAPEILALLTAVWLPKRV AVMHCKGHQKDDAPTSTGNRRADEVARFVAIRPLSTQATISAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1381	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV

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	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSEAAAKPAPGGTAPLEEEYRLFLEAPIQNVT
	LLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGTSEYRMVQDLREVNKR
	VETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEEGESGQLTWTRLPQGFKNSPTLFNEALNRDLQGFRLDHPSVSLLQY
	VDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAILQIPVPKTKRQVREFLGKIGYCRLFIPGFAELAQP
	LYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSKRLDPVAAGWPRCLRAIAAALLTREA
	SKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTSTRPDLTDQPLAQEATLFT
	DGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWLTAGGKAIKNAPEILALLTAV
	WLPKRVAVMHCKGHQKDDAPTSTGNRRADEVARE VAIRPLSTQATISAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1382	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
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	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
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	APIQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGTSEYRMVQD
	LREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEEGESGQLTWTRLPQGFKNSPTLFNEALNRDLQGFRLDHP
	SVSLLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAILQIPVPKTKRQVREFLGKIGYCRLFIPG
	FAELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSKRLDPVAAGWPRCLRAIAAA
	ALLTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTSTRPDLTDQPLAQ
	AEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWLTAGGKAIKNAPEI
	LALLTAVWLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1383	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK

	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSPAPGGGGGTAPLEEEYRLFLEAPIQNVTLL
	EQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGTSEYRMVQDLREVNKRVE
	TIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEEGESGQLTWTRLPQGFKNSPTLFNEALNRDLQGFRLDHPSVSLLQYVD
	DLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAILQIPVPKTKRQVREFLGKIGYCRLFIPGFAELAQPLY
	AATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSKRLDPVAAGWPRCLRAIAAAALLTREASK
	LTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTSTRPDLTDQPLAQAEATLFTDG
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1384	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
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	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
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	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
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	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSPAPGGTAPLEEEYRLFLEAPIQNVT
	LLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGTSEYRMVQDLREVNKR
	VETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEEGESGQLTWTRLPQGFKNSPTLFNEALNRDLQGFRLDHPSVSLLQY
	VDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAILQIPVPKTKRQVREFLGKIGYCRLFIPGFAELAQP
	LYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSKRLDPVAAGWPRCLRAIAAAALLTREA
	SKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTSTRPDLTDQPLAQAEATLFT
	DGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWLTAGGKAIKNAPEILALLTAV
	WLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1385	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
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	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD

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1389	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
1390	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK

	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
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	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGSGGTAPLEEEYRLFLEAPIQNVT
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	VETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEEGESGQLTWTRLPQGFKNSPTLFNEALNRDLQGFRLDHPSVSLLQY
	VDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAILQIPVPKTKRQVREFLGKIGYCRLFIPGFAELAQP
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	SKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLSTRPDLTDQPLAQAEATLFT
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1394	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
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	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
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1397	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
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	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
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	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
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	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGSEAAAKGGTAPLEEEYRLFLEAPI
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	IAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAILQIPVPKTKRQVREFLGKIGYCRLFIPGFAELAQPLYAAT
	RPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSKRLDPVAAGWPRCLRAIAAAALLTREASKLTF
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	IRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWLTAGGKAIKNAPEILALLTAVWLPKR
	VAVMHCKGHQKDDAPTSTGNRRADEVARE
1399	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
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	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
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	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGSEAAAKGGTAPLEEEYRLFLEAPI
	QNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGTSEYRMVQDLRE
	VNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEEGESGQLTWTRLPQGFKNSPTLFNEALNRDLQGFRLDHPSVS
	LLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAILQIPVPKTKRQVREFLGKIGYCRLFIPGFAE
	LAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSKRLDPVAAGWPRCLRAIAAAALL
	TREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTSTRPDLTDQPLAQAEA
	TLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWLTAGGKAIKNAPEILAL
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1400	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
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	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
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	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH

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	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	EYRMVQDLREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEEGESGQLTWTRLPQGFKNSPTLFNEALNRDLQGFRLDHPSVSLLQYVD
	GFRLDHPSVSLLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAILQIPVPKTKRQVREFLGKIGYCRLFIPGFAELAQPLY
	CRLFIPGFAELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSKRLDPVAAGWPRC
	LRAIAAAALLTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTSTRPDL
	TDQPLAQAEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWLTAGGKA
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140 1	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
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	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
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	EQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGTSEYRMVQDLREVNKRVE
	TIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEEGESGQLTWTRLPQGFKNSPTLFNEALNRDLQGFRLDHPSVSLLQYVD
	DLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAILQIPVPKTKRQVREFLGKIGYCRLFIPGFAELAQPLY
	AATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSKRLDPVAAGWPRCLRAIAAAALLTREASK
	LTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTSTRPDLTDQPLAQAEATLFTDG
	SSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWLTAGGKAIKNAPEILALLTAVWL
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140 2	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
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	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
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	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGPAPGGSGGTAPLEEEYRLFLEAPIQNVTLL EQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGTSEYRMVQDLREVNKR TIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEEGESGQLTWTRLPQGFKNSPTLFNEALNRDLQGFRLDHPSVSLLQY DLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAILQIPVPKTKRQVREFLGKIGYCRLFIPGFAELAQP LLAEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGTSEYRMVQDLREVNKR VETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEEGESGQLTWTRLPQGFKNSPTLFNEALNRDLQGFRLDHPSVSLLQY VDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAILQIPVPKTKRQVREFLGKIGYCRLFIPGFAELAQP LYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSKRLDPVAAGWPRCLRAIAAAALLTREA SKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTSTRPDLTDQPLAQAEATLFT DGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWLTAGGKAIKNAPEILALLTAV WLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1404	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGPAPGGSGGTAPLEEEYRLFLEAPIQNVTL LLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGTSEYRMVQDLREVNKR VETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEEGESGQLTWTRLPQGFKNSPTLFNEALNRDLQGFRLDHPSVSLLQY VDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAILQIPVPKTKRQVREFLGKIGYCRLFIPGFAELAQP LYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSKRLDPVAAGWPRCLRAIAAAALLTREA SKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTSTRPDLTDQPLAQAEATLFT DGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWLTAGGKAIKNAPEILALLTAV WLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1405	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL

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	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
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	QWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGTSEYRMVQDLREVNKR
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	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
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	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSEAAAKGGTAPLEEEYRLFLEAPIQNVTT
	LLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGTSEYRMVQDLREVNKR
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	VDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAILQIPVPKTKRQVREFLGKIGYCRLFIPGFAELAQP
	LYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSKRLDPVAAGWPRCLRAIAAAALLTREA
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	DGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWLTAGGKAIKNAPEILALLTAV
	WLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1406	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSEAAAKGGTAPLEEEYRLFLEAPIQNVTT LLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGTSEYRMVQDLREVNKR VETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEEGESGQLTWTRLPQGFKNSPTLFNEALNRDLQGFRLDHPSVSLLQY VDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAILQIPVPKTKRQVREFLGKIGYCRLFIPGFAELAQP LYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSKRLDPVAAGWPRCLRAIAAAALLTREA SKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTSTRPDLTDQPLAQAEATLFT DGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWLTAGGKAIKNAPEILALLTAV WLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1410	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA

	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPEAAAKGGTAPLEEEYRLFLEAPIQNVT
	KREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGTSEYRMVQDLREVNKRVETIH
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	PTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEEGESGQLTWTRLPQGFKNSPTLFNEALNRDLQGFRLDHPSVSLLQYVDDLL
	IAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAILQIPVPKTKRQVREFLGKIGYCRLFIPGFAELAQPLYAAT
	RPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSKRLDPVAAGWPRCLRAIAAAALLTREASKLTF
	GQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTSTRPDLTDQPLAQAEATLFTDGSSY
	IRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWLTAGGKAIKNAPEILALLTAVWLPKR
	VAVMHCKGHQKDDAPTSTGNRRADEVARE VAIRPLSTQATISAGKRTADGSEFEKRTADGSEFESPKKKAKVE
141 5	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGPAPEAAAKGGTAPLEEEYRLFLEAPIQNVT
	LLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGTSEYRMVQDLREVNKR
	VETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEEGESGQLTWTRLPQGFKNSPTLFNEALNRDLQGFRLDHPSVSLLQY
	VDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAILQIPVPKTKRQVREFLGKIGYCRLFIPGFAELAQP
	LYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSKRLDPVAAGWPRCLRAIAAAALLTREA
	SKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTSTRPDLTDQPLAQAEATLFT
	DGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWLTAGGKAIKNAPEILALLTAV
	WLPKRVAVMHCKGHQKDDAPTSTGNRRADEVARE VAIRPLSTQATISAGKRTADGSEFEKRTADGSEFESPKKKAKVE

1419	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV LYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSKRLDPVAAGWPRCLRAIAAAALLTREA SKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTSTRPDLTDQPLAQAEATLFTDGS DGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWLTAGGKAIKNAPEILALLTAV WLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFESPKKKAKVE
1422	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGSSGGGGTAPLEEEYRLFLEAPIQNVT QWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGTSEYRMVQDLREVNKR IHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEEGESGQLTWTRLPQGFKNSPTLFNEALNRDLQGFRLDHPSVSLLQYVDD LLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAILQIPVPKTKRQVREFLGKIGYCRLFIPGFAELAQPLYA ATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSKRLDPVAAGWPRCLRAIAAAALLTREASKL TFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTSTRPDLTDQPLAQAEATLFTDGS

	SYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWLTAGGKAIKNAPEILALLTAVWLP KRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFESPKKKAKVE
1423	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGGSGGGTAPLEEEYRLFLEAPIQNVTL LEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGTSEYRMVQDLREVNKRV ETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEEGESGQLTWTRLPQGFKNSPTLFNEALNRDLQGFRLDHPSVSLLQYV DDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAILQIPVPKTKRQVREFLGKIGYCRLFIPGFAELAQPL YAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSKRLDPVAAGWPRCLRAIAAAALLTREAS KLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTSTRPDLTDQPLAQAEATLFTD GSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWLTAGGKAIKNAPEILALLTAVW LPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFESPKKKAKVE
1424	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGGGEAAAKGGTAPLEEEYRLFLEAPIQNVT LLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGTSEYRMVQDLREVNKR VETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEEGESGQLTWTRLPQGFKNSPTLFNEALNRDLQGFRLDHPSVSLLQY VDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAILQIPVPKTKRQVREFLGKIGYCRLFIPGFAELAQP LYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSKRLDPVAAGWPRCLRAIAAAALLTREA

	SKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTSTRPDLTDQPLAQAEATLFT DGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWLTAGGKAIKNAPEILALLTAV WLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFEKRTADGSEFESPKKKAKVE
144 1	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSGGGGGTAPLEEEYRLFLEAPIQNVT LLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGTSEYRMVQDLREVNKR VETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEEGESGQLTWTRLPQGFKNSPTLFNEALNRDLQGFRLDHPSVSLLQY VDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAILQIPVPKTKRQVREFLGKIGYCRLFIPGFAELAQP LYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSKRLDPVAAGWPRCLRAIAAAALLTREA SKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTSTRPDLTDQPLAQAEATLFT DGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWLTAGGKAIKNAPEILALLTAV WLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFEKRTADGSEFESPKKKAKVE
154 0	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSSEAAAKGGTVSLQDEHRLFDIPVTTSLP DVWLQDFPQAWAETGGLGRAKCQAPIIIDLKPTAVPVSIKQYPMSLEAHMGIRQHIIKFLELGVLRPCRSPWNTPLLPVKKPGTQDYRPVQDLREINKRTV DIHPTVPNPYNLLSTLKPDYSWYTVLDLKDAFFCLPLAPQSQELFAFEWKDPERGISGQLTWTRLPQGFKNSPTLFNEALHRDLTDFRTQHPEVTLLQYVD DLLLAAPTKKACTQGTRHLLQELGEKGYRASAKKAQICQTKVTYLGYILSEGKRWLTPGRIETVARIPPPRNPREVREFLGTAGFCRLWIPGFAELAAPLY

	ALTKPSTPFTWQTEHQLAFEALKKALLSAPALGLPDTSKPFTLFLDERQGIAKGVLTQKLGPWKRPVAYLSKKLDPVAAGWPPCLRIMAATAMLVKDSAKL
	TLGQPLTVITPHTLEAIVRQPPDRWITNARLTHYQALLLDTDRVQFGPPVTLNPATLLPVPENQPSPHDCRQVLAETHGTREDLKDQELPDADHTWYTDGS
	SYLDSGTRRAGAAVVDGHNTIWAQSLPPGTSAQKAELIALTKALELSKGKKANIYTDSRYAFATAHTHGSIYERRGWLTSEGKEIKNKAEIIALLKALFLP
	QEVAIIHCPGHQKGQDPVAVGNRQADRVARQAAMAEVLTLATEPDNTSHITAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1543	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGGGSGGGGSGGTVSLQD
	EHRLFDIPVTTSLPDVWLQDFPQAWAETGGLGRAKCQAPIIIDLKPTAVPVSIKQYPMSLEAHMGIRQHIIKFLELGVLRPCRSPWNTPLLPVKKPGTQDY
	RPVQDLREINKRTVDIHPTVPNPYNLLSTLKPDYSWYTVLDLKDAFFCLPLAPQSQELFAFEWKDPERGISGQLTWTRLPQGFKNSPTLFNEALHRDLTDF
	RTQHPEVTLLQYVDDLLLAAPTKKACTQGTRHLLQELGEKGYRASAKKAQICQTKVTYLGYILSEGKRWLTPGRIETVARIPPPRNPREVREFLGTAGFCR
	LWIPGFAELAAPLYALTKPSTPFTWQTEHQLAFEALKKALLSAPALGLPDTSKPFTLFLDERQGIAKGVLTQKLGPWKRPVAYLSKKLDPVAAGWPPCLRI
	MAATAMLVKDSAKLTLGQPLTVITPHTLEAIVRQPPDRWITNARLTHYQALLLDTDRVQFGPPVTLNPATLLPVPENQPSPHDCRQVLAETHGTREDLKDQ
	ELPDADHTWYTDGSSYLDSGTRRAGAAVVDGHNTIWAQSLPPGTSAQKAELIALTKALELSKGKKANIYTDSRYAFATAHTHGSIYERRGWLTSEGKEIKN
	KAEIIALLKALFLPQEVAIIHCPGHQKGQDPVAVGNRQADRVARQAAMAEVLTLATEPDNTSHITAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1550	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGSSGGGGGTVSLQDEHRLFDIPVTTSLPDV
	WLQDFPQAWAETGGLGRAKCQAPIIIDLKPTAVPVSIKQYPMSLEAHMGIRQHIIKFLELGVLRPCRSPWNTPLLPVKKPGTQDYRPVQDLREINKRTVDI
	HPTVPNPYNLLSTLKPDYSWYTVLDLKDAFFCLPLAPQSQELFAFEWKDPERGISGQLTWTRLPQGFKNSPTLFNEALHRDLTDFRTQHPEVTLLQYVDDL

	LLAAPTKKACTQGTRHLLQELGEKGYRASAKKAQICQTKVTYLGYILSEGKRWLTPGRIETVARIPPPRNPREVREFLGTAGFCRLWIPGFAELAAPLYALTKPSTPFTWQTEHQLAFEALKKALLSAPALGLPDTSKPFTLFLDERQGIAKGVLTQKLGPWKRPVAYLSKKLDPVAAGWPPCLRIMAATAMLVKDSAKLTLGQPLTVITPHTLEAIVRQPPDRWITNARLTHYQALLLDTDRVQFGPPVTLNPATLLPVPENQPSPHDCRQVLAETHGTREDLKDQELPDADHTWYTDGSSYLDSGTRRAGAAVVDGHNTIWAQSLPPGTSAQKAELIALTKALELSKGKKANIYTDSRYAFATAHTHGSIYERRGWLTSEGKEIKNKAEIIALLKALFLPQEVAIIHCPGHQKGQDPVAVGNRQADRVARQAAMAEVLTLATEPDNTSHITAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1553	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPGGLLGRDLLTKLKAQIQFSTEGPQVT WEDRPAMCLVLNLEEYRLHEKPVPPSIDPSWLQLFPMVAAEKAGMGLANQVPPVVVELKSDASPVAVRQYPMSKEARAREGIRPHIQRFLDLGILVPCQSPW
1616	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPGGLLGRDLLTKLKAQIQFSTEGPQVT WEDRPAMCLVLNLEEYRLHEKPVPPSIDPSWLQLFPMVAAEKAGMGLANQVPPVVVELKSDASPVAVRQYPMSKEARAREGIRPHIQRFLDLGILVPCQSPW

	NTPLLPVKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNS PTLFNEALHRDLASFRALNPQVVMLQYVDDLLVAAPTYRDCKEGTRRLLQELSKLGYRVSAKKAQLCREEVTYLGYLLKGGKRWLTPARKATVMKIPTPTT PRQVREFLGTAGFCRLWIPGFASLAAPLYPLTRPKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFALYVDEKEGVARGVLTQTLGPWRRPVAYLSK KLDPVASGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAILNPATLLPVESDDTPIHICSEI LAEETGTRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQ RGWLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTETTKNAGKRTADGSEFEKRTADGSEFESPKKKAK VE
1618	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKPAPGSSGGLLGRDLLITKLKAQIQFSTEG PQVTWEDRPAMCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPMVWAEKAGMGLANQVPPVVVELKSDASPVAVRQYPMSKEAREGIRPHIQRFLDLGILVPC QSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQG FKNSPTLFNEALHRDLASFRALNPQVVMLQYVDDLLVAAPTYRDCKEGTRRLLQELSKLGYRVSAKKAQLCREEVTYLGYLLKGGKRWLTPARKATVMKIP TPTTPRQVREFLGTAGFCRLWIPGFASLAAPLYPLTRPKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFALYVDEKEGVARGVLTQTLGPWRRPVA YLSKKLDPVASGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAILNPATLLPVESDDTPIHI CSEILAEETGTRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALTQALRLAEGKSINIYTDSRYAFATAHVHGA IYKQRGWLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTETTKNAGKRTADGSEFEKRTADGSEFESPK KKAKVE
1619	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY

	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPAPGGLLGRDLLTKLKAQIQFSTEG PQVTWEDRPAMCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPMVWAEKAGMGLANQVPPVVVELKSDASPVAVRQYPMSKEAREGIRPHIQRFLDLGILVPC QSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQG FKNSPTLFNEALHRDLASFRALNPQVVMLQYVDDLLVAAPTYRDCKEGTRRLLQELSKLGYRVSAKKAQLCREEVTYLGYLLKGGKRWLTPARKATVMKIP TPTTPRQVREFLGTAGFCRLWIPGFASLAAPLYPLTRPKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFALYVDEKEGVARGVLTQTLGPWRRPVA YLSKKLDPVASGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAILNPATLLPVESDDTPIHI CSEILAEETGTRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALTQALRLAEGKSINIYTDSRYAFATAHVHGA IYKQRGWLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTETTKNAGKRTADGSEFEKRTADGSEFESPK KKAKVE
1666	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSPAPEAAAKGGLLGRDLLTKLKAQIQFSTEG PQVTWEDRPAMCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPMVWAEKAGMGLANQVPPVVVELKSDASPVAVRQYPMSKEAREGIRPHIQRFLDLGILVPC QSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQG FKNSPTLFNEALHRDLASFRALNPQVVMLQYVDDLLVAAPTYRDCKEGTRRLLQELSKLGYRVSAKKAQLCREEVTYLGYLLKGGKRWLTPARKATVMKIP TPTTPRQVREFLGKAGFCRLFIPGFASLAAPLYPLTRPKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFALYVDEKEGVARGVLTQTLGPWRRPVA YLSKKLDPVASGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAILNPATLLPVESDDTPIHI CSEILAEETGTRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALTQALRLAEGKSINIYTDSRYAFATAHVHGA IYKQRGWLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTETTKNAGKRTADGSEFEKRTADGSEFESPK KKAKVE
1668	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD

	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGGGGGLLGRDLLTKLKAQIQFSTEGPQVTW EDRPAMCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPMVWAEKAGMGLANQVPPVVVELKSDASPVAVRQYPMSKEARE GIRPHIQRFLDLGILVPCQSPWN TPLLPVVKKPGTNDYIRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSP TLFNEALHRDLASFRALNPQVVMLQYVDDLLVAAPTYRDCKEGTRRLLQELSKLGYRVSAKKAQLCREEVTYLGYLLKGGKRWLTPARKATVMKIPTPTTP RQVREFLGKAGFCRLFIPGFASLAAPLYPLTRPKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFALYVDEKEGVARGVLTQTLGPWRRPVAYLSKK LDPVASGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAILNPATLLPVESDDTPIHICSEIL AEETGTRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQR GWLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTETTKNAGKRTADGSEFEKRTADGSEFESPKKKAKV E
1672	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGGGGGEAAAKPAPGGLLGRDLLTKLKAQIQFSTEG PQVTWEDRPAMCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPMVWAEKAGMGLANQVPPVVVELKSDASPVAVRQYPMSKEAREGIRPHIQRFLDLGILVPC QSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQG FKNSPTLFNEALHRDLASFRALNPQVVMLQYVDDLLVAAPTYRDCKEGTRRLLQELSKLGYRVSAKKAQLCREEVTYLGYLLKGGKRWLTPARKATVMKIP TPTTPRQVREFLGKAGFCRLFIPGFASLAAPLYPLTRPKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFALYVDEKEGVARGVLTQTLGPWRRPVA YLSKKLDPVASGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAILNPATLLPVESDDTPIHI CSEILAEETGTRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALTQALRLAEGKSINIYTDSRYAFATAHVHGA IYKQRGWLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTETTKNAGKRTADGSEFEKRTADGSEFESPK KKAKVE
1677	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH

	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGSSGGLLGRDLLTKLKAQIQFSTEG PQVTWEDRPAMCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPMVWAEKAGMGLANQVPPVVVELKSDASPVAVRQYPMSKEARGEGIRPHIQRFLDLGILVPC QSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKN FKNSPTLFNEALHRDLASFRALNPQVVMLQYVVDDLLVAAPTYRDCKEGTRRLLQELSKLGYRVSAKKAQLCREEVTYLGYLLKGGKRWLTPARKATVMKIPTPT TPTTPRQVREFLGKAGFCRLFIPGFASLAAPLYPLTRPKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFALYVDEKEGVARGVLTQTLGPWRRPVAYLS YLSKKLDPVASGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAILNPATLLPVESDDTPIHI CSEILAEETGTRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALTQALRLAEGKSINIYTDSRYAFATAHVHGA IYKQRGWLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTETTKNAGKRTADGSEFEKRTADGSEFESPK KKAKVE
167 9	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGSSGGLLGRDLLTKLKAQIQFSTEGPQV TWEDRPAMCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPMVWAEKAGMGLANQVPPVVVELKSDASPVAVRQYPMSKEARGEGIRPHIQRFLDLGILVPCQSP WNTPLLPVKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKN SPTLFNEALHRDLASFRALNPQVVMLQYVVDDLLVAAPTYRDCKEGTRRLLQELSKLGYRVSAKKAQLCREEVTYLGYLLKGGKRWLTPARKATVMKIPTPT TPRQVREFLGKAGFCRLFIPGFASLAAPLYPLTRPKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFALYVDEKEGVARGVLTQTLGPWRRPVAYLS KKLDPVASGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAILNPATLLPVESDDTPIHICSE ILAEETGTRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYK QRGWLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTETTKNAGKRTADGSEFEKRTADGSEFESPKKKA KVE
168 2	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA

	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSEAAAKGGLLGRDLLTKLKAQIQFSTEG PQVTWEDRPAMCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPMVWAEKAGMGLANQVPPVVVELKSDASPVAVRQYPMSKEARE GIRPHIQRFLDLGILVPC QSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQG FKNSPTLFNEALHRDLASFRALNPQVVMLQYVDDLLVAAPTYRDCKEGTRRLLQELSKLGYRVSAKKAQLCREEVTYLGYLLKGGKRWLTPARKATVMKIP TPTTPRQVREFLGKAGFCRLFIPGFASLAAPLYPLTRPKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFALYVDEKEGVARGVLTQTLGPWRRPVA YLSKKLDPVASGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAILNPATLLPVESDDTPIHI CSEILAEETGTRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALTQALRLAEGKSINIYTDSRYAFATAHVHGA IYKQRGWLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTETTKNAGKRTADGSEFEKRTADGSEFESPKK KKAKVE
168 6	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGGSGGGSEAAAKGGLLGRDLLTKLKAQIQFSTEGPQ VTWEDRPAMCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPMVWAEKAGMGLANQVPPVVVELKSDASPVAVRQYPMSKEAREGIRPHIQRFLDLGILVPCQS PWNTPLLPVKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFK NSPTLFNEALHRDLASFRALNPQVVMLQYVDDLLVAAPTYRDCKEGTRRLLQELSKLGYRVSAKKAQLCREEVTYLGYLLKGGKRWLTPARKATVMKIPTP TTPRQVREFLGKAGFCRLFIPGFASLAAPLYPLTRPKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFALYVDEKEGVARGVLTQTLGPWRRPVAYL SKKLDPVASGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAILNPATLLPVESDDTPIHICS EILAEETGTRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALTQALRLAEGKSINIYTDSRYAFATAHVHGAIY KQRGWLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTETTKNAGKRTADGSEFEKRTADGSEFESPKKK AKVE

1690	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGSSGGSGGLLGRDLLTKLKAQIQFSTEG PQVTWEDRPAMCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPMVWAEKAGMGLANQVPPVVVELKSDASPVAVRQYPMSKEAREGIRPHIQRFLDLGILVPC QSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQG FKNSPTLFNEALHRDLASFRALNPQVVMLQYVDDLLVAAPTYRDCKEGTRRLLQELSKLGYRVSAKKAQLCREEVTYLGYLLKGGKRWLTPARKATVMKIP TPTTPRQVREFLGKAGFCRLFIPGFASLAAPLYPLTRPKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFALYVDEKEGVARGVLTQTLGPWRRPVA YLSKKLDPVASGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAILNPATLLPVESDDTPIHI CSEILAEETGTRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALTQALRLAEGKSINIYTDSRYAFATAHVHGA IYKQRGWLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTETTKNAGKRTADGSEFEKRTADGSEFESPK KKAKVE
1691	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGGGSSGGLLGRDLLTKLKAQIQFSTEGPQ VTWEDRPAMCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPMVWAEKAGMGLANQVPPVVVELKSDASPVAVRQYPMSKEAREGIRPHIQRFLDLGILVPCQS PWNTPLLPVKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFK NSPTLFNEALHRDLASFRALNPQVVMLQYVDDLLVAAPTYRDCKEGTRRLLQELSKLGYRVSAKKAQLCREEVTYLGYLLKGGKRWLTPARKATVMKIPTP TTPRQVREFLGKAGFCRLFIPGFASLAAPLYPLTRPKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFALYVDEKEGVARGVLTQTLGPWRRPVAYL SKKLDPVASGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAILNPATLLPVESDDTPIHICS

	EILAEETGTRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALTQALRLAEGKSINIYTDSRYAFATAHVHGAIY KQRGWLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTETTKNAGKRTADGSEFEKRTADGSEFESPKKK AKVE
1695	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGSSGGLLGRDLLTKLKAQIQFSTEGPQVTW EDRPAMCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPMVWAEKAGMGLANQVPPVVVELKSDASPVAVRQYPMSKEARAEGIRPHIQRFLDLGILVPCQSPWN TPLLPVVKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSP TLFNEALHRDLASFRALNPQVVMLQYVDDLLVAAPTYRDCKEGTRRLLQELSKLGYRVSAKKAQLCREEVTYLGYLLKGGKRWLTPARKATVMKIPTPTTP RQVREFLGKAGFCRLFIPGFASLAAPLYPLTRPKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFALYVDEKEGVARGVLTQTLGPWRRPVAYLSKK LDPVASGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAILNPATLLPVESDDTPIHICSEIL AEETGTRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQR GWLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTETTKNAGKRTADGSEFEKRTADGSEFESPKKKAKV E
1698	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGGGGLLGRDLLTKLKAQIQFSTEGPQVTW EDRPAMCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPMVWAEKAGMGLANQVPPVVVELKSDASPVAVRQYPMSKEARAEGIRPHIQRFLDLGILVPCQSPWN TPLLPVVKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSP

	TLFNEALHRDLASFRALNPQVVMLQYVDDLLVAAPTYRDCKEGTRRLLQELSKLGYRVSAKKAQLCREEVTYLGYLLKGGKRWLTPARKATVMKIPTPTTP RQVREFLGKAGFCRLFIPGFASLAAPLYPLTRPKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFALYVDEKEGVARGVLTQTLGPWRRPVAYLSKK LDPVASGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAILNPATLLPVESDDTPIHICSEIL AEETGTRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQR GWLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTETTKNAGKRTADGSEFFESPKKKAKV E
172 1	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSPAPEAAAKGGLLGRDLLTKLKAQIQFSTEG PQVTWEDRPAMCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPMVWAEKAGMGLANQVPPVVVELKSDASPVAVRQYPMSKEAREGIRPHIQRFLDLGILVPC QSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQG FKNSPTLFNEALHRDLASFRALNPQVVMLQYVDDLLVAAPTYRDCKEGTRRLLQELSKLGYRVSAKKAQLCREEVTYLGYLLKGGKRWLTPARKATVMKIP TPTTPRQVREFLGKAGFCRLFIPGFASLAAPLYPLTRPKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFALYVDEKEGVARGVLTQTLGPWRRPVA YLSKKLDPVASGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAILNPATLLPVESDDTPIHI CSEILAEETGTRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALTQALRLAEGKSINIYTDSRYAFATAHVHGA IYKQRGWLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTETTKNAGKRTADGSEFESPK KKAKVE
175 4	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI

	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGSEAAAKGGTLGDQGSRGSDDPLPEPRVTL TVEGIPTEFLVNTGAEHSVLTKPMGKMGSKRTVVAGATGSKVYPWTTKRLLKIGQKQVTHSFLVIPECPAPLLGRDLLTKLKAQIQFSTEGPQVTWEDRPA MCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPMVWAEKAGMGLANQVPPVVVELKSDASPVAVRQYPMSKEAREGIRPHIQRFLDLGILVPCQSPWNTPLLP VKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNE ALHRDLASFRALNPQVVMLQYVDDLLVAAPTYRDCKEGTRRLLQELSKLGYRVSAKKAQLCREEVTYLGYLLKGGKRWLTPARKATVMKIPTPTTPRQVRE FLGTAGFCRLWIPGFASLAAPLYPLTRPKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFALYVDEKEGVARGVLTQTLGPWRRPVAYLSKKLDPVA SGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAILNPATLLPVESDDTPIHICSEILAEETG TRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTS AGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTETTKNAGKRTADGSEFESPKKKAKVE
1759	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGGEAAAKGGTLGDQGSRGSDDPLPEPRVTL TVEGIPTEFLVNTGAEHSVLTKPMGKMGSKRTVVAGATGSKVYPWTTKRLLKIGQKQVTHSFLVIPECPAPLLGRDLLTKLKAQIQFSTEGPQVTWEDRPA MCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPMVWAEKAGMGLANQVPPVVVELKSDASPVAVRQYPMSKEAREGIRPHIQRFLDLGILVPCQSPWNTPLLP VKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNE ALHRDLASFRALNPQVVMLQYVDDLLVAAPTYRDCKEGTRRLLQELSKLGYRVSAKKAQLCREEVTYLGYLLKGGKRWLTPARKATVMKIPTPTTPRQVRE FLGTAGFCRLWIPGFASLAAPLYPLTRPKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFALYVDEKEGVARGVLTQTLGPWRRPVAYLSKKLDPVA SGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAILNPATLLPVESDDTPIHICSEILAEETG TRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTS AGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTETTKNAGKRTADGSEFESPKKKAKVE
1769	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK

	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSEAAAKGSSGGTLGDQGSRGSDPLPEPRVTL
	TVEGIPTEFLVNTGAEHSVLTKPMGKMGSKRTVVAGATGSKVYPWTTKRLLKIGQKQVTHSFLVIPECPAPLLGRDLLTKLKAQIQFSTEGPQVTWEDRPA
	MCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPMVWAEKAGMGLANQVPPVVVELKSDASPVAVRQYPMSKEARE GIRPHIQRFLDLGILVPCQSPWNTPLLP
	VKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNE
	ALHRDLASFRALNPQVVMLQYVDDLLVAAPTYRDCKEGTRRLLQELSKLGYRVSAKKAQLCREEVTYLGYLLKGGKRWLTPARKATVMKIPTPTTPRQVRE
	FLGKAGFCRLFIPGFASLAAPLYPLTRPKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFALYVDEKEGVARGVLTQTLGPWRRPVAYLSKKLDPVA
	SGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAILNPATLLPVESDDTPIHICSEILAEETG
	TRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTS
	AGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTETTKNAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1770	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGEAAAKGGGPAPGGTLGDQGSRGSDPLPEPRVTL
	TVEGIPTEFLVNTGAEHSVLTKPMGKMGSKRTVVAGATGSKVYPWTTKRLLKIGQKQVTHSFLVIPECPAPLLGRDLLTKLKAQIQFSTEGPQVTWEDRPA
	MCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPMVWAEKAGMGLANQVPPVVVELKSDASPVAVRQYPMSKEAREGIRPHIQRFLDLGILVPCQSPWNTPLLP
	VKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNE
	ALHRDLASFRALNPQVVMLQYVDDLLVAAPTYRDCKEGTRRLLQELSKLGYRVSAKKAQLCREEVTYLGYLLKGGKRWLTPARKATVMKIPTPTTPRQVRE
	FLGKAGFCRLFIPGFASLAAPLYPLTRPKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFALYVDEKEGVARGVLTQTLGPWRRPVAYLSKKLDPVA
	SGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAILNPATLLPVESDDTPIHICSEILAEETG
	TRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTS
	AGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTETTKNAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1772	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL

	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSSGGTLGDQGSRGSDPLPEPRVTLTVEGI
	PTEFLVNTGAEHSVLTKPMGKMGSKRTVVAGATGSKVYPWTTKRLLKIGQKQVTHSFLVIPECPAPLLGRDLLTKLKAQIQFSTEGPQVTWEDRPAMCLVL
	CLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAILNPATLLPVESDDTPIHICSEILAEETGTRPDL
	NLEEEYRLHEKPVPPSIDPSWLQLFPMVWAEKAGMGLANQVPPVVVELKSDASPVAVRQYPMSKEAREGIRPHIQRFLDLGILVPCQSPWNTPLLPVKKPG
	RDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGKDI
	TNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRD
	LASFRALNPQVVMLQYVDDLLVAAPTYRDCKEGTRRLLQELSKLGYRVSAKKAQLCREEVTYLGYLLKGGKRWLTPARKATVMKIPTPTTPRQVREFLGKA
	GFCRLFIPGFASLAAPLYPLTRPKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFALYVDEKEGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPT
	KNKEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTETTKNAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1773	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKGGTLGDQGSRGSDPLPEPRVTLT
	VEGIPTEFLVNTGAEHSVLTKPMGKMGSKRTVVAGATGSKVYPWTTKRLLKIGQKQVTHSFLVIPECPAPLLGRDLLTKLKAQIQFSTEGPQVTWEDRPAM
	CLVLNLEEEYRLHEKPVPPSIDPSWLQLFPMVWAEKAGMGLANQVPPVVVELKSDASPVAVRQYPMSKEAREGIRPHIQRFLDLGILVPCQSPWNTPLLPV
	KKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEA
	LHRDLASFRALNPQVVMLQYVDDLLVAAPTYRDCKEGTRRLLQELSKLGYRVSAKKAQLCREEVTYLGYLLKGGKRWLTPARKATVMKIPTPTTPRQVREF
	LGKAGFCRLFIPGFASLAAPLYPLTRPKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFALYVDEKEGVARGVLTQTLGPWRRPVAYLSKKLDPVAS
	GWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAILNPATLLPVESDDTPIHICSEILAEETGT
	RPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSA
	GKDIKNKEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTETTKNAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1856	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL

	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGGEAAAKGGTLNLEDEYRLYETSAEPEVS
	PGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEAKLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR
	VEDIHPTVPNPYNLLSGLPPSHRWYTVLDLKDAFFCLRLHPTSQFLKFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVD
	VDDILLAATSELDCQQGTRALLLTLGNLGYRASAKKAQLCQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP
	LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLRKDAG
	KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQPIPDADHTWYTDG
	SSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALFL
	PKRLSIIHCLGHQKGDSAEARGNRLADQAARE AAIKTPPDTSTLLAGKRTADGSEFESPKKKAKVE
1857	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGSSGGTLNLEDEYRLYETSAEPEVSPG STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEAKLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE DIHPTVPNPYNLLSGLPPSHRWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVD DILLAATSELDCQQGTRALLLTLGNLGYRASAKKAQLCQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLY PLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLRKDAGKL TMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQPIPDADHTWYTDGSS FLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALFLPK RLSIIHCLGHQKGDSAEARGNRLADQAARE AAIKTPPDTSTLLAGKRTADGSEFESPKKKAKVE
1860	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA

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	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAKGGGGSEAAAKGGGGSEEAAAKGGGGSEPEVS
	PEVSPGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEAKLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR
	KDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQPIPDADHTW
	YTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLK
	ALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
186 1	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSEAAAKGGGGTLNLEDEYRLYETSAEPEVS
	PGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEAKLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR
	VEDIHPTVPNPYNLLSGLPPSHRWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY
	VDDILLAATSELDCQQGTRALLLTLGNLGYRASAKKAQLCQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP
	LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLRKDAG
	KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQPIPDADHTWYTDG
	SSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALFL
	PKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE

1863	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPAPGGTLNLEDEYRLYETSAEPE VSPGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEAKLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVN KRVEDIHPTVPNPYNLLSGLPPSHRWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILL QYVDDILLAATSELDCQQGTRALLLTLGNLGYRASAKKAQLCQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMA APLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLRKD AGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQPIPDADHTWYTT DGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKAL FLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLAGKRTADGSEFESPKKKAKVE
1864	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPEAAAKGGGGGTLNLEDEYRLYETSAEPEVS PGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEAKLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHRWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY VDDILLAATSELDCQQGTRALLLTLGNLGYRASAKKAQLCQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLRKDAG KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQPIPDADHTWYTDG

	SSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALFL PKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1865	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAAKGGTLNLEDEYRLY PGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEAKLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHRWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY VDDILLAATSELDCQQGTRALLLTLGNLGYRASAKKAQLCQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLRKDAG

	KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQPIPDADHTWYTDG
	SSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALFL
	PKRLSIIHCLGHQKGDSAEARGNRLADQAARE AAIKTPPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1868	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGTLNLEDEYRLYETSAEPEVSPGSTWL
	SDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEAKLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHP
	TVPNPYNLLSGLPPSHRWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILL
	AATSELDCQQGTRALLLTLGNLGYRASAKKAQLCQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTK
	PGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLRKDAGKLTMGQ
	PLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQPIPDADHTWYTDGSSFLQE
	GQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALFLPKRLSI
	IHCLGHQKGDSAEARGNRLADQAARE AAIKTPPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1870	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGSAGSGEFGGTLNLEDEYRLYETSAEPEV
	SPGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEAKLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNK
	RVEDIHPTVPNPYNLLSGLPPSHRWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQ
	YVDDILLAATSELDCQQGTRALLLTLGNLGYRASAKKAQLCQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAA

	PLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLRKDA
	GKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQPIPDADHTWYTD
	GSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALF
	LPKRLSIIHCLGHQKGDSAEARGNRLADQAARE
187 1	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKPAPGGSGGTLNLEDEYRLYETSAEPEVS
	PGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEAKLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR
	VEDIHPTVPNPYNLLSGLPPSHRWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY
	VDDILLAATSELDCQQGTRALLLTLGNLGYRASAKKAQLCQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP
	LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLRKDAG
	KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQPIPDADHTWYTDG
	SSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALFL
	PKRLSIIHCLGHQKGDSAEARGNRLADQAARE
187 4	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
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	STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEAKLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE
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	RLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLAGKRTADGSEFESPKKKAKVE
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	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
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	ADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEI
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	SPGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEAKLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNK
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1899	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSPAPGGGGGTLNLEDEYRLYETSAEPEVSPG STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEAKLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE DIHPTVPNPYNLLSGLPPSHRWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVD DILLAATSELDCQQGTRALLLTLGNLGYRASAKKAQLCQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLY PLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLRKDAGKL TMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQPIPDADHTWYTDGSS FLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALFLPK RLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1937	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY

	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGGSEAAAKGGTVSLQDEHRLFDIPVTTSLP
	DVWLQDFPQAWAETGGLGRAKCQAPIIIDLKPTAVPVSIKQYPMSLEAHMGIRQHIIKFLELGVLRPCRSPWNTPLLPVKKPGTQDYRPVQDLREINKRTV
	DIHPTVPNPYNLLSTLKPDYSWYTVLDLKDAFFCLPLAPQSQELFAFEWKDPERGISGQLTWTRLPQGFKNSPTLFNEALHRDLTDFRTQHPEVTLLQYVD
	DLLLAAPTKKACTQGTRHLLQELGEKGYRASAKKAQICQTKVTYLGYILSEGKRWLTPGRIETVARIPPPRNPREVREFLGKAGFCRLFIPGFAELAAPLY
	ALTKPSTPFTWQTEHQLAFEALKKALLSAPALGLPDTSKPFTLFLDERQGIAKGVLTQKLGPWKRPVAYLSKKLDPVAAGWPPCLRIMAATAMLVKDSAKL
	TLGQPLTVITPHTLEAIVRQPPDRWITNARLTHYQALLLDTDRVQFGPPVTLNPATLLPVPENQPSPHDCRQVLAETHGTREDLKDQELPDADHTWYTDGS
	SYLDSGTRRAGAAVVDGHNTIWAQSLPPGTSAQKAELIALTKALELSKGKKANIYTDSRYAFATAHTHGSIYERRGWLTSEGKEIKNKAEIIALLKALFLP
	QEVAIIHCPGHQKGQDPVAVGNRQADRVARQAAMAEVLTLATEPDNTSHITAGKRTADGSEFEKRTADGSEFESPKKKAKVE
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	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGPAPEAAAKGGTVSLQDEHRLFDIPVTTSLP
	DVWLQDFPQAWAETGGLGRAKCQAPIIIDLKPTAVPVSIKQYPMSLEAHMGIRQHIIKFLELGVLRPCRSPWNTPLLPVKKPGTQDYRPVQDLREINKRTV
	DIHPTVPNPYNLLSTLKPDYSWYTVLDLKDAFFCLPLAPQSQELFAFEWKDPERGISGQLTWTRLPQGFKNSPTLFNEALHRDLTDFRTQHPEVTLLQYVD
	DLLLAAPTKKACTQGTRHLLQELGEKGYRASAKKAQICQTKVTYLGYILSEGKRWLTPGRIETVARIPPPRNPREVREFLGKAGFCRLFIPGFAELAAPLY
	ALTKPSTPFTWQTEHQLAFEALKKALLSAPALGLPDTSKPFTLFLDERQGIAKGVLTQKLGPWKRPVAYLSKKLDPVAAGWPPCLRIMAATAMLVKDSAKL
	TLGQPLTVITPHTLEAIVRQPPDRWITNARLTHYQALLLDTDRVQFGPPVTLNPATLLPVPENQPSPHDCRQVLAETHGTREDLKDQELPDADHTWYTDGS
	SYLDSGTRRAGAAVVDGHNTIWAQSLPPGTSAQKAELIALTKALELSKGKKANIYTDSRYAFATAHTHGSIYERRGWLTSEGKEIKNKAEIIALLKALFLP
	QEVAIIHCPGHQKGQDPVAVGNRQADRVARQAAMAEVLTLATEPDNTSHITAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1939	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV

	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGSEAAAKGGTVSLQDEHRLFDIPVTTSLP DVWLQDFPQAWAETGGLGRAKCQAPIIIDLKPTAVPVSIKQYPMSLEAHMGIRQHIIKFLELGVLRPCRSPWNTPLLPVKKPGTQDYRPVQDLREINKRTV DIHPTVPNPYNLLSTLKPDYSWYTVLDLKDAFFCLPLAPQSQELFAFEWKDPERGISGQLTWTRLPQGFKNSPTLFNEALHRDLTDFRTQHPEVTLLQYVD DLLLAAPTKKACTQGTRHLLQELGEKGYRASAKKAQICQTKVTYLGYILSEGKRWLTPGRIETVARIPPPRNPREVREFLGKAGFCRLFIPGFAELAAPLY ALTKPSTPFTWQTEHQLAFEALKKALLSAPALGLPDTSKPFTLFLDERQGIAKGVLTQKLGPWKRPVAYLSKKLDPVAAGWPPCLRIMAATAMLVKDSAKL TLGQPLTVITPHTLEAIVRQPPDRWITNARLTHYQALLLDTDRVQFGPPVTLNPATLLPVPENQPSPHDCRQVLAETHGTREDLKDQELPDADHTWYTDGS SYLDSGTRRAGAAVVDGHNTIWAQSLPPGTSAQKAELIALTKALELSKGKKANIYTDSRYAFATAHTHGSIYERRGWLTSEGKEIKNKAEIIALLKALFLP QEVAIIHCPGHQKGQDPVAVGNRQADRVARQAAMAEVLTLATEPDNTSHITAGKRTADGSEFESPKKKAKVE
1940	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGGGTVSLQDEHRLFDIPVTTSLPDVWLQ DFPQAWAETGGLGRAKCQAPIIIDLKPTAVPVSIKQYPMSLEAHMGIRQHIIKFLELGVLRPCRSPWNTPLLPVKKPGTQDYRPVQDLREINKRTVDIHPT VPNPYNLLSTLKPDYSWYTVLDLKDAFFCLPLAPQSQELFAFEWKDPERGISGQLTWTRLPQGFKNSPTLFNEALHRDLTDFRTQHPEVTLLQYVDDLLLA APTKKACTQGTRHLLQELGEKGYRASAKKAQICQTKVTYLGYILSEGKRWLTPGRIETVARIPPPRNPREVREFLGKAGFCRLFIPGFAELAAPLYALTKP STPFTWQTEHQLAFEALKKALLSAPALGLPDTSKPFTLFLDERQGIAKGVLTQKLGPWKRPVAYLSKKLDPVAAGWPPCLRIMAATAMLVKDSAKLTLGQP LTVITPHTLEAIVRQPPDRWITNARLTHYQALLLDTDRVQFGPPVTLNPATLLPVPENQPSPHDCRQVLAETHGTREDLKDQELPDADHTWYTDGSSYLDS GTRRAGAAVVDGHNTIWAQSLPPGTSAQKAELIALTKALELSKGKKANIYTDSRYAFATAHTHGSIYERRGWLTSEGKEIKNKAEIIALLKALFLPQEVAI IHCPGHQKGQDPVAVGNRQADRVARQAAMAEVLTLATEPDNTSHITAGKRTADGSEFESPKKKAKVE
1942	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK

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	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
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	HPTVPNPYNLLSTLKPDYSWYTVLDLKDAFFCLPLAPQSQELFAFEWKDPERGISGQLTWTRLPQGFKNSPTLFNEALHRDLTDFRTQHPEVTLLQYVDDL
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	TKPSTPFTWQTEHQLAFEALKKALLSAPALGLPDTSKPFTLFLDERQGIAKGVLTQKLGPWKRPVAYLSKKLDPVAAGWPPCLRIMAATAMLVKDSAKLTL
	GQPLTVITPHTLEAIVRQPPDRWITNARLTHYQALLLDTDRVQFGPPVTLNPATLLPVPENQPSPHDCRQVLAETHGTREDLKDQELPDADHTWYTDGSSY
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1943	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
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	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
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	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGGPAPGGTVSLQDEHRLFDIPVTTSLP
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1949	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSEAAAKGGGGSGGTVSLQDEHRLFDIPVT TSLPDVWLQDFPQAWAETGGLGRAKCQAPIIIDLKPTAVPVSIKQYPMSLEAHMGIRQHIIKFLELGVLRPCRSPWNTPLLPVKKPGTQDYRPVQDLREIN KRTVDIHPTVPNPYNLLSTLKPDYSWYTVLDLKDAFFCLPLAPQSQELFAFEWKDPERGISGQLTWTRLPQGFKNSPTLFNEALHRDLTDFRTQHPEVTLL QYVDDLLLAAPTKKACTQGTRHLLQELGEKGYRASAKKAQICQTKVTYLGYILSEGKRWLTPGRIETVARIPPPRNPREVREFLGKAGFCRLFIPGFAELA APLYALTKPSTPFTWQTEHQLAFEALKKALLSAPALGLPDTSKPFTLFLDERQGIAKGVLTQKLGPWKRPVAYLSKKLDPVAAGWPPCLRIMAATAMLVKD SAKLTLGQPLTVITPHTLEAIVRQPPDRWITNARLTHYQALLLDTDRVQFGPPVTLNPATLLPVPENQPSPHDCRQVLAETHGTREDLKDQELPDADHTWY TDGSSYLDSGTRRAGAAVVDGHNTIWAQSLPPGTSAQKAELIALTKALELSKGKKANIYTDSRYAFATAHTHGSIYERRGWLTSEGKEIKNKAEIIALLKA LFLPQEVAIIHCPGHQKGQDPVAVGNRQADRVARQAAMAEVLTLATEPDNTSHITAGKRTADGSEFEKRTADGSEFESPKKKAKVE
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	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
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	QGFKNSPTLFNEALHRDLTDFRTQHPEVTLLQYVDDLLLAAPTKKACTQGTRHLLQELGEKGYRASAKKAQICQTKVTYLGYILSEGKRWLTPGRIETVAR
	IPPPRNPREVREFLGKAGFCRLFIPGFAELAAPLYALTKPSTPFTWQTEHQLAFEALKKALLSAPALGLPDTSKPFTLFLDERQGIAKGVLTQKLGPWKRP
	VAYLSKKLDPVAAGWPPCLRIMAATAMLVKDSAKLTLGQPLTVITPHTLEAIVRQPPDRWITNARLTHYQALLLDTDRVQFGPPVTLNPATLLPVPENQPS
	PHDCRQVLAETHGTREDLKDQELPDADHTWYTDGSSYLDSGTRRAGAAVVDGHNTIWAQSLPPGTSAQKAELIALTKALELSKGKKANIYTDSRYAFATAH
	THGSIYERRGWLTSEGKEIKNKAEIIALLKALFLPQEVAIIHCPGHQKGQDPVAVGNRQADRVARQAAMAEVLTLATEPDNTSHITAGKRTADGSEFEKRT
	ADGSEFESPKKKAKVE
1968	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
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	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER

	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGSSEAAAKGGTVSLQDEHRLFDIPVTTSLP DVWLQDFPQAWAETGGLGRAKCQAPIIIDLKPTAVPVSIKQYPMSLEAHMGIRQHIIKFLELGVLRPCRSPWNTPLLPVKKPGTQDYRPVQDLREINKRTV DIHPTVPNPYNLLSTLKPDYSWYTVLDLKDAFFCLPLAPQSQELFAFEWKDPERGISGQLTWTRLPQGFKNSPTLFNEALHRDLTDFRTQHPEVTLLQYVD DLLLAAPTKKACTQGTRHLLQELGEKGYRASAKKAQICQTKVTYLGYILSEGKRWLTPGRIETVARIPPPRNPREVREFLGKAGFCRLFIPGFAELAAPLY ALTKPSTPFTWQTEHQLAFEALKKALLSAPALGLPDTSKPFTLFLDERQGIAKGVLTQKLGPWKRPVAYLSKKLDPVAAGWPPCLRIMAATAMLVKDSAKL TLGQPLTVITPHTLEAIVRQPPDRWITNARLTHYQALLLDTDRVQFGPPVTLNPATLLPVPENQPSPHDCRQVLAETHGTREDLKDQELPDADHTWYTDGS SYLDSGTRRAGAAVVDGHNTIWAQSLPPGTSAQKAELIALTKALELSKGKKANIYTDSRYAFATAHTHGSIYERRGWLTSEGKEIKNKAEIIALLKALFLP QEVAIIHCPGHQKGQDPVAVGNRQADRVARQAAMAEVLTLATEPDNTSHITAGKRTADGSEFEKRTADGSEFESPKKKAKVE
197 0	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGSSGSSGGTVSLQDEHRLFDIPVTTSLPDVWLQ DFPQAWAETGGLGRAKCQAPIIIDLKPTAVPVSIKQYPMSLEAHMGIRQHIIKFLELGVLRPCRSPWNTPLLPVKKPGTQDYRPVQDLREINKRTVDIHPT VPNPYNLLSTLKPDYSWYTVLDLKDAFFCLPLAPQSQELFAFEWKDPERGISGQLTWTRLPQGFKNSPTLFNEALHRDLTDFRTQHPEVTLLQYVDDLLLA APTKKACTQGTRHLLQELGEKGYRASAKKAQICQTKVTYLGYILSEGKRWLTPGRIETVARIPPPRNPREVREFLGKAGFCRLFIPGFAELAAPLYALTKP STPFTWQTEHQLAFEALKKALLSAPALGLPDTSKPFTLFLDERQGIAKGVLTQKLGPWKRPVAYLSKKLDPVAAGWPPCLRIMAATAMLVKDSAKLTLGQP LTVITPHTLEAIVRQPPDRWITNARLTHYQALLLDTDRVQFGPPVTLNPATLLPVPENQPSPHDCRQVLAETHGTREDLKDQELPDADHTWYTDGSSYLDS GTRRAGAAVVDGHNTIWAQSLPPGTSAQKAELIALTKALELSKGKKANIYTDSRYAFATAHTHGSIYERRGWLTSEGKEIKNKAEIIALLKALFLPQEVAI IHCPGHQKGQDPVAVGNRQADRVARQAAMAEVLTLATEPDNTSHITAGKRTADGSEFEKRTADGSEFESPKKKAKVE
197 6	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL

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	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
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	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
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	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
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	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
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	TDGSSYLDSGTRRAGAAVVDGHNTIWAQSLPPGTSAQKAELIALTKALELSKGKKANIYTDSRYAFATAHTHGSIYERRGWLTSEGKEIKNKAEIIALLKA
	LFLPQEVAIIHCPGHQKGQDPVAVGNRQADRVARQAAMAEVLTLATEPDNTSHITAGKRTADGSEFEKRTADGSEFESPKKKAKVE

2048	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGSEAAAKGGLGIEDEYRLHETSTEPDVSL GSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRV EDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYV DDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPL YPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGK LTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQPIPDADHTWYTDGS SFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALFLP KRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFESPKKKAKVE
2048	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGSEAAAKGGLGIEDEYRLHETSTEPDVSL GSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRV EDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYV DDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPL YPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGK LTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQPIPDADHTWYTDGS

	SFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALFLP KRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2049	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGSEAAAKGGLGIEDEYRLHETSTEP DVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREV NKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYV LQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPL AAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGK DAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQPIPDADHTWY TDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKA LFLPKRLSIIHCLGHQKGDSAEARGNRLADQAARFAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2050	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGSSEAAAKGGLGIEDEYRLHETSTEPDVSL GSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRV EDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYV DDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPL YPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGK

	LTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQPIPDADHTWYTDGS
	SFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALFLP
	KRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFESPKKKAKVE
2054	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGPAPGGLGIEDEYRLHETSTEPDVSL
	GSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRV
	EDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYV
	DDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLGSQVLPLSEDAKKDLLSIKETLLRKGTLSLGKPGHKLGELGAPAEFLCKGD
2055	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGSGSSGGLGIEDEYRLHETSTEPDVSL
	GSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRV
	EDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYV
	DDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPL

	YPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGK LTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQPIPDADHTWYTDGS SFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALFLP KRLSIIHCLGHQKGDSAEARGNRLADQAARE AAIKTPPDTSTLLIAGKRTADGSEFESPKKKAKVE
2058	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSPAPGGGGGLGIEDEYRLHETSTEPDVSLGS TWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVED IHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDD ILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYP LTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLT MGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQPIPDADHTWYTDGSSF LQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALFLPKR LSIIHCLGHQKGDSAEARGNRLADQAARE AAIKTPPDTSTLLIAGKRTADGSEFESPKKKAKVE
2060	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSPAPGGGGGLGIEDEYRLHETSTEPDVSLGS TWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVED IHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDD

	ILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYP
	LTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLT
	MGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQPIPDADHTWYTDGSSF
	LQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALFLPKR
	LSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFESPKKKAKVE
2085	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAAKGGLGIEDE
	DHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEIL
	ALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFESPKKKAKVE
2086	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAAKGGLGIEDE
	YRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND

	YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAD FRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKAGFC RLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLR MVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQ PIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKN KSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAARE
2087	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPAPGGLGIEDEYRLHETSTEPDV SLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNK RVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQ YVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAA PLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDA GKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQPIPDADHTWYTD GSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALF LPKRLSIIHCLGHQKGDSAEARGNRLADQAARE
2089	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGSSEAAAKGGLGIEDEYRLHETSTEPDVSL

	GSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRV EDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYV DDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPL YPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGK LTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQPIPDADHTWYTDGS SFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALFLP KRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFESPKKKAKVE
209 0	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
209 1	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI

	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGSSGGGGGLGIEDEYRLHETSTEPDVSLGS
	TWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVED
	IHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDD
	ILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYP
	LTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLT
	MGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQPIPDADHTWYTDGSSF
	LQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALFLPKR
	LSIIHCLGHQKGDSAEARGNRLADQAARE AAIKTPPDTSTLLIAGKRTADGSEFESPKKKAKVE
2092	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAAKGGLGIEDEYRLHE
	TSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQ
	DLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQH
	PDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKAGFCRLFIP
	GFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAI
	AVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQPIPDA
	DHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEIL
	ALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAARE AAIKTPPDTSTLLIAGKRTADGSEFESPKKKAKVE
2093	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY

	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGSEAAAKGGLGIEDEYRLHETSTEPDVSL
	GSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRV
	EDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYV
	DDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPL
	YPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGK
	LTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQPIPDADHTWYTDGS
	SFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALFLP
	KRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFESPKKKAKVE
2093	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGSEAAAKGGLGIEDEYRLHETSTEPDVSL
	GSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRV
	EDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYV
	DDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPL
	YPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGK
	LTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQPIPDADHTWYTDGS
	SFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALFLP
	KRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFESPKKKAKVE
2094	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV

	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSGGGGSGGGGSGGGGSGGGGSGGGL
	GIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKK
	PGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALH
	RDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLG
	KAGFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGK
	PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRP
	DLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG
	REIKNKSEIIALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAARE AAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2095	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
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	GSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRV
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	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
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	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
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	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
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	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSGGLGIEDEYRLHETSTEPDVSLGST
	WLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDI
	HPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDI
	LLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPL
	TKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTM
	GQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQPIPDADHTWYTDGSSFL
	QEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEIILALLKALFLPKRL
	SIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
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	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
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	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSEAAAKGGLGIEDEYRLHETSTEPDVSLGST
	WLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDI
	HPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDI
	LLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPL
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	GQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQPIPDADHTWYTDGSSFL
	QEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEIILALLKALFLPKRL
	SIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
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	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
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	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSEAAAKGGGGSGGLGIEDEYRLHETSTEP
	DVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREV
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	LQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLEGQRWLTEARKETVMGQPVPKTPRQLREFLGKAGFCRLFIPGFAEM
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	TDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKA
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	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
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	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
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	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSEAAAKPAPGGLGIEDEYRLHETSTEPDVSL
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	LTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQPIPDADHTWYTDGS
	SFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALFLP
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211 2	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSPAPGGLGIEDEYRLHETSTEPDVSL GSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRV EDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYV DDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPL YPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGK LTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQPIPDADHTWYTDGS SFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALFLP KRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
211 4	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL

	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
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	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
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	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSPAPGGGGGLGIEDEYRLHETSTEPDVSLGS
	TWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVED
	IHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDD
	ILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYP
	LTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLT
	MGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQPIPDADHTWYTDGSSF
	LQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALFLPKR
	LSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2115	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSEAAAKGGLGIEDEYRLHETSTEPDVSLGST
	WLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDI
	HPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDI
	LLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPL
	TKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTM
	GQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQPIPDADHTWYTDGSSFL
	QEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALFLPKRL
	SIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2116	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA

	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGGSGEAAAKGGLGIEDEYRLHETSTEPDVSL
	DVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRV
	DAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQPIPDADHTWY
	TDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKA
	LFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2117	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGGSGEAAAKGGLGIEDEYRLHETSTEPDVSL
	GSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRV
	EDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYV
	DDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPL
	YPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGK
	LTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQPIPDADHTWYTDGS
	SFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALFLP
	KRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE

2120	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV EDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYV DDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPL YPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGK LTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQPIPDADHTWYTDGS SFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALFLP KRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFESPKKKAKVE
2122	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPEAAAKGGGGGLGIEDEYRLHETSTEPDVSL ILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYP LTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLT MGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQPIPDADHTWYTDGSSF

	LQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALFLPKR
	LSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2123	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGPAPGGLGIEDEYRLHETSTEPDVSL
	GSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRV
	EDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYV
	DDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPL
	YPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGK
	LTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQPIPDADHTWYTDGS
	SFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALFLP
	KRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2131	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGGLGIEDEYRLHETSTEPDVSLGSTWLSDF
	PQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVP
	NPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAAT
	SELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGT
	LFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLV

	ILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQPIPDADHTWYTDGSSFLQEGQR KAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALFLPKRLSIIHC LGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFESPKKKAKVE
2132	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGEAAAKGGSGGLGIEDEYRLHETSTEPDVSL GSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRV EDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYV DDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPL YPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGK LTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQPIPDADHTWYTDGS SFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALFLP KRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFESPKKKAKVE
2133	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSPAPGGLGIEDEYRLHETSTEPDVSLGS TWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVED IHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDD ILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYP

	LTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLT
	MGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQPIPDADHTWYTDGSSF
	LQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALFLPKR
	LSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2137	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGSGS

	LILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKAGFCRLFIPGF
	AEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAV
	LTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQPIPDADH
	TWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILAL
	LKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFESPKKKAKVE
2142	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPGGLGIEDEYRLHETSTEPDVSLGSTWLS
	DFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPT
	LILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKAGFCRLFIPGF
	AEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAV
	LTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQPIPDADH
	TWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILAL
	LKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFESPKKKAKVE
2143	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPGGLGIEDEYRLHETSTEPDVSLGSTWLS
	DFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPT

	VPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLA ATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKP GTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQP LVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQPIPDADHTWYTDGSSFLQEG QRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALFLPKRLSII HCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFESPKKKAKVE
2145	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSSEAAAKPAPGGLGIEDEYRLHETSTEPDVSL
2146	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSSEAAAKPAPGGLGIEDEYRLHETSTEPDVSL

	GSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRV EDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYV DDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPL YPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGK LTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQPIPDADHTWYTDGS SFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALFLP KRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFESPKKKAKVE
2148	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
2149	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI

	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSPAPEAAAKGGLGIEDEYRLHETSTEPDVSL
	GSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRV
	EDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYV
	DDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPL
	YPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGK
	LTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQPIPDADHTWYTDGS
	SFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALFLP
	KRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2151	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGGLGIEDEYRLHETSTEPDVSLGS
	TWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVED
	IHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDD
	ILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYP
	LTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLT
	MGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQPIPDADHTWYTDGSSF
	LQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALFLPKR
	LSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2154	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY

	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGPAPGGSGGLGIEDEYRLHETSTEPDVSLGS TWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVED IHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDD ILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYP LTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLT MGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQPIPDADHTWYTDGSSF LQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALFLPKR LSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2158	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGSSGGLGIEDEYRLHETSTEPDVSLGSTWL SDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHP TVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILL AATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTK PGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQ PLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQPIPDADHTWYTDGSSFLQE GQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALFLPKRLSI IHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2159	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV

	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSGSSGGLGIEDEYRLHETSTEPDVSL
	GSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRV
	EDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYV
	DDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPL
	YPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQEGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGK
	LTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQPIPDADHTWYTDGS
	SFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALFLP
	KRLSIIHCLGHQKGDSAEARGNRLADQAARE AAIKTPPDTSTLLIAGKRTADGSEFESPKKKAKVE
2161	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSGSSGGLGIEDEYRLHETSTEPDVSL
	GSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRV
	EDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYV
	DDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPL
	YPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGK
	LTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQPIPDADHTWYTDGS
	SFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALFLP
	KRLSIIHCLGHQKGDSAEARGNRLADQAARE AAIKTPPDTSTLLIAGKRTADGSEFESPKKKAKVE
2165	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK

	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGSGGGGLGIEDEYRLHETSTEPDVSLGS
	TWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVED
	IHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDD
	ILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYP
	LTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLT
	MGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQPIPDADHTWYTDGSSF
	LQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALFLPKR
	LSIIHCLGHQKGDSAEARGNRLADQAARE AAIKTPPDTSTLLIAGKRTADGSEFESPKKKAKVE
2172	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGSGGGGLGIEDEYRLHETSTEPDVSLGS
	TWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVED
	IHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDD
	ILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYP
	LTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLT
	MGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQPIPDADHTWYTDGSSF
	LQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALFLPKR
	LSIIHCLGHQKGDSAEARGNRLADQAARE AAIKTPPDTSTLLIAGKRTADGSEFESPKKKAKVE
2174	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD

	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGEAAAKGSSGGLGIEDEYRLHETSTEPDVSL
	GSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRV
	EDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYV
	DDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPL
	YPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGK
	LTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLITDQPIPDADHTWYTDG
	SFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALFL
	KRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2187	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
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	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPGGTLGIEDEYRLHETSTEPDVS
	LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR
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	SSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALFL
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	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
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	DFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGTAGF
	CRLWIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCL
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	QPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIK
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	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
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	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
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	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
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	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGSSGGSGGTLGIEDEYRLHETSTEPDVS
	LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR
	VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY
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	SSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALFL
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	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
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	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSPAPEAAAKGGTLGIEDEYRLHETSTEPDVS
	VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY
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	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH

	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLI VDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGTAGFCRLWIPGFAE LYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLT LKQVKDLLAAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGTAGFCRLWIPGFAE KTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMDQPLPDADHTWYTDG LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGTAGFCRLWIPGFAEMAAP REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGSSEAAAKGGTLNIEDEYRLHETSKEPDVS SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI RLQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGSSEAAAKGGTLNIEDEYRLHETSKEPDVS KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQY VDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGTAGFCRLWIPGFAEMAAP LYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMDQPLPDADHTWYTDG SSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL PKRLSIIHCPGHQKGNSAEARGNRMADQAARFVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2226	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGTLNIEDEYRLHETSKE PDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLRE VNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLI LLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGTAGFCRLWIPGFAE MAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLT KDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMDQPLPDADHTW YTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAARFVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2227	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER

	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGSGSGGTLNIEDEYRLHETSKEPDVSLGSTW LSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVED IH PTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVDDLL LAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLT KPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMG QPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMDQPLPDADHTWYTDGSSFLQ EGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLS IIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
223 1	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGSGSGGTLNIEDEYRLHETSKEPDVSLG STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE DIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVD DLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLY PLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKL TMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMDQPLPDADHTWYTDGSS FLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPK RLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
223 5	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL

	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGSSPAPGGTLNIEDEYRLHETSKEPDVS
	LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR
	VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	VDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGTAGFCRLWIPGFAEMAAP
	LYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG
	KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMDQPLPDADHTWYTDG
	SSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL
	PKRLSIIHCPGHQKGNSAEARGNRMADQAARE VATRETPETSTLLAGKRTADGSEFESPKKKAKVE
2236	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKGGTLNIEDEYRLHETSKEPDVSL
	GSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRV
	EDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYV
	DDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGTAGFCRLWIPGFAEMAAPL
	YPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGK
	LTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMDQPLPDADHTWYTDGS
	SFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLP
	KRLSIIHCPGHQKGNSAEARGNRMADQAARE VATRETPETSTLLAGKRTADGSEFESPKKKAKVE
2249	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA

	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAAKEAAAKGGT
	LNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVK
	KPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEAL
	HRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFL
	GTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAG
	WPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTR
	SDLMDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSE
	GKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAARE
2280	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGSGSGSGSGSGSGGTLNIEDEYRLHETSKE
	PDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLRE
	VNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLI
	LLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGTAGFCRLWIPGFAE
	MAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLT
	KDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMDQPLPDADHTW
	YTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK
	ALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE

2299	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGTLNIEDEYRLHETSKEPDVSLGSTWLSD FPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTV PNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVDDLLLAA TSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPG TLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPL VILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMDQPLPDADHTWYTDGSSFLQEGQ RKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIH CPGHQKGNSAEARGNRMADQAARGVATRETPETSTLLAGKRTADGSEFESPKKKAKVE
2300	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGTLNIEDEYRLHETSKEPDVSLGSTWLSD FPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTV PNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVDDLLLAA TSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPG TLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPL VILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMDQPLPDAD

	HTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILA LLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAARFVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
230 1	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPGGTLNIEDEYRLHETSKEPDVS LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQY VDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGKAGFCRLFIPGFAEMAAP LYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMDQPLPDADHTWYTDG SSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL PKRLSIIHCPGHQKGNSAEARGNRMADQAARFVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
230 2	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGPAPGGTLNIEDEYRLHETSKEPDVSLGSTW LSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIH PTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVDDLL LAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLT KPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMG

	QPLVIILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMDQPLPDADHTWYTDGSSFLQ EGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLS IIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2303	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGGGSGGGGSGGGGSGGT LNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVK KPGTNDYIRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEAL HRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFL GKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAG WPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTR SDLMDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSE GKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2304	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGGGGSGGGGSGGGGSGGTLNIEDEYRLHET SKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQD LREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHP DLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGKAGFCRLFIPG

	FAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIA VLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMDQPLPDAD HTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILA LLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAARE
2305	VATRETPETSTLLAGKRTADGSEFESPKKKAKVE MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGSEAAAKGGGGSEAAAKGGTLNIEDEYRLHETSKE PDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLRE VNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLI LLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGKAGFCRLFIPGFAE MAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLT KDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMDQPLPDADHTW YTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAARE
2308	VATRETPETSTLLAGKRTADGSEFESPKKKAKVE MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGGGSSGGTLNIEDEYRLHETSKEPDVSLG STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE DIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVD

	DLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLY
	PLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKL
	TMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMDQPLPDADHTWYTDGSS
	FLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPK
	RLSIIHCPGHQKGNSAEARGNRMADQAARFVATRETPETSTLLAGKRTADGSEFESPKKKAKVE
2309	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGGGSGGGGSGGTLNIEDEYRLH ETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPV
2311	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGGGSGGGGSGGTLNIEDEYRLH ETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPV

	QDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQ
	HPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGKAGFCRLFI
	PGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAA
	IAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMDQPLPD
	ADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEI
	LALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAARE VATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2312	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGSSGGTLNIEDEYRLHETSKEPDVSLG
	STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE
	DIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVD
	DLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLY
	PLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKL
	TMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMDQPLPDADHTWYTDGSS
	FLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPK
	RLSIIHCPGHQKGNSAEARGNRMADQAARE VATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2313	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSAGSAAGSGEFGGTLNIEDEYRLHETSKEPDV

	SLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNK RVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQ YVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGKAGFCRLFIPGFAEMAA PLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDA GKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMDQPLPDADHTWYTD GSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALF LPKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFESPKKKAKVE
2314	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
2315	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI

	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKPAPGGSGGTLNIEDEYRLHETSKEPDVS LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQY VDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGKAGFCRLFIPGFAEMAAP LYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDIIAEAHGTRSDLMDQPLPDADHTWYTDG SSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL PKRLSIIHCPGHQKGNSAEARGNRMADQAARGVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2316	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGEAAAKGSSGGTLNIEDEYRLHETSKEPDVS LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQY VDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGKAGFCRLFIPGFAEMAAP LYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDIIAEAHGTRSDLMDQPLPDADHTWYTDG SSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL PKRLSIIHCPGHQKGNSAEARGNRMADQAARGVATRETPETSTLLAGKRTADGSEFESPKKKAKVE
2317	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY

	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGGPAPGGTLNIEDEYRLHETSKEPDVSLG STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE DIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVD DLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLY PLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKL TMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMDQPLPDADHTWYTDGSS FLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPK RLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2319	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGGSGGGSGGTLNIEDEYRLHETSKEPDV SLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNK RVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQ YVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGKAGFCRLFIPGFAEMAA PLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDA GKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMDQPLPDADHTWYTD GSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALF LPKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFESPKKKAKVE
2320	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV

	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGPAPGGSGGTLNIEDEYRLHETSKEPDVSLG STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE DIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVD DLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLY PLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKL TMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMDQPLPDADHTWYTDGSS FLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPK RLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFESPKKKAKVE
2322	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAAKEAAAKGGT LNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVK KPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEAL HRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFL GKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAG WPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTR SDLMDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSE GKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFESPKKKAKVE
2323	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK

	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGTLNIEDEYRLHETSKEPDVSLGSTWLSD
	FPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTV
	PNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVDDLLLAA
	TSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPG
	TLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPL
	VILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMDQPLPDADHTWYTDGSSFLQEGQ
	RKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIH
	CPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFESPKKKAKVE
2324	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAAKGGTLNIED
	EYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTN
	DYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA
	GFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGKAGF
	CRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCL
	RMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMD
	QPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIK
	NKDEIILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFESPKKKAKVE
2325	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD

	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKGGTLNIEDEYRLH ETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPV QDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQ HPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGKAGFCRLFI PGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAA IAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMDQPLPDADHTWYTDG ADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL LALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAARKVATRETPETSTLLAGKRTADGSEFESPKKKAKVE
2326	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
2327	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK

	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSSEAAAKGGTLNIEDEYRLHETSKEPDVS LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQY VDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGKAGFCRLFIPGFAEMAAP LYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQ KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMDQPLPDADHTWYTDGSSFLQE SSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSI PKRLSIIHCPGHQKGNSAEARGNRMADQAARKVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2328	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGTLNIEDEYRLHETSKEPDVSLGSTWL SDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHP TVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVDDLLL AATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTK PGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQ PLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMDQPLPDADHTWYTDGSSFLQE GQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSI IHCPGHQKGNSAEARGNRMADQAARKVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2329	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL

	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSPAPGGGGTLNIEDEYRLHETSKEPDVSLG
	STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE
	DIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVD
	DLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLY
	PLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKL
	TMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMDQPLPDADHTWYTDGSS
	FLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPK
	RLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2331	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGSGGGGGTLNIEDEYRLHETSKEPDVSLG
	STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE
	DIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVD
	DLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLY
	PLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKL
	TMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMDQPLPDADHTWYTDGSS
	FLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPK
	RLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2332	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH

	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGSEAAAKGGTLNIEDEYRLHETSKEPDVS
	LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR
	VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQY
	VDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGKAGFCRLFIPGFAEMAAP
	LYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG
	KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMDQPLPDADHTWYTDG
	SSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL
	PKRLSIIHCPGHQKGNSAEARGNRMADQAARE VATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2333	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGSEAAAKGGTLNIEDEYRLHETSKE
	PDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLRE
	VNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLI
	LLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGKAGFCRLFIPGFAE
	MAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLT
	KDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMDQPLPDADHTW
	YTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK
	ALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAARE VATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2335	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER

	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGGGGGTLNIEDEYRLHETSKEPDVSLGSTW LSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIH PTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVDDLL LAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLT KPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMG QPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMDQPLPDADHTWYTDGSSFLQ EGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLS IIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2338	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGGGGGTLNIEDEYRLHETSKEPDVS LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQY VDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGKAGFCRLFIPGFAEMAAP LYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMDQPLPDADHTWYTDG SSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL PKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2342	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL

	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGEAAAKGGTLNIEDEYRLHETSKEPDVSLGS
	TWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVED
	IHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVDD
	LLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYP
	LTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLT
	MGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMDQPLPDADHTWYTDGSSF
	LQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKR
	LSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKPKKKAKVE
2343	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKEAAAKEAAAKEAAA
	AKEAAAKEAAAKAGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGI
	LVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTR
	LPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV
	MGQPIPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWR
	RPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEG
	LQHDCLDILAEAHGTRSDLMDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATA
	HIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEF
	ESPKKKAKVE

2345	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQY VDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGKAGFCRLFIPGFAEMAAP LYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDIIAEAHGTRSDLMDQPLPDADHTWYTDG SSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL PKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFESPKKKAKVE
2346	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSPAPEAAAKGGTLNIEDEYRLHETSKEPDVS LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQY VDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLY PLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKL TMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDIILAEAHGTRSDLMDQPLPDADHTWYTDGSS

	FLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPK RLSIIHCPGHQKGNSAEARGNRMADQAARFVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2347	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPEAAAKGSSGGTLNIEDEYRLHETSKEPDVS LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQY VDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGKAGFCRLFIPGFAEMAAP LYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMDQPLPDADHTWYTDG SSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL PKRLSIIHCPGHQKGNSAEARGNRMADQAARFVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2353	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGSSGGTLNIEDEYRLHETSKEPDVSLGSTW LSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIH PTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVDDLL LAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLT KPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMG

	QPLVIILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMDQPLPDADHTWYTDGSSFLQ EGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLS IIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2359	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSEAAAKPAPGGTLNIEDEYRLHETSKEPDVS LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQY VDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGKAGFCRLFIPGFAEMAAP LYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMDQPLPDADHTWYTDG SSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL PKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2360	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGGSGGSTLNIEDEYRLHETSKEPDVSLG STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE DIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVD DLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLY

	PLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKL TMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMDQPLPDADHTWYTDGSS FLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPK RLSIIHCPGHQKGNSAEARGNRMADQAARE VATRETPETSTLLAGKRTADGSEFESPKKKAKVE
2363	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSEAAAKGGTLNIEDEYRLHETSKEPDVSLGS TWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVED IHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVDD LLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYP LTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLT MGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMDQPLPDADHTWYTDGSSF LQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKR LSIIHCPGHQKGNSAEARGNRMADQAARE VATRETPETSTLLAGKRTADGSEFESPKKKAKVE
2364	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGPAPAPGGTLNIEDEYRLHETSKEPDVSLGSTWL SDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHP TVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVDDLLL

	AATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTK PGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQ PLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMDQPLPDADHTWYTDGSSFLQE GQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSI IHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2365	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSGSSGGTLNIEDEYRLHETSKEPDVS LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR
2370	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSGSSGGTLNIEDEYRLHETSKEPDVS LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR

	VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQY
	VDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGKAGFCRLFIPGFAEMAAP
	LYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG
	KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMDQPLPDADHTWYTDG
	SSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL
	PKRLSIIHCPGHQKGNSAEARGNRMADQAARGVATRETPETSTLLAGKRTADGSEFESPKKKAKVE
237 1	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGGGGSGGTLNIEDEYRLHETSKEPDVSLGS
238 2	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSEAAAKGGTLNIEDEYRLHETSKEPDVSLGS

	TWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVED
	IHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVDD
	LLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYP
	LTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLT
	MGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMDQPLPDADHTWYTDGSSF
	LQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKR
	LSIIHCPGHQKGNSAEARGNRMADQAARE VATRETPETSTLLAGKRTADGSEFESPKKKAKVE
2395	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	PTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVDDLL
	LAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLT
	KPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMG
	QPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMDQPLPDADHTWYTDGSSFLQ
	EGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLS
	IIHCPGHQKGNSAEARGNRMADQAARE VATRETPETSTLLAGKRTADGSEFESPKKKAKVE
2400	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI

	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPEAAAKGGGGGTLNIEDEYRLHETSKEPDVS
	LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR
	VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQY
	VDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGKAGFCRLFIPGFAEMAAP
	LYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG
	KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDIIAEAHGTRSDLMDQPLPDADHTWYTDG
	SSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL
	PKRLSIIHCPGHQKGNSAEARGNRMADQAARGVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2403	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGSGGGGGTLNIEDEYRLHETSKEPDVSLG
	STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE
	DIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVD
	DLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLY
	PLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKL
	TMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDIILAEAHGTRSDLMDQPLPDADHTWYTDGSS
	FLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPK
	RLSIIHCPGHQKGNSAEARGNRMADQAARGVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2405	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY

	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGSGGSSGGSGGTLNIEDEYRLHETSKE PDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLRE VNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLI LLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGKAGFCRLFIPGFAE MAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLT KDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMDQPLPDADHTW YTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAARGVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2449	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPAPGGTLNIEDEYRLHETSKGPD VPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVN KRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILL QYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMA APLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKD AGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLTDQPLPDADHTWYT DGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKAL FLPKRLSIIHCPGHQKGNRAEARGNRMADQAARGVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2503	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV

	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSEAAAKGGTLNIEDEYRLHETSKGPDVPLGS TWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVED IHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDD LLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYP LTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLT MGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSF LQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKR LSIIHCPGHQKGNRAEARGNRMADQAARE
2504	VATRETPETSTLLAGKRTADGSEFEKPSPKKKAKVE MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGTLNIEDEYRLHETSKGPDVPLGSTWL SDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHP TVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLL AATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTK PGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQ PLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSFLQE GQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSI IHCPGHQKGNRAEARGNRMADQAARE
2505	VATRETPETSTLLAGKRTADGSEFEKPSPKKKAKVE MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK

	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPEAAAKGGTLNIEDEYRLHETSKGPDVPLGS
	TWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVED
	IHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDD
	LLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYP
	LTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLT
	MGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSF
	LQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKR
	LSIIHCPGHQKGNRAEARGNRMADQAARFVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2506	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKPAPGGGGTLNIEDEYRLHETSKGPDVP
	LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR
	VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY
	VDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP
	LYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG
	KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLTDQPLPDADHTWYTDG
	SSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL
	PKRLSIIHCPGHQKGNRAEARGNRMADQAARFVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2507	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD

	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKGGTLNIEDEYRLHETSKG PDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLRE VNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLI LLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAE MAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLT KDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLTDQPLPDADHTW YTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIH ALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAARFVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2508	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGTLNIEDEYRLHETSKGPDVPLGSTWLSD FPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTV PNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAA TSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPG TLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPL VILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSFLQEGQ RKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIH CPGHQKGNRAEARGNRMADQAARFVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2510	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK

	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPGGTLNIEDEYRLHETSKGPDVP
	LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR
	VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY
	VDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP
	LYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLVKDAG
	KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLTDQPLPDADHTWYTDG
	SSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL
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2511	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGGGSGGTLNIEDEYRLHETSKGPDVPL
	GSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRV
	EDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYV
	DDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPL
	YPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGK
	LTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLTDQPLPDADHTWYTDGS
	SFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLP
	KRLSIIHCPGHQKGNRAEARGNRMADQAARGVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2512	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL

	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKPAPGGSGGTLNIEDEYRLHETSKGPDVP LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY VDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPG LYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIA KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLTDQPLPDADHTWYTDG SSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL PKRLSIIHCPGHQKGNRAEARGNRMADQAARKVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2513	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGGSGGSGGSGGTLNIEDEYRLHET SKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQD LREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHP DLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPG FAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIA VLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLTDQPLPDAD HTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILA LLKALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAARKVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2514	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH

	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPEAAAKGSSGGTLNIEDEYRLHETSKGPDVP
	LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR
	VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY
	VDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP
	LYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG
	KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLTDQPLPDADHTWYTDG
	SSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL
	PKRLSIIHCPGHQKGNRAEARGNRMADQAARAVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2515	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGSSGGGEAAAKGGTLNIEDEYRLHETSKGPDVP
	LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR
	VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY
	VDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP
	LYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG
	KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLTDQPLPDADHTWYTDG
	SSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL
	PKRLSIIHCPGHQKGNRAEARGNRMADQAARAVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2518	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER

	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGSGSETPGTSESATPESGGTLNIEDEYRLHETSK GPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR EVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY ILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP EMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVL TKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLTDQPLPDADHT WYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALL KALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2519	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGSGSETPGTSESATPESGGTLNIEDEYRLHETSKGPDVP LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY VDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP LYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLTDQPLPDADHTWYTDG SSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL PKRLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2521	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL

	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGEAAAKGGSGGTLNIEDEYRLHETSKGPDVP
	LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR
	VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY
	VDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP
	LYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG
	KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLTDQPLPDADHTWYTDG
	SSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL
	PKRLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFESPKKKAKVE
2525	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGPAPAPAPAPGGTLNIEDEYRLHETSKGPDVPLG
	STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE
	DIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVD
	DLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLY
	PLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKL
	TMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSS
	FLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPK
	RLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFESPKKKAKVE
2526	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA

	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSPAPEAAAKGGTLNIEDEYRLHETSKGPDVP
	LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR
	VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY
	VDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP
	LYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG
	KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLTDQPLPDADHTWYTDG
	SSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL
	PKRLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFESPKKKAKVE
2527	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSPAPEAAAKGGTLNIEDEYRLHETSKGPDVP
	LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR
	VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY
	VDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP
	LYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG
	KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLTDQPLPDADHTWYTDG
	SSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL
	PKRLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFESPKKKAKVE

2528	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSEAAAKGGGGSGGTLNIEDEYRLHETSKG PDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLRE VNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLI LLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAE MAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLT KDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLTDQPLPDADHTW YTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFESPKKKAKVE
2529	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKALEAEAAAAKEAA AKEAAAKEAAAKAGGTLNIEDEYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGI LVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTR LPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWR RPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEG LQHDCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATA

	HIHGEIYRRRGWLTSEGKEIKNKDEIILALLKALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAARE VATRETPETSTLLAGKRTADGSEFEKRTADGSEF ESPKKKAKVE
2530	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSEAAAKPAPGGTLNIEDEYRLHETSKGPDVP STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRV DIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVD DLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLY PLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKL

	TMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSS FLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPK RLSIIHCPGHQKGNRAEARGNRMADQAARFVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2534	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPAPGGTLNIEDEYRLHETSKGPD VPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVN KRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILL QYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAA APLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKD AGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLTDQPLPDADHTWYT DGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKAL FLPKRLSIIHCPGHQKGNRAEARGNRMADQAARFVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2535	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSEAAAKPAPGGTLNIEDEYRLHETSKGPDVP LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY VDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP

	LYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLTDQPLPDADHTWYTDG SSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL PKRLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFESPKKKAKVE
2536	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKGGTLNIED EYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTN DYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGF CRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCL RMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLTD QPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIK NKDEILALLKALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFESPKKKAKVE
2539	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGTLNIEDEYRLHETSKGPDVPLGSTWL SDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHP TVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLL

	AATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTK PGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQ PLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSFLQE GQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSI IHCPGHQKGNRAEARGNRMADQAARAVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2542	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGGSGGSGGTLNIEDEYRLHETSKGPDV PLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNK
2544	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGGSGGSGGTLNIEDEYRLHETSKGPDV PLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNK

	RVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQ
	YVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAA
	PLYPLITKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDA
	GKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLTDQPLPDADHTWYTD
	GSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALF
	LPKRLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFESPKKKAKVE
2547	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGPAPGGTLNIEDEYRLHETSKGPDVPLGSTW
	LSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIH
	PTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLL
	LAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLT
	KPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMG
	QPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSFLQ
	EGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLS
	IIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFESPKKKAKVE
2548	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGPAPGGTLNIEDEYRLHETSKGPDVP

	LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY VDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP LYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLTDQPLPDADHTWYTDG SSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL PKRLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFESPKKKAKVE
2550	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
2551	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI

	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSGGGGGTLNIEDEYRLHETSKGPDVP LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY VDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP LYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLTDQPLPDADHTWYTDG SSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL PKRLSIIHCPGHQKGNRAEARGNRMADQAARGVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2553	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSEAAAKGGSGGTLNIEDEYRLHETSKGPDVP LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY VDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP LYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLTDQPLPDADHTWYTDG SSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL PKRLSIIHCPGHQKGNRAEARGNRMADQAARGVATRETPETSTLLAGKRTADGSEFESPKKKAKVE
2556	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY

	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGPAPGGTLNIEDEYRLHETSKGPDVP LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY VDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP LYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLTDQPLPDADHTWYTDG SSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL PKRLSIIHCPGHQKGNRAEARGNRMADQAARGVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2559	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGGGTLNIEDEYRLHETSKGPDVPLGSTW LSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIH PTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLL LAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLT KPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMG QPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSFLQ EGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLS IIHCPGHQKGNRAEARGNRMADQAARGVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2561	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV

	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGSEAAAKGGGTLNIEDEYRLHETSKG PDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLRE VNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLI LLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAE MAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLT KDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLTDQPLPDADHTW YTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAARE
2562	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGGGTLNIEDEYRLHETSKGPDVPLGSTW LSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIH PTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLL LAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLT KPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMG QPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSFLQ EGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLS IIHCPGHQKGNRAEARGNRMADQAARE
2566	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK

	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGGGSGGGGSGGGGSGGT LNIEDEYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVK KPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEAL HRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFL GKAGFCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAG WPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSE GKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2568	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPGGTLNIEDEYRLHETSKGPDVPLGSTWL SDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHP TVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLL AATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTK PGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQ PLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSFLQE GQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEIILALLKALFLPKRLSI IHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2573	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD

	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSPAPGGGGTLNIEDEYRLHETSKGPDVPLG STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE DIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVD DLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLY PLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKL TMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSS FLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPK RLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFESPKKKAKVE
2578	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK	
2583	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK	

	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSAGSAAGSGEFGGTLNIEDEYRLHETSKGPDV PLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNK RVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQ YVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAA PLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLT GKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSF GSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKR LPKRLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
258 5	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGSSGGTLNIEDEYRLHETSKGPDVPLGS TWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVED IHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDD LLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYP LTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLT MGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSF LQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKR LSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
259 2	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL

	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSPAPEAAAKGGTLNIEDEYRLHETSKGPDVP
	LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR
	VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY
	VDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP
	LYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG
	KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLTDQPLPDADHTWYTDG
	SSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL
	PKRLSIIHCPGHQKGNRAEARGNRMADQAARGVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2599	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSPAPEAAAKGGTLNIEDEYRLHETSKGPDVP
	LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR
	VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY
	VDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP
	LYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG
	KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLTDQPLPDADHTWYTDG
	SSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL
	PKRLSIIHCPGHQKGNRAEARGNRMADQAARGVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2610	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH

	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKGGTLNIEDEYRLH IAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPD ADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEI LALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEKRTADGSEFESPKKK AKVE
261 1	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKALEAEAAAKEAA AKEAAAKEAAAKAGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGI LVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTR LPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWR RPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEG LQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATA HIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEA GKRTADGSEFEKRTADGSEFESPKKKAKVE
261 2	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA

	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGGSGGSGGSGGSGGTLNIEDEYRLHET SKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQD LREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHP DLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPG FAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIA VLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDAD HTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILA LLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE
2614	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGPAPGGTLNIEDEYRLHETSKEPDVS LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE

2615	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGGGSGGGGSGGTLNIEDEYRLH ETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPV QDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQ HPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFI PGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAA IAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPD ADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEI LALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKK AKVE
2618	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGGGSGGGGSGGTLNIEDEYRLHETSKEPDVSLG STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE DIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVD DLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLY PLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKL TMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSS

	LLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPK RLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE
2619	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPGGTLNIEDEYRLHETSKEPDVS LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE
2620	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGTLNIEDEYRLHETSKEPDVSLGSTWL SDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHP TVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLL AATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTK PGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQ

	PLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQE
	GQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSI
	IHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE
2622	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGGGPAPGGTLNIEDEYRLHETSKEPDVSLG
	STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE
	DIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVD
	DLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLY
	PLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQE
	GQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSI
	IHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE
2622	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGGGPAPGGTLNIEDEYRLHETSKEPDVSLG
	STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE
	DIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVD
	DLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLY

	PLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKL
	TMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSS
	LLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPK
	RLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE
2623	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGSEAAAKGGGGSEAAAKGGTLNIEDEYRLHETSKE
	PDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLRE
	VNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLI
	LLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAE
	MAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLT
	KDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTW
	YTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK
	ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE
2624	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGTLNIEDEYRLHETSKEPDVSLGSTWLSD
	FPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTV
	PNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAA

	TSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPG TLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPL VILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQ RKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIH CPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEKRTADGSEFESPKKKAKVE
2624	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKGGTLNIEDEYRLHETSKE PDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLRE
2627	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKGGTLNIEDEYRLHETSKE PDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLRE

	VNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLI
	LLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAE
	MAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLT
	KDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTW
	YTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK
	ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE
2629	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSEAAAKGGGGGTLNIEDEYRLHETSKEPDVS
	LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG
	KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG
	SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL
	PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE
2631	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGTLNIEDEYRLHETSKEPDVSLGSTWLSD

	FPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTV
	PNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAA
	TSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPG
	TLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPL
	VILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQ
	RKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIH
	CPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE
2632	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSGGSGGTLNIEDEYRLHETSKEPDVSLG
	STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE
	DIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVD
	DLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLY
	PLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKL
	TMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSS
	LLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPK
	RLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE
2633	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI

	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSPAPGGGGTLNIEDEYRLHETSKEPDVSLG
	STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE
	DIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVD
	DLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLY
	PLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKL
	TMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSS
	LLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPK
	RLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE
2634	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGSGSSGGTLNIEDEYRLHETSKEPDVSLG
	STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE
	DIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVD
	DLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLY
	PLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKL
	TMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSS
	LLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPK
	RLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE
2636	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY

	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSEAAAKGGGGSGGTLNIEDEYRLHETSKE
	PDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLRE
	VNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLI
	LLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAE
	MAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLT
	KDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTW
	YTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK
	ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE
2637	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSGSGGGGTLNIEDEYRLHETSKEPDVS
	LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR
	VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY
	VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP
	LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG
	KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG
	SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL
	PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE
2638	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV

	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGEAAAKGGSGGTLNIEDEYRLHETSKEPDVS LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEKRTADGSEFESPKKKAKVE
2638	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGEAAAKGGSGGTLNIEDEYRLHETSKEPDVS LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEKRTADGSEFESPKKKAKVE
2639	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK

	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGGGSGGTLNIEDEYRLHETSKEPDVSL
	GSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRV
	EDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYV
	DDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPL
	YPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGK
	LTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGS
	SLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLP
	KRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE
2639	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGGGSGGTLNIEDEYRLHETSKEPDVSL
	GSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRV
	EDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYV
	DDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPL
	YPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGK
	LTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGS
	SLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLP
	KRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE
2641	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD

	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSEAAAKPAPGGTLNIEDEYRLHETSKEPDVS LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAQIGDQYADLFLA SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYKRRGWLTSEGKEIKNKDEILALLKALF PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFESPKKKAKVE
2644	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGGGSGGGSGGGSGGGSGGGSGGT LNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVK KPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEAL HRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFL GKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAG WPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSE GKEIKNKDEIILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTAD GSEFESPKKKAKVE
2647	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL

	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKKGGTLNIEDEYRLHETSKEPDVSL
	GSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRV
	EDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYV
	DDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPL
	YPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGK
	LTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGS
	SLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLP
	KRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE
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	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
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	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
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	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKKGGTLNIEDEYRLHETSKEPDVSL
	GSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRV
	EDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYV
	DDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPL
	YPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGK
	LTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGS
	SLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLP
	KRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE
2648	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
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	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH

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	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
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	LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR
	VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY
	VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP
	LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQEGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG
	KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG
	SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL
	PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE
2649	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
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	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
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	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
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	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGPAPGGSGGGGGTLNIEDEYRLHETSKEPDVSLG
	STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE
	DIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVD
	DLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLY
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	TMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSS
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	RLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
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	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER

	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGSGGGGTLNIEDEYRLHETSKEPDVSLG STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE DIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY DLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE
2651	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGSSSEAAAKGGTLNIEDEYRLHETSKEPDVS LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE
2653	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL

	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGGGGTLNIEDEYRLHETSKEPDVSLGSTW
	LSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVED
	PTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQFLAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLL
	LAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLT
	KPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMG
	QPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQ
	EGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLS
	IIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE
2654	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSPAPGGTLNIEDEYRLHETSKEPDVS
	LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR
	VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY
	VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP
	LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG
	KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG
	SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL
	PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE
2655	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA

	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGTLNIEDEYRLHETSKEPDVSLGTSS
	FPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTV
	PNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAA
	TSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPG
	TLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPL
	VILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQ
	RKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIH
	CPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE
2656	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPGGTLNIEDEYRLHETSKEPDVSLG
	STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE
	DIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVD
	DLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLY
	PLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKL
	TMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSS
	LLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPK
	RLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE

2657	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSGGTLNIEDEYRLHETSKEPDVSLGS TWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVED IHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDD LLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYP LTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLT MGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSL LQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKR LSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE
2660	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGSSEAAAKGGTLNIEDEYRLHETSKEPDVS LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG

	SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE
2663	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGSGSETPGTSESATPESGGTLNIEDEYRLHETSK EPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLR EVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLI ILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFA EMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVL TKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHT WYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALL KALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE
2665	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGSGSGSGSGGTLNIEDEYRLHETSKEPDV SLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNK RVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQ YVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAA PLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDA

	GKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTD
	GSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALF
	LPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE
2666	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSGSSGGTLNIEDEYRLHETSKEPDVS
	LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR
	VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY
	VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP
	LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG
	KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG
	SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL
	PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE
2667	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSPAPGGGGTLNIEDEYRLHETSKEPDVSLG
	STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE
	DIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVD
	DLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLY

	PLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKL
	TMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSS
	LLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPK
	RLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE
2669	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGSGSGSGSGSGGTLNIEDEYRLHETSKEP
	PDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREV
	VNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLI
	LLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAE
	MAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLT
	KDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTW
	YTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK
	ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE
2675	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGSGSGSGSGSGGTLNIEDEYRLHETSKEPDVSLG
	STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE
	DIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVD

	DLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLY
	PLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKL
	TMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSS
	LLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPK
	RLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEKRTADGSEFESPKKKAKVE
2676	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGGGGGTLNIEDEYRLHETSKEPDVSLGSTW LSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIH PTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLL LAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLT KPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMG QPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQ EGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLS IIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE
2676	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGGGGGTLNIEDEYRLHETSKEPDVSLGSTW LSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIH

	PTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLL LAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLT KPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMG QPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQ EGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLS IIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE
2677	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGEAAAKGSSGGTLNIEDEYRLHETSKEPDVS LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE
2678	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAAKGGTLNIED

	EYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTN DYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGF CRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCL RMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTD QPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIK NKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAATETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFE SPKKKAKVE
2681	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKPAPGGGGTLNIEDEYRLHETSKEPDVS LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEIILALLKALFL PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAATETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE
2684	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY

	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSPAPGSSGGTLNIEDEYRLHETSKEPDVSLG STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE DIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVD DLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLY PLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKL TMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSS LLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPK RLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE
2688	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSSEAAAKGGTLNIEDEYRLHETSKEPDVS LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE
2692	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV

	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGGEAAAKGGTLNIEDEYRLHETSKEPDVS LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEKRTADGSEFESPKKKAKVE
2696	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSAGSAAGSGEFGGTLNIEDEYRLHETSKEPDV SLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNK RVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQ YVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAA PLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDA GKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTD GSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALF LPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEKRTADGSEFESPKKKAKVE
2700	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK

	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSEAAAKGGTLNIEDEYRLHETSKEPDVSLGS
	TWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVED
	IHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDD
	LLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYP
	LTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLT
	MGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSL
	LQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKR
	LSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE
270 1	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSPAPEAAAKGGTLNIEDEYRLHETSKEPDVS
	LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR
	VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY
	VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP
	LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG
	KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG
	SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL
	PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE
271 1	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD

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2712	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGSEAAAKGGTLNIEDEHRLHETSKE PDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLRE VNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLI LLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAE MAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLT KDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTW YTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2712	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL

	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGSEAAAKGGTLNIEDEHRLHETSKE
	PDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLRE
	VNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLI
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	MAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG
	KDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTW
	YTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK
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2713	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
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	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
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	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSEAAAKGGGGGTLNIEDEHRLHETSKEPDVS
	LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR
	VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY
	VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAP
	LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG
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	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH

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	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSEAAAKPAPGGSGGTLNIEDEHRLHETSKEPDVS
	LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR
	VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY
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	KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG
	SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL
	PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2714	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
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	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
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	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKPAPGGSGGTLNIEDEHRLHETSKEPDVS
	LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR
	VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY
	VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAP
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	SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL
	PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFESPKKKAKVE

2722	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAP LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFESPKKKAKVE
2723	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSEAAAKGGTLNIEDEHRLHETSKEPDVS LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAP LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG

	SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFESPKKKAKVE
2723	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGSSPAPGGTLNIEDEHRLHETSKEPDVS LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAP LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFESPKKKAKVE
2724	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKPAPGGTLNIEDEHRLHETSKEPDVSLGS TWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVED IHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDD LLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYP LTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLT

	MGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSL LQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKR LSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2726	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSGGTLNIEDEHRLHETSKEPDVSLGS TWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVED IHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDD LLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYP LTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLT MGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSL LQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKR LSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2731	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPGGTLNIEDEHRLHETSKEPDVSLG STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE DIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVD DLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLY

	PLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKL
	TMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSS
	LLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPK
	RLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKPSPKKKAKVE
2734	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGSGGSGGSGSETPGTSESATPESSGGSSGGSS
	GGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLL
	PVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFN
	EALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLR
	EFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPV
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2737	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
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	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
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	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
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	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
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	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI

	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGSEAAAKGGTLNIEDEHRLHETSKEPDVS LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAP LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFESPKKKAKVE
2760	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGSEAAAKGGTLNIEDEHRLHETSKEPDVS LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAP LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFESPKKKAKVE
2764	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY

	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSSEAAAKGGTLNIEDEHRLHETSKEPDVS LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAP LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFQPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFESPKKKAKVE
2771	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSGGGGSGGGGSGGTLNIEDEHRLH ETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPV QDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQ HPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWI PGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAA IAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPD ADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEI LALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEFESPKKKAKVE
2772	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV

	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKGGTLNIEDEHRLHETSKE
	PDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLRE
	VNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLI
	LLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAE
	MAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLT
	KDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTW
	YTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK
	ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFESPKKKAKVE
2776	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSPAPEAAAKGGTLNIEDEHRLHETSKEPDVS
	LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR
	VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY
	VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAP
	LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG
	KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG
	SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL
	PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFESPKKKAKVE
2780	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK

	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSGGTLNIEDEHRLHETSKEPDVSLGSTW
	LSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIH
	PTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLL
	LAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLT
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	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL

	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKALEAEAAAKEAA AKEAAAKEAAAKAGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGI LVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTR LPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWR RPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEG LQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATA HIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEF ESPKKKAKVE
2786	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKALEAEAAAKEAA LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2787	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER

	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIISQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSEAAAKGGGGGTLNIEDEHRLHETSKEPDVS LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2787	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIISQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSEAAAKGGGGGTLNIEDEHRLHETSKEPDVS LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2788	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL

	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGSEAAAKGGTLNIEDEHRLHETSKE PDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY LLQVVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP LAQLVSDFRKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGSSGGTLNIEDEHRLHETSKEPDVS LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2789	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA

	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGGGGTLNIEDEHRLHETSKEPDVSLGST
	WLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDI
	HPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDL
	LLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPL
	TKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTM
	GQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLL
	QEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRL
	SIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
279 1	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKGGTLNIEDEHRLHETSKE
	PDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLRE
	VNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLI
	LLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAE
	MAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLT
	KDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTW
	YTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK
	ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE

2792	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFESPKKKAKVE
2793	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAKGSSPAPGGTLNIEDEHRLHETSKEPDVS LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLY PLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKL TMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSS

	LLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPK RLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2794	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSGGGGGTLNIEDEHRLHETSKEPDVS LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2795	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGSGGSGGTLNIEDEHRLHETSKEPDV SLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNK RVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQ YVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAA PLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDA

	GKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTD GSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVVTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALF LPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFESPKKKAKVE
2795	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGSGGSGGTLNIEDEHRLHETSKEPDV SLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNK RVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQ YVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAA PLYPLITKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDA GKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTD GSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVVTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALF LPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFESPKKKAKVE
2797	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPAPAPGGTLNIEDEHRLHETSKEPD VSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVN KRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILL QYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMA

	APLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKD AGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYT DGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKAL FLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2797	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPGGTLNIEDEHRLHETSKEPD VSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVN KRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILL QYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMA APLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKD AGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYT DGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKAL FLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2798	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPGSSEAAAKGGTLNIEDEHRLHETSKEPDVS LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY

	VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP
	LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG
	KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG
	SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL
	PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFESPKKKAKVE
2798	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGPAPGGSGGTLNIEDEHRLHETSKEPDVSLG
	VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP
	LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG
	KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG
	SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL
	PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFESPKKKAKVE
2800	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
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	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGPAPGGSGGTLNIEDEHRLHETSKEPDVSLG
	STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE

	DIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVD
	DLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLY
	PLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKL
	TMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSS
	LLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPK
	RLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFESPKKKAKVE
2800	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSPAPGGGGGTLNIEDEHRLHETSKEPDVSLG
	DIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVD
	DLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLY
	PLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKL
	TMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSS
	LLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPK
	RLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFESPKKKAKVE
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	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
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	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSPAPGGGGGTLNIEDEHRLHETSKEPDVSLG

	STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE
	DIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVD
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	PLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKL
	TMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSS
	LLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPK
	RLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFESPKKKAKVE
2801	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
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	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSPAPGGGGGTLNIEDEHRLHETSKEPDVSLG
	STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE
	DIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVD
	DLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLY
	PLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKL
	TMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSS
	LLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPK
	RLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFESPKKKAKVE
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	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
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	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
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	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGSSGSSGSSGGTLNIEDEHRLHETSKE
	PDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLRE
	VNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLI
	LLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAE
	MAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLT
	KDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTW
	YTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK
	ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFESPKKKAKVE
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	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
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	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
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	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
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	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
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	EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTN
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	DFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGF
	CRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCL
	RMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTD
	QPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIK
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	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY

	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGGPAPGGTLNIEDEHRLHETSKEPDVSLG STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE DIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVD DLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLY PLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKL TMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSS LLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPK RLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
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2805	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV

	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSPAPEAAAKGGTLNIEDEHRLHETSKEPDVS LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2808	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSPAPGGTLNIEDEHRLHETSKEPDVSLGSTW LSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIH PTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVVDDLL LAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLT KPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMG QPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQ EGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLS IIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2808	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK

	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSPAPGGTLNIEDEHRLHETSKEPDVSLGSTW
	LSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIH
	PTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLL
	LAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLT
	KPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMG
	QPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQ
	EGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLS
	IIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2809	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
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	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVVTLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGGSGGTLNIEDEHRLHETSKEPDVSLG
	STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE
	DIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVD
	DLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLY
	PLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKL
	TMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSS
	LLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPK
	RLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2810	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD

	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGGEAAAKGGTLNIEDEHRLHETSKEPDVS
	LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR
	VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY
	VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP
	LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG
	KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG
	SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL
	PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2810	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
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	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGGEAAAKGGTLNIEDEHRLHETSKEPDVS
	LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR
	VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY
	VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP
	LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG
	KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG
	SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL
	PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2812	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
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	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK

	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGTLNIEDEHRLHETSKEPDVSLGSTWLSD
	FPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTV
	PNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAA
	TSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPG
	TLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPL
	VILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQ
	RKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIH
	CPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2813	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAAKEAAAKGGT
	LNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVK
	KPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEAL
	HRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFL
	GKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAG
	WPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR
	PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSE
	GKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2815	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL

	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGSGGTLNIEDEHRLHETSKEPDVS VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2815	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGSGGTLNIEDEHRLHETSKEPDVS LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2817	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH

	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSGSSGGTLNIEDEHRLHETSKEPDVS
	LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR
	VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY
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	LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG
	KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG
	SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL
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2817	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSGSSGGTLNIEDEHRLHETSKEPDVS
	LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR
	VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY
	VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP
	LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG
	KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG
	SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL
	PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2818	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
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	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER

	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGSGGGGGTLNIEDEHRLHETSKEPDVSLG STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE DIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVD DLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLY PLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKL TMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSS LLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPK RLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2818	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGSGGGGGTLNIEDEHRLHETSKEPDVSLG STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE DIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVD DLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLY PLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKL TMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSS LLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPK RLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2819	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL

	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSGGGGSGGTLNIEDEHRLHETSKE
	PDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLRE
	VNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLI
	LLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAE
	MAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLT
	KDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTW
	YTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK
	ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2820	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSGGGGSGGTLNIEDEHRLHETSKEPDVSLGSTW
	LSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIH
	PTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLL
	LAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLT
	KPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMG
	QPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQ
	EGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLS
	IIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2822	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA

	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGGEAAAKGGTLNIEDEHRLHETSKEPDVS
	LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR
	VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY
	VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP
	LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG
	KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG
	SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL
	PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFESPKKKAKVE
2823	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGTLNIEDEHRLHETSKEPDVSLGSTWL
	SDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHP
	TVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLL
	AATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTK
	PGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQ
	PLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQE
	GQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSI
	IHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFESPKKKAKVE

2825	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGTLNIEDEHRLHETSKEPDVSLGSTWL SDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHP TVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLL AATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTK PGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQ PLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGS GQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSI IHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2826	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSEAAAKGSSGGTLNIEDEHRLHETSKEPDVS LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG

	SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2827	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGGGSGGGGSGGGGSGGT LNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVK KPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEAL HRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFL GKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAG WPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSE GKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2828	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSEAAAKGGTLNIEDEHRLHETSKEPDVSLGS TWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVED IHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDD LLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYP LTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLT

	MGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSL LQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKR LSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2829	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPEAAAKGGSGGTLNIEDEHRLHETSKEPDVS LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP
2830	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGEAAAKPAPGGTLNIEDEHRLHETSKEPDVS LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP

	LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2830	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGEAAAKPAPGGTLNIEDEHRLHETSKEPDVS LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2831	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSSEAAAKGGTLNIEDEHRLHETSKEPDVS LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY

	VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP
	LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG
	KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG
	SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL
	PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFESPKKKAKVE
2833	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGGGTLNIEDEHRLHETSKEPDVSLGSTWL
	SDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHP
2834	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGGGTLNIEDEHRLHETSKEPDVSLGSTWL
	SDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHP

	TVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLL AATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTK PGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQ PLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQE GQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSI IHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFESPKKKAKVE
2835	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSEAAAKGGGGSGGTLNIEDEHRLHETSKE
2836	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSEAAAKGGGGSGGTLNIEDEHRLHETSKE

	PDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLRE VNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLI LLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAE MAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLT KDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTW YTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFESPKKKAKVE
2838	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
2839	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI

	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSPAPEAAAKGGTLNIEDEHRLHETSKEPDVS
	LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR
	VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY
	VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP
	LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG
	KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG
	SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL
	PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2840	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSPAPGGTLNIEDEHRLHETSKEPDVSLG
	STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE
	DIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVD
	DLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLY
	PLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKL
	TMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSS
	LLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPK
	RLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2840	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY

	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSPAPGGTLNIEDEHRLHETSKEPDVSLG STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE DIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVD DLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLY PLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKL TMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSS LLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPK RLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2844	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAAKEAAAKEAAAKGGTLNIEDEHRLH ETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPV QDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQ HPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFI PGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAA IAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPD ADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEI LALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2845	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV

	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKGGTLNIEDEHRLHETSKEPDVSL
	GSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRV
	EDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYV
	DDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPL
	YPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGK
	LTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGS
	SLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLP
	KRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2846	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
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	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGSSGGTLNIEDEHRLHETSKEPDVSLG
	STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE
	DIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVD
	DLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLY
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	TMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSS
	LLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPK
	RLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2848	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
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	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
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	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
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	STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE
	DIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVD
	DLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLY
	PLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKL
	TMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSS
	LLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKR
	RLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFESPKKKAKVE
2849	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
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	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
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	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSEAAAKGGTLNIEDEHRLHETSKEPDVSLGS
	TWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVED
	IHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDD
	LLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYP
	LTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLT
	MGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSL
	LQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKR
	LSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFESPKKKAKVE
2850	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
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	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD

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2850	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
2851	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK

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	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
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	LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR
	VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY
	VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP
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	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
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	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
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	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
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	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSPAPGSSGGTLNIEDEHRLHETSKEPDVSLG
	STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE
	DIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVD
	DLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLY
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	TMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSS
	LLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPK
	RLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2855	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
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	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL

	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGSGTLNIEDEHRLHETSKEPDVSLGSTW
	LSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIH
	EGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLS
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2857	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
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	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSEAAAKPAPGGTLNIEDEHRLHETSKEPDVS
	LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR
	VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY
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	LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG
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	SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL
	PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
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	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH

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	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGSEAAAKGGTLNIEDEHRLHETSKEPDVS
	LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR
	VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY
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	LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG
	KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG
	SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL
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2862	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
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	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSGGGGTLNIEDEYRLHETSKEPDVS
	LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR
	VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY
	VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP
	LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG
	KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG
	SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL
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2863	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
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	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER

	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGSGGTLNIEDEYRLHETSKEPDVS LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE
2864	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGSSGGTLNIEDEYRLHETSKEPDVSLGSTWLSD FPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTV PNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAA TSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPG TLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPL VILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQ RKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIH CPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE
2865	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL

	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
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	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGTLNIEDEYRLHETSKEPDVSLGSTWLSD
	FPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTV
	PNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAA
	VILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQ
	RKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIH
	CPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE
2865	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGTLNIEDEYRLHETSKEPDVSLGSTWLSD
	FPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTV
	PNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAA
	TSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPG
	TLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPL
	VILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQ
	RKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIH
	CPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE
2866	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
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	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
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	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
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	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGGGGEAAAKGGTLNIEDEYRLHETSKEPDVS
	LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR
	VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY
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	LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG
	KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG
	SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL
	PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE
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	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
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	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGGSGGSGGSGGTLNIEDEYRLHETSKEPDV
	SLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNK
	RVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQ
	YVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAA
	PLYPLITKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDA
	GKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTD
	GSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALF
	LPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE

2868	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV KVPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPAPGGTLNIEDEYRLHETSKEPD VSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVN KRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILL QYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMA APLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKD AGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYT DGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKAL FLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE
2869	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPGGGSSGGTLNIEDEYRLHETSKEPDVSLG STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE DIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVD DLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLY PLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKL TMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSS

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	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
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	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGEAAAKGSSGGTLNIEDEYRLHETSKEPDVS
	LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR
	VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY
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	LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG
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	PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE
2871	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
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	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
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	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGGGTLNIEDEYRLHETSKEPDVSLGSTW
	LSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIH
	PTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLL
	LAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLT
	KPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMG

	QPLVIILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQ EGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLS IIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE
2871	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGGGGGTLNIEDEYRLHETSKEPDVSLGSTW LSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIH PTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLL LAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLT KPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMG QPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQ EGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLS IIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE
2872	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGGEAAAKGGTLNIEDEYRLHETSKEPDVS LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP

	LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE
2873	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGSSEAAAKGGTLNIEDEYRLHETSKEPDVS LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE
2874	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGEAAAKGGSGGTLNIEDEYRLHETSKEPDVS LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY

	VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP
	LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG
	KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG
	SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL
	PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE
2874	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKGGTLNIEDEYRLHETSKE
	PDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLRE
2877	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKGGTLNIEDEYRLHETSKE
	PDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLRE

	VNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLI
	LLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAE
	MAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLT
	KDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTW
	YTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK
	ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE
2878	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGSGGGGTLNIEDEYRLHETSKEPDVSLG
	STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE
	DIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVD
	DLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLY
	PLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKL
	TMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSS
	LLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPK
	RLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE
2878	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGSGGGGTLNIEDEYRLHETSKEPDVSLG

	STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE DIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVD DLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLY PLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKL TMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSS LLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPK RLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEKRTADGSEFESPKKKAKVE
2879	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
2880	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI

	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAAKEAAAKGGTLNIED EYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTN DYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGF CRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCL RMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTD QPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIK NKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFE SPKKKAKVE
2881	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGTLNIEDEYRLHETSKEPDVSLGSTWL SDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHP TVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLL AATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTK PGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQ PLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQE GQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSI IHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE
2883	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV

	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPEAAAKGGTLNIEDEYRLHETSKEPDVSLGS
	TWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVED
	IHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDD
	LLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYP
	LTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLT
	MGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSL
	LQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKR
	LSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE
2885	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSSEAAAKGGTLNIEDEYRLHETSKEPDVS
	LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR
	VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY
	VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP
	LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG
	KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG
	SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL
	PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE
2886	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK

	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGGGGTLNIEDEYRLHETSKEPDVSLGSTW
	LSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIH
	PTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLL
	LAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLT
	KPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMG
	QPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQ
	EGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLS
	IIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE
2887	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
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	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVVTLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKGGTLNIEDEYRLHETSKEPDVSL
	GSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRV
	EDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYV
	DDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPL
	YPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGK
	LTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGS
	SLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLP
	KRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE
2887	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD

	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKGGTLNIEDEYRLHETSKEPDVSL GSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRV EDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQFLAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYV DDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPL YPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGK LTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGS SLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLP KRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE
2888	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKGGTLNIEDEYRLH ETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPV QDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQ HPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFI PGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAA IAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPD ADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEI LALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKK AKVE
2890	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL

	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
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	STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE
	LLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPK
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2891	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
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	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
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	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
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	LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR
	VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY
	VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP
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	KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG
	SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL
	PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE
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	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
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	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH

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	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSPAPEAAAKGGTLNIEDEYRLHETSKEPDVS
	LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR
	VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY
	VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP
	LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQEGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG
	KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG
	SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL
	PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE
2894	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSPAPGSSGGTLNIEDEYRLHETSKEPDVSLG
	STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE
	DIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVD
	DLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLY
	PLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKL
	TMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSS
	LLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPK
	RLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2895	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
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	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER

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2895	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGGGPAPGGTLNIEDEYRLHETSKEPDVSLG STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE DIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVD DLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLY PLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKL TMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSS LLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPK RLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE
2901	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL

	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSEAAAKGGGGTLNIEDEYRLHETSKEPDVS LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNK VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQ VVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEIILALLKALFL PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEKRTADGSEFESPKKKAKVE
2902	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSAGSGEFGGTLNIEDEYRLHETSKEPDV SLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNK RVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQ YVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAA PLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDA GKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTD GSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEIILALLKALF LPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEKRTADGSEFESPKKKAKVE
2903	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA

	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGGSGGSGGTLNIEDEYRLHETSKEPDVSLG
	STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE
	DIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVD
	DLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLY
	PLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKL
	TMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSS
	LLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPK
	RLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE
2904	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGGSGGSGGTLNIEDEYRLHETSKEPDVSLG
	STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE
	DIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVD
	DLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLY
	PLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKL
	TMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSS
	LLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPK
	RLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE

2905	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV LSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIH PTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLL LAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLT KPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMG QPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHT EGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLS IIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE
2907	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGSSGSGSGGTLNIEDEYRLHETSKEPDVSLGSTW EPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLR EVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDL ILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFA EMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVL TKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHT

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	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGGGSGGTLNIEDEYRLHETSKEPDVSL
	GSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRV
	EDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYV
	DDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPL
	YPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGK
	LTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGS
	SLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLP
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	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
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	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGGGSGGTLNIEDEYRLHETSKEPDVSL
	GSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRV
	EDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYV
	DDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPL
	YPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGK

	LTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGS
	SLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLP
	KRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE
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	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGSSEAAAKGGTLNIEDEYRLHETSKEPDVS
	LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR
	VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY
	VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP
	LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG
	KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG
	SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL
	PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE
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	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGSSGGTLNIEDEYRLHETSKEPDVSLGSTW
	LSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIH
	PTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLL
	LAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLT

	KPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMG QPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQ EGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLS IIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE
2916	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSEAAAKGGTLNIEDEYRLHETSKEPDVSLGS TWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVED IHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDD LLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYP LTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLT MGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSL LQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKR LSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE
2920	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSPAPEAAAKGGTLNIEDEYRLHETSKEPDVS LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY

	VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP
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	KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG
	SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL
	PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE
2922	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPEAAAKGGSGGTLNIEDEYRLHETSKEPDVS
	LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR
	VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY
	VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP
	LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG
	KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG
	SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL
	PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE
2924	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM
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	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPEAAAKGGSGGTLNIEDEYRLHETSKEPDVS
	LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR

	VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY
	VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP
	LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG
	KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG
	SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL
	PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE
2927	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
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	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGGGTLNIEDEYRLHETSKEPDVSLGSTWLS
	DFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPT
	VPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLA
	ATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKP
	GTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQP
	LVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEG
	QRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSII
	HCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE
2928	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
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	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
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	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGGSEAAAKGGTLNIEDEYRLHETSKEPDVS

	LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEKRTADGSEFESPKKKAKVE
2929	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
2930	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI

	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPGGTLNIEDEYRLHETSKEPDVSLG
	STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE
	DIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVD
	DLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLY
	PLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKL
	TMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSS
	LLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPK
	RLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE
2932	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGSEAAAKGGGTLNIEDEYRLHETSKE
	PDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLRE
	VNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLI
	LLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAE
	MAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLT
	KDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTW
	YTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK
	ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE
2933	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY

	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSGGTLNIEDEYRLHETSKEPDVSLGS TWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVED IHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDD LLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYP LTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLT MGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSL LQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKR LSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE
2937	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSEAAAKGGGGSGGTLNIEDEYRLHETSKE PDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLRE VNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLI LLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAE MAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLT KDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTW YTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE
2941	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV

	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGSSGSSGSSGGTLNIEDEYRLHETSKE PDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLRE VNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLI LLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAE MAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLT KDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTW YTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE
2943	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGSSGSSGSSGGTLNIEDEYRLHET SKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQD LREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHP DLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPG FAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIA VLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDAD HTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILA LLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAK VE	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD

	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGSSGGGGTLNIEDEYRLHETSKEPDVSLG
	STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE
	DIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVD
	DLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLY
	PLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKL
	TMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSS
	LLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPK
	RLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEKRTADGSEFESPKKKAKVE
2950	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGSSGGGGTLNIEDEYRLHETSKEPDVSLG
	STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE
	DIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVD
	DLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLY
	PLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKL
	TMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSS
	LLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPK
	RLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE
2953	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK

	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGEAAAKGGTLNIEDEYRLHETSKEPDVSLGS TWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVED IHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDD LLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYP LTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEG MGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATA LQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAIHGEIYKRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEKRTADGSEFESPKKKAKVE LSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE HIHGEIYRRRGLLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEF ESPKKKAKVE
2957	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKALEAEAAAKEAA AKEAAAKEAAAKAGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGI LVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTR LPQGFKNSPTLFDEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKTGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWR RPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEG LQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATA HIHGEIYRRRGLLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEF ESPKKKAKVE
2957	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH

	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKALEAEAAAKEAA AKEAAAKEAAAKAGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGI LVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQFLKFAFEWRDPEMGISGQLTWTR LPQGFKNSPTLFDEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKTGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWR RPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEG LQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATA HIHGEIYRRRGLLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEF ESPKKKAKVE
2965	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGSGSGSGSGSGSGSGGTLNIEDEHRLHET SKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQD LREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQFLKFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHP DLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPG FAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIA VLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDAD HTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILA LLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2966	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL

	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSEAAAKGGGGGTLNIEDEHRLHETSKEPDVS
	LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR
	VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY
	VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAP
	LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG
	KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG
	SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL
	PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2966	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSEAAAKGGGGGTLNIEDEHRLHETSKEPDVS
	LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR
	VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY
	VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAP
	LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG
	KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG
	SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL
	PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2967	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA

	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGGGGSGGGGSGGGGSGGTLNIEDEHRLH
	LSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIH
	PTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLL
	LAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLT
	KPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMG
	QPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQ
	EGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLS
	IIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2968	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGGGGSGGGGSGGGGSGGTLNIEDEHRLH
	ETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPV
	QDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQ
	HPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWI
	PGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAA
	IAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPD
	ADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEI
	LALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE

2969	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAP LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFESPKKKAKVE
2971	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGSEAAAKGGTLNIEDEHRLHETSKEPDVS TWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVED IHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDD LLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYP LTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLT MGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSL

	LQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKR LSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2972	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKALEAEAAAKEAA AKEAAAKEAAAKAGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGI LVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTR LPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAP MGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWR RPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEG LQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATA HIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEF ESPKKKAKVE
2976	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGSSPAPGGTLNIEDEHRLHETSKEPDVS LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAP

	LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2976	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGSSPAPGGTLNIEDEHRLHETSKEPDVS LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAP LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2979	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGSSGGGGGTLNIEDEHRLHETSKEPDVSLG STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE DIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVD

	DLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLY
	PLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKL
	TMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSS
	LLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPK
	RLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFESPKKKAKVE
2982	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
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	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
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	LLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYP
	LTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLT
	MGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSL
	LQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKR
	LSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFESPKKKAKVE
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	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
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2987	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSPAPEAAAKGGTLNIEDEHRLHETSKEPDVS

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	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
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	SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL
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	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
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	CRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCL
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	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
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	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
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	EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTN
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	DFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGF
	CRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCL
	RMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTD
	QPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIK
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2995	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM
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	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY

	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSAGSAAGSGEFGGTLNIEDEHRLHETSKEPDV SLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNK RVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQ YVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAA PLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDA GKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTD GSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALF LPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2999	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGEAAAKPAPGGTLNIEDEHRLHETSKEPDVS LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAP LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFESPKKKAKVE
3007	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV

	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGSSEAAAKGGTLNIEDEHRLHETSKEPDVS
	LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR
	VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY
	VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAP
	LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG
	KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG
	SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL
	PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3014	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKPAPGGSGGTLNIEDEHRLHETSKEPDVS
	LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR
	VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY
	VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAP
	LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG
	KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG
	SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL
	PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3015	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK

	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSEAAAKGGTLNIEDEHRLHETSKEPDVSLGS
	TWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVED
	IHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDD
	LLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYP
	LTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLT
	MGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSL
	LQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKR
	LSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3018	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGEAAAKGGSGGTLNIEDEHRLHETSKEPDVS
	LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR
	VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY
	VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAP
	LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG
	KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG
	SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL
	PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
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	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
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	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD

	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGGGSGGTLNIEDEHRLHETSKEPDVSLG STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE DIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVD DLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLY PLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKL TMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSS LLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALFLPK RLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFESPKKKAKVE
3035	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGGGSGGGSGGTLNIEDEHRLHET SKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQD LREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHP DLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPG FAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIA VLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDAD HTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILA LLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFESPKKKAKVE
3036	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK

	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAAKGGTLNIEDEHRLH
	ETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPV
	QDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQ
	HPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFI
	PGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAA
	IAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPD
	ADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEI
	LALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3037	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGTLNIEDEHRLHETSKEPDVSLGSTWLSD
	FPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTV
	PNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAA
	TSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPG
	TLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPL
	VILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQ
	RKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEIILALLKALFLPKRLSIIH
	CPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3039	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL

	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGGSGGSGGTLNIEDEHRLHETSKEPDV
	RVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQ
	YVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAA
	PLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDA
	GKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTD
	GSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEIILALLKALF
	LPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3039	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGGSGGSGGTLNIEDEHRLHETSKEPDV
	SLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNK
	RVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQ
	YVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAA
	PLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDA
	GKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTD
	GSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEIILALLKALF
	LPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3040	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
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	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH

	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSSEAAAKGGTLNIEDEHRLHETSKEPDVS
	LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR
	VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY
	VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP
	LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG
	KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG
	SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL
	PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
304 1	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKGGTLNIEDEHRLHETSKEPDVSL
	GSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRV
	EDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYV
	DDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPL
	YPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGK
	LTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGS
	SLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLP
	KRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
304 2	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER

	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGSSGGGGTLNIEDEHRLHETSKEPDVSLG STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE DIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVD DLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLY PLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKL TMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSS LLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPK RLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
304 2	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGSSGGGGTLNIEDEHRLHETSKEPDVSLG STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE DIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVD DLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLY PLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKL TMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSS LLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPK RLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
304 3	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL

	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
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	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
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	EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTN
	DYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA
	DFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGF
	CRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCL
	RMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTD
	QPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIK
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	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAAKGGTLNIED
	LAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLT
	KPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMG
	QPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQ
	EGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEIILALLKALFLPKRLS
	IIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
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	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGGGGTLNIEDEHRLHETSKEPDVSLGSTW
	LSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIH
	PTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLL
	LAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLT
	KPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMG
	QPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQ
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3045	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
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	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGGGGTLNIEDEHRLHETSKEPDVS
	LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR
	VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY
	VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP
	LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG
	KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG
	SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL
	PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE

3045	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFESPKKKAKVE
3046	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGEAAAKGGSGGTLNIEDEHRLHETSKEPDVS LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG

	SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3047	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGGGGGSGGGGTLNIEDEHRLHETSKEPDVSLG STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE DIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVD DLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLY PLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKL TMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSS LLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPK RLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3048	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGGGGGSGGGGTLNIEDEHRLHETSKEPDVSLG STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE DIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVD DLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLY PLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKL

	TMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSS LLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPK RLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3052	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGGEAAAKGGTLNIEDEHRLHETSKEPDVS LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE

	LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3053	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSGSSGGTLNIEDEHRLHETSKEPDVS LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3054	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPAPGGTLNIEDEHRLHETSKEPDVS LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY

	VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP
	LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG
	KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG
	SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL
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3055	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM
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	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGGPAPGGTLNIEDEHRLHETSKEPDVSLG
	STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE
3056	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM
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	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
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	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGGPAPGGTLNIEDEHRLHETSKEPDVSLG
	STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE

	DIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVD
	DLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLY
	PLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKL
	TMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSS
	LLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPK
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3057	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
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	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGGEAAAKGGTLNIEDEHRLHETSKEPDVS
	DIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVD
	DLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLY
	PLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKL
	TMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSS
	LLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPK
	RLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFESPKKKAKVE
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	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
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	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGGEAAAKGGTLNIEDEHRLHETSKEPDVS

	LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR
	VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY
	VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP
	LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG
	KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG
	SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL
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	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
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	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGGPAPGGTLNIEDEHRLHETSKEPDVSLG
	STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE
	DIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVD
	DLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLY
	PLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKL
	TMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSS
	LLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPK
	RLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3059	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI

	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGGGPAPGGTLNIEDEHRLHETSKEPDVSLG
	STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE
	DIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVD
	DLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLY
	PLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKL
	TMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSS
	LLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPK
	RLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3060	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGSGGTLNIEDEHRLHETSKEPDVSLGSTW
	LSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIH
	PTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLL
	LAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLT
	KPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMG
	QPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQ
	EGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLS
	IIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3061	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY

	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPEAAAKGGTLNIEDEHRLHETSKEPDVSLGS TWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVED IHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDD LLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYP LTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLT MGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSL LQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKR LSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3062	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSEAAAKGGTLNIEDEHRLHETSKEPDVSLGS TWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVED IHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDD LLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYP LTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLT MGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSL LQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKR LSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3063	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV

	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSGGGGSGGGGSGGTLNIEDEHRLH
	ETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPV
	QDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQ
	HPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFI
	PGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAA
	IAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPD
	ADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEI
	LALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3063	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
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	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
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	ETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPV
	QDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQ
	HPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFI
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	IAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPD
	ADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEI
	LALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3064	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM
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	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK

	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGSGSSGGTLNIEDEHRLHETSKEPDVSLG STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE DIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVD DLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLY PLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKL TMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSS LLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKR RLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3065	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSGGTLNIEDEHRLHETSKEPDVSLGSTWL SDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHP TVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLL AATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTK PGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQ PLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQE GQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSI IHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3067	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD

	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSEAAAKGGGGTLNIEDEHRLHETSKEPDVS LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFESPKKKAKVE
3067	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
3068	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK

	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPEAAAKGGGGTLNIEDEHRLHETSKEPDVS
	LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR
	VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY
	VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP
	LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG
	KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG
	SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL
	PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3070	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGSGGSGGTLNIEDEHRLHETSKEPDVSLG
	STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE
	DIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVD
	DLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLY
	PLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKL
	TMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSS
	LLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPK
	RLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3075	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL

	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGSPAPGGTLNIEDEHRLHETSKEPDVSLG
	STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE
	LLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPK
	RLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3076	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGTLNIEDEHRLHETSKEPDVSLGSTW
	LSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIH
	PTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLL
	LAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLT
	KPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMG
	QPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQ
	EGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLS
	IIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3076	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH

	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGTLNIEDEHRLHETSKEPDVSLGSTW PTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLI LAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAE KPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMG QPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQ EGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLS IIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3079	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGSEAAAKGGTLNIEDEHRLHETSKE PDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLRE VNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLI LLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAE MAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLT KDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTW YTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3080	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER

	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKPAPGGSGGTLNIEDEHRLHETSKEPDVS LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
308 1	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKPAPGGSGGTLNIEDEHRLHETSKEPDVS LNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVK KPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEAL HRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFL GKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAG WPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSE GKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
308 3	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL

	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKVVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGSEAAAKGGTLNIEDEHRLHETSKEPDVS
	LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR
	VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILL
	VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP
	LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG
	KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG
	SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL
	PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3084	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKVVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPAPGGTLNIEDEHRLHETSKEPD
	VSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVN
	KRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILL
	QYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMA
	APLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKD
	AGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYT
	DGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKAL
	FLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3084	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA

	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPGGTLNIEDEHRLHETSKEPD
	VSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVN
	KRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILL
	QYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMA
	APLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKD
	AGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYT
	DGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKAL
	FLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3085	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPGGTLNIEDEHRLHETSKEPDVS
	LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR
	VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY
	VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP
	LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG
	KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG
	SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL
	PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE

3085	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFESPKKKAKVE
3086	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGEAAAKPAPGGTLNIEDEHRLHETSKEPDVS STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR DIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVD DLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLY PLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKL TMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSS

	LLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPK RLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3087	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSPAPGGTLNIEDEHRLHETSKEPDVSLGSTW LSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIH PTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLL LAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLT KPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMG QPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQ EGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLS IIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3087	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSPAPGGTLNIEDEHRLHETSKEPDVSLGSTW LSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIH PTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLL LAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLT KPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMG

	QPLVIILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQ
	EGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLS
	IIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3088	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSEAAAKPAPGGTLNIEDEHRLHETSKEPDVS
	LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR
	VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY
	VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP
	LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG
	KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG
	SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL
	PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3089	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGGSGGTLNIEDEHRLHETSKEPDVSLGSTW
	LSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIH
	PTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVVDDLL
	LAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLT

	KPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMG QPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQ EGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLS IIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
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309 1	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGSSEAAAKGGTLNIEDEHRLHETSKEPDVS LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY

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	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
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	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
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3093	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM
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	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSPAPGGGGGTLNIEDEHRLHETSKEPDVSLG
	STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE

	DIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVD
	DLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLY
	PLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKL
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	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
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	LVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEG
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	HCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFESPKKKAKVE
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	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
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	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
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	TKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTM
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	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV

	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGGSGGTLNIEDEHRLHETSKEPDVS LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3107	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGTLNIEDEHRLHETSKEPDVSLGSTW LSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIH PTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVVDDLL LAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLT KPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMG QPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQ EGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLS IIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3108	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK

	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSPAPGGTLNIEDEHRLHETSKEPDVS
	LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR
	VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY
	VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP
	LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG
	KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG
	SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL
	PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3108	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSPAPGGTLNIEDEHRLHETSKEPDVS
	LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR
	VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY
	VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP
	LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG
	KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG
	SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL
	PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3109	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD

	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGGGSEAAAKGGTLNIEDEHRLHETSKEPDVS
	LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR
	VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY
	VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP
	LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG
	KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG
	SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL
	PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3110	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGGGSEAAAKGGTLNIEDEHRLHETSKEPDVSL
	GSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRV
	EDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYV
	DDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPL
	YPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGK
	LTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGS
	SLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLP
	KRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3111	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK

	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGPAPGGSGGTLNIEDEHRLHETSKEPDVSLG
	STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE
	DIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVD
	DLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLY
	PLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKL
	TMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSS
	LLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPK
	RLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3111	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGPAPGGSGGTLNIEDEHRLHETSKEPDVSLG
	STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE
	DIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVD
	DLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLY
	PLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKL
	TMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSS
	LLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPK
	RLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3112	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL

	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGSSGGTLNIEDEHRLHETSKEPDVSLGSTW VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3113	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGSSGGTLNIEDEHRLHETSKEPDVSLGSTW LSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIH PTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLL LAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLT KPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMG QPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQ EGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLS IIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3114	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH

	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGGTLNIEDEHRLHETSKEPDVSLGSTWL SDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHP TVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLL AATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP PGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQ PLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQE GQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEIILALLKALFLPKRLSI IHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3116	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGSSGGTLNIEDEHRLHETSKEPDVS LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEIILALLKALFL PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3117	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER

	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSSPAPGGTLNIEDEHRLHETSKEPDVSLG STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE DIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY DLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3118	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSSPAPEAAAKGGTLNIEDEHRLHETSKEPDVS LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3120	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL

	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAAKEAAAKGGT
	LNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVD
	KPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEAL
	HRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFL
	GKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAG
	WPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR
	PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSE
	GKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
312 1	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAAKEAAAKGGT DLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLY PLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKL TMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSS LLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPK RLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
312 1	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA

	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGGGGSSGGTLNIEDEHRLHETSKEPDVSLG
	STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKREV
	DIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVD
	DLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLY
	PLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKL
	TMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSS
	LLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPK
	RLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3123	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGTLNIEDEHRLHETSKEPDVSLGSTWL
	SDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHP
	TVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLL
	AATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTK
	PGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQ
	PLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQE
	GQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSI
	IHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE

3124	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGSGGGGTLNIEDEHRLHETSKEPDVSLG STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE DIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVD DLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLRRFLGKAGFCRLFIPGFAEMAAPLY PLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKL TMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSS LLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPK RLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3125	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGSGGGGTLNIEDEHRLHETSKEPDVS LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLRRFLGKAGFCRLFIPGFAEMAAP LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG

	SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3126	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGGSGGSGGSGGTLNIEDEHRLHETSKE PDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLRE VNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLI LLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP MAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLT KDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTW YTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLK ALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3127	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSPAPEAAAKGGTLNIEDEHRLHETSKEPDVS LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG

	KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG
	SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL
	PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3130	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSPAPGGGGGTLNIEDEHRLHETSKEPDVSLG
	STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE
	DIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVD
	DLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLY
	RLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3130	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSPAPGGGGGTLNIEDEHRLHETSKEPDVSLG
	STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE
	DIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVD
	DLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLY

	PLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKL
	TMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSS
	LLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPK
	RLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3131	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSEAAAKGGSGGTLNIEDEHRLHETSKEPDVS
	LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR
	VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY
	VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP
	LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG
	KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG
	SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL
	PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3136	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGPAPEAAAKGGTLNIEDEHRLHETSKEPDVS
	LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR
	VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY

	VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP
	LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG
	KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG
	SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL
	PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFESPKKKAKVE
450 1	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGSGGSGGSGGVLNLEEEYRLHEKPVP SSIDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMSKEAREGIRPHIQRFLDLGVLVPCQSPWNTPLLPVKKPGTNDYRPVQDLREIN
450 2	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGSGGSGGSGGVLNLEEEYRLHEKPVP SSIDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMSKEAREGIRPHIQRFLDLGVLVPCQSPWNTPLLPVKKPGTNDYRPVQDLREIN

	KRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLAPFRALNPQVVLL QYVDDLLVAAPTYRDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLLKEGKRWLTPARKATVMKIPPPTTPRQVREFLGTAGFCRLWIPGFASLA APLYPLTKPSIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAVAAVALLLKD ADKLTLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVHRCSEILAEETGTRRDLKDQPLPGVPAWYTD GSSFIAEGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDINIYTDSRYAFATAHIHGAIYKQRGWLTSAGKDIKNKEEILALLEAIH LPKRVAIIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4503	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGSGGSGGSGGSGGSGGSGGTLNIED
4504	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGSGGSGGSGGSGGSGGSGGTLNIED

	EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTN
	DYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA
	DFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGF
	CRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCL
	RMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTD
	QPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIK
	NKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4505	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGSGSGSGGTLNIEDEHRLHETSKEPDVSLG
	STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE
	DIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVD
	DLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLY
	PLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKL
	TMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSS
	LLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPK
	RLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4506	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI

	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKGGTLNIEDEYRLHETSKE
	PDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLRE
	VNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLI
	LLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAE
	MAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLT
	KDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDLTDQPIPDADYTW
	YTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIKNKNEILALLK
	ALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAARE AAMKAVLETSTLLAGKRTADGSEFESPKKKAKVE
4507	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAAKGGTLNIED
	EYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTN
	DYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA
	GFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGTAGF
	CRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCL
	RMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMD
	QPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIK
	NKDEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAARE VATRETPETSTLLAGKRTADGSEFESPKKKAKVE
4508	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY

	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPGGTLNIEDEYRLHETSKEPDVSLGST WLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDI HPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDL LLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPL TKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTM GQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLL QEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRL SIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFESPKKKAKVE
4509	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPGGVLNLEEEYRLHEKPVPSS IDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMSKEARAEGIRPHIQRFLDLGVLVPCQSPWNTPLLPVKKPGTNDYRPVQDLREINKR VQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLAPFRALNPQVVLLQY VDDLLVAAPTYRDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLLKEGKRWLTPARKATVMKIPPPTTPRQVREFLGTAGFCRLWIPGFASLAAP LYPLTKPSIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAVAAVALLLKDAD KLTLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVHRCSEILAEETGTRRDLKDQPLPGVPAWYTDGS SFIAEGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDININIYTDSRYAFATAHIHGAIYKQRGWLTSAGKDIKNKEEILALLEAIHLP KRVAIIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKPAGKRTADGSEFESPKKKAKVE
4510	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV

	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPAPAPGGTLNIEDEYRLHETSKEPD VPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVN KRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILL QYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMA APLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKD AGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDLTDQPIPDADYTWYT DGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIKNKNEILALLKAL FLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4511	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSGGLGIEDEYRLHETSTEPDVSLGSTWL SDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHP TVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILL AATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTK PGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQ PLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQPIPDADHTWYTDGSSFLQE GQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEIILALLKALFLPKRLSI IHCLGHQKGDSAEARGNRLADQAARFAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4512	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK

	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGSSGGLGIEDEYRLHETSTEPDVSLGST
	WLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDI
	HPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDI
	LLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPL
	TKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTM
	GQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQPIPDADHTWYTDGSSFL
	QEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALFLPKRL
	SIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4513	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVVTLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGSSGGTLNIEDEHRLHETSKEPDVSLGSTW
	LSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIH
	PTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLL
	LAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLT
	KPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMG
	QPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQ
	EGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEIILALLKALFLPKRLS
	IIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4514	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD

	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGSSGGTLNIEDEHRLHETSKEPDVSLGSTW LSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIH PTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLL LAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLT KPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMG QPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQ EGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLS IIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4515	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK	
4516	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK

	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPEAAAKGGLGIEDEYRLHETSTEPDVSLGST
	WLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDI
	HPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDI
	LLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPL
	TKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTM
	GQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQPIPDADHTWYTDGSSF
	QIIHCLGHQKGDSAEARGNRLADQAARGAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
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	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
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	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
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	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
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	TWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVED
	IHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDD
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	LTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLT
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	LSIIHCLGHQKGDSAEARGNRLADQAARGAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
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	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
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	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
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	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGGGSGGTLNIEDEYRLHETSKEPDVPLG
	STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE
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	RLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
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	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
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	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
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	LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR
	VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY
	VDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP
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	KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDLTDQPIPDADYTWYTDG
	SSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIKNKNEILALLKALFL
	PKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4520	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH

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	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
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	STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEAKLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE
	DIHPTVPNPYNLLSGLPPSHRWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVD
	DILLAATSELDCQQGTRALLLTLGNLGYRASAKKAQLCQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLY
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	TMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQPIPDADHTWYTDGSS
	FLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALFLPK
	RLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
452 1	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGGGSGSGGTLNIEDEHRLHETSKEPDVSLG
	STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE
	DIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVD
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	LLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPK
	RLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
452 2	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
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	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
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452 3	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSEAAAKGGSGSSGGTLNIEDEYRLHETSKEPDVP LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY VDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAP LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDLTDQPIPDADYTWYTDG SSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIKNKNEILALLKALFL PKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFESPKKKAKVE
452 4	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL

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	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
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	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGSSGGSGGTLNIEDEYRLHETSKEPDVP
	LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR
	VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY
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	PKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFESPKKKAKVE
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	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
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	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSPAPGSSGGTLNIEDEYRLHETSKEPDVPLG
	STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE
	DIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVD
	DLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLY
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	RLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFESPKKKAKVE
4526	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA

	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSPAPGGSGGLLGRDLLTKLKAQIQFSTEGPQ VTWEDRPAMCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPMVWAEKAGMGLANQVPPVVVELKSDASPVAVRQYPMSKEAREGIRPHIQRFLDLGILVPCQS PWNTPLLPVKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFK NSPTLFNEALHRDLASFRALNPQVVMLQYVDDLLVAAPTYRDCKEGTRRLLQELSKLGYRVSAKKAQLCREEVTYLGYLLKGGKRWLTPARKATVMKIPTP TTPRQVREFLGTAGFCRLWIPGFASLAAPLYPLTRPKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFALYVDEKEGVARGVLTQTLGPWRRPVAYL SKKLDPVASGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAILNPATLLPVESDDTPIHICS EILAEETGTRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALTQALRLAEGKSINIYTDSRYAFATAHVHGAIY KQRGWLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTETTKNAGKRTADGSEFEKRTADGSEFESPKKKK AKVE
452 7	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKPAPGGSGGTLNIEDEYRLHETSKEPDVP LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY VDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDLTDQPIPDADYTWYTDG SSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIKNKNEILALLKALFL PKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFESPKKKAKVE

4528	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV PGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEAKLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHRWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY VDDILLAATSELDCQQGTRALLLTLGNLGYRASAKKAQLCQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAP LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLRKDAG KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQPIPDADHTWYTDG SSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALFL PKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLAGKRTADGSEFESPKKKAKVE
4529	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPEAAAKGGSGGTLNLEDEYRLYETSAEPEVS RLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPEAAAKGGSGGTLNLEDEYRLYETSAEPEVS WLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDI HPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDL LLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPL TKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTL GQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLAIEETGVRKDLTDIPLTGEVLTWFTDGSSYV

	VEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRL AIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFESPKKKAKVE
4530	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGEAAAKGSSGGTLNIEDEHRLHETSKEPDVS PSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMSKEAREGIRPHIQRFLDLGVLVPCQSPWNTPLLPVKKPGTNDYRPVVQDLREINKRVQ DIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLAPFRALNPQVVLLQYVD DLLVAAPTYRDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLLKEGKRWLTPARKATVMKIPPPTTPRQVREFLGKAGFCRLFIPGFASLAAPLY PLTKPSIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAVAAVALLLKDADKL
4531	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGEAAAKGSSGGTLNIEDEHRLHETSKEPDVS PSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMSKEARGGIRPHIQRFLDLGVLVPCQSPWNTPLLPVKKPGTNDYRPVVQDLREINKRVQ DIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLAPFRALNPQVVLLQYVD DLLVAAPTYRDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLLKEGKRWLTPARKATVMKIPPPTTPRQVREFLGKAGFCRLFIPGFASLAAPLY PLTKPSIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAVAAVALLLKDADKL

	TLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVHRCSEILAEETGTRRDLKDQPLPGVPAWYTDGSSF IAEGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDININYTDSRYAFATAHIHGAIYKQRGWLTSAGKDIKNKEEILALLEAIHLPKR VAIIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4532	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGGGPAPGGTLQLDDEYRLYSPLVKPDQNIQ FWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQD IHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDD LLLAGATKQDCLEGTKALLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYP LTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLT LGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSY VVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSININIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKR LAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4533	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGSSGGGGTLNLEDEYRLYETSAEPEVSPG STWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEAKLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVE DIHPTVPNPYNLLSGLPPSHRWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVD DILLAATSELDCQQGTRALLLTLGNLGYRASAKKAQLCQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLY

	PLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLRKDAGKL TMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQPIPDADHTWYTDGSS FLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALFLPK RLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4534	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGPAPEAAAKGGTLNIEDEHRLHETSKEPDVS LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAP LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4535	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGEAAAKGGGPAPGGTLNIEDEHRLHETSKEPDVS LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKR VEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQY

	VDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAP
	LYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG
	KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDG
	SSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFL
	PKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFESPKKKAKVE
4536	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPEAAAKGGGGGLLGRDLLTKLKAQIQFSTEG
	PQVTWEDRPAMCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPMVWAEKAGMGLANQVPPVVVELKSDASPVAVRQYPMSKEAREGIRPHIQRFLDLGILVPC
4537	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM
	AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT
	YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA
	AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL
	NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER
	MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
	DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL
	IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK
	EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD
	NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
	KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
	SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPEAAAKGGGGGLLGRDLLTKLKAQIQFSTEG
	PQVTWEDRPAMCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPMVWAEKAGMGLANQVPPVVVELKSDASPVAVRQYPMSKEAREGIRPHIQRFLDLGILVPC

	QSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQG FKNSPTLFNEALHRDLASFRALNPQVVMLQYVDDLLVAAPTYRDCKEGTRRLLQELSKLGYRVSAKKAQLCREEVTYLGYLLKGGKRWLTPARKATVMKIP TPTTPRQVREFLGTAGFCRLWIPGFASLAAPLYPLTRPKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFALYVDEKEGVARGVLTQTLGPWRRPVA YLSKKLDPVASGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAILNPATLLPVESDDTPIHI CSEILAEETGTRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALTQALRLAEGKSINIYTDSRYAFATAHVHGA IYKQRGWLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTETTKNAGKRTADGSEFEKRTADGSEFESPK KKAKVE
4538	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
4539	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHADAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI

	REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSPAPEAAAKGGTAPLEEEYRLFLEAPIQNVT LLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGTSEYRMVQDLREVNKR VETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEEGESGQLTWTRLPQGFKNSPTLFNEALNRDLQGFRLDHPSVSLLQY VDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAILQIPVPKTKRQVREFLGKIGYCRLFIPGFAELAQP LYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSKRLDPVAAGWPRCLRAIAAAALLTREA SKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTSTRPDLTDQPLAQAEATLFT DGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWLTAGGKAIKNAPEIIALLTAV WLPKRVAVMHCKGHQKDDAPTSTGNRRADEVARE VAIRPLSTQATISAGKRTADGSEFESPKKKAKVE
4540	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKALEAEAAAKEAA AKEAAAKEAAAKAGGTLNIEDEYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGI LVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTR LPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV MGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWR RPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEG LQHDCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATA HIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEF ESPKKKAKVE
4541	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRYTRRKNRICYLQEIFSNEM AKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQT YNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLA AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKL NREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIER MTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQL IHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILK EHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFD NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV

QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKY
SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPI
REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKALEAEAAAKEAA
AKEAAAKEAAAKAGGIPWLMKKPLQLTTLVPLQEYEERLLKQTMLTGSYKEKLQSLFLKYDALWQHWENQVGHRRIKPHHIATGTVNPRPQKQYPINPKAK
ASIQTVINDLLKQGVLIQQNSIMNTPVYPVPKPDGKWRMVLDYREVNKTIPLIAAQNQHSAGILSSIFRGKYKTTLDLSNGFWAHSITPESYWLTAFTWLG
QQYCWTRLPQGFLNSPALFNADVVDLLKEVPNVQVYVDDIYISHDDPREHLEQLEKVFSLLLNAGYVVSLKKSEIAQHEVEFLGFNITKEGRGLTETFKQK
LLNITPPRDLKQLQSILGKLNFARNFIPNFSELVKPLYNIIATAPGKYITWTTDNSQQLQNIISMLNSAENLEERNPEVRLIMKVNTSPSAGYIRFYNEFA
KRPIMYLNYVVYTKAEVKFTNTEKLLTTIHKGLIKALDLGMGQEILVYSPIVSMTKIQKTPLPERKALPIRWITWMSYLEDPRIQFHYDKTLPELQQVPTVT
DDIIAKIKHPSEFSMVFYTDGSAIKHPNVVNKSHNAGMGIAQVQFKPEFTVINTWSIPLGDHTAQLAEVAAVEFACKKALKIDGPVLIVTDSFYVAESVNKE
LPYWQSNGFFNNKKKPLKHVSKWKSIADCIQLKPDIIIIHEKGHQPTASTFHTEGNNLADKLATQGSYVVNAGKRTADGSEFEKRTADGSEFESPKKKAKV
E

Localization sequences for gene modifying systems

In certain embodiments, a gene editor system RNA further comprises an intracellular localization sequence, e.g., a nuclear localization sequence (NLS). In some embodiments, a gene modifying polypeptide comprises an NLS as comprised in SEQ ID NO: 4000 and/or SEQ ID NO: 4001, or an NLS having an amino acid sequence having at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto.

The nuclear localization sequence may be an RNA sequence that promotes the import of the RNA into the nucleus. In certain embodiments the nuclear localization signal is located on the template RNA. In certain embodiments, the gene modifying polypeptide is encoded on a first RNA, and the template RNA is a second, separate, RNA, and the nuclear localization signal is located on the template RNA and not on an RNA encoding the gene modifying polypeptide. While not wishing to be bound by theory, in some embodiments, the RNA encoding the gene modifying polypeptide is targeted primarily to the cytoplasm to promote its translation, while the template RNA is targeted primarily to the nucleus to promote insertion into the genome. In some embodiments the nuclear localization signal is at the 3′ end, 5′ end, or in an internal region of the template RNA. In some embodiments the nuclear localization signal is 3′ of the heterologous sequence (e.g., is directly 3′ of the heterologous sequence) or is 5′ of the heterologous sequence (e.g., is directly 5′ of the heterologous sequence). In some embodiments the nuclear localization signal is placed outside of the 5′ UTR or outside of the 3′ UTR of the template RNA. In some embodiments the nuclear localization signal is placed between the 5′ UTR and the 3′ UTR, wherein optionally the nuclear localization signal is not transcribed with the transgene (e.g., the nuclear localization signal is an anti-sense orientation or is downstream of a transcriptional termination signal or polyadenylation signal). In some embodiments the nuclear localization sequence is situated inside of an intron. In some embodiments a plurality of the same or different nuclear localization signals are in the RNA, e.g., in the template RNA. In some embodiments the nuclear localization signal is less than 5, 10, 25, 50, 75, 100, 150, 200, 250, 300, 350, 400, 450, 500, 600, 700, 800, 900 or 1000 bp in length. Various RNA nuclear localization sequences can be used. For example, Lubelsky and Ulitsky, *Nature* 555 (107-111), 2018 describe RNA sequences which drive RNA localization into the nucleus. In some embodiments, the nuclear localization signal is a SINE-derived nuclear RNA localization (SIRLOIN) signal. In some embodiments the nuclear localization signal binds a nuclear-enriched protein. In some

embodiments the nuclear localization signal binds the HNRNPK protein. In some embodiments the nuclear localization signal is rich in pyrimidines, e.g., is a C/T rich, C/U rich, C rich, T rich, or U rich region. In some embodiments the nuclear localization signal is derived from a long non-coding RNA. In some embodiments the nuclear localization signal is derived from MALAT1 long non-coding RNA or is the 600 nucleotide M region of MALAT1 (described in Miyagawa et al., *RNA* 18, (738-751), 2012). In some embodiments the nuclear localization signal is derived from BORG long non-coding RNA or is a AGCCC motif (described in Zhang et al., *Molecular and Cellular Biology* 34, 2318-2329 (2014). In some embodiments the nuclear localization sequence is described in Shukla et al., *The EMBO Journal* e98452 (2018). In some embodiments the nuclear localization signal is derived from a retrovirus.

In some embodiments, a polypeptide described herein comprises one or more (e.g., 2, 3, 4, 5) nuclear targeting sequences, for example a nuclear localization sequence (NLS). In some embodiments, the NLS is a bipartite NLS. In some embodiments, an NLS facilitates the import of a protein comprising an NLS into the cell nucleus. In some embodiments, the NLS is fused to the N-terminus of a gene modifying polypeptide as described herein. In some embodiments, the NLS is fused to the C-terminus of the gene modifying polypeptide. In some embodiments, the NLS is fused to the N-terminus or the C-terminus of a Cas domain. In some embodiments, a linker sequence is disposed between the NLS and the neighboring domain of the gene modifying polypeptide.

In some embodiments, an NLS comprises the amino acid sequence MDSLLMNRRKFLYQFKNVRWAKGRRETYLC (SEQ ID NO: 5009), PKKRKVEGADKRTADGSEFESPKKKRKV(SEQ ID NO: 5010), RKSGKIAAIWKRPRKPKKKRKV (SEQ ID NO: 5011) KRTADGSEFESPKKKRKV(SEQ ID NO: 5012), KKTELQTTNAENKTKKL (SEQ ID NO: 5013), or KRGINDRNFWRGENGRKTR (SEQ ID NO: 5014), KRPAATKKAGQAKKKK (SEQ ID NO: 5015), PAAKRVKLD (SEQ ID NO: 4644), KRTADGSEFEKRTADGSEFESPKKKAKVE (SEQ ID NO: 4649), KRTADGSEFE (SEQ ID NO: 4650), KRTADGSEFESPKKKAKVE (SEQ ID NO: 4651), AGKRTADGSEFEKRTADGSEFESPKKKAKVE (SEQ ID NO: 4001), or a functional fragment or variant thereof. Exemplary NLS sequences are also described in PCT/EP2000/011690, the contents of which are incorporated herein by reference for their disclosure of exemplary nuclear localization sequences. In some embodiments, an NLS

comprises an amino acid sequence as disclosed in Table 11. An NLS of this table may be utilized with one or more copies in a polypeptide in one or more locations in a polypeptide, e.g., 1, 2, 3 or more copies of an NLS in an N-terminal domain, between peptide domains, in a C-terminal domain, or in a combination of locations, in order to improve subcellular localization to the nucleus. Multiple unique sequences may be used within a single polypeptide. Sequences may be naturally monopartite or bipartite, e.g., having one or two stretches of basic amino acids, or may be used as chimeric bipartite sequences. Sequence references correspond to UniProt accession numbers, except where indicated as SeqNLS for sequences mined using a subcellular localization prediction algorithm (Lin et al BMC Bioinformat 13:157 (2012), incorporated herein by reference in its entirety).

Table 11 Exemplary nuclear localization signals for use in gene modifying systems

Sequence	Sequence References	SEQ ID No.
AHFKISGEKRPSTDPGKKAK NPKKKKKKDP	Q76IQ7	5223
AHRAKKMSKTHA	P21827	5224
ASPEYVNLPINGNG	SeqNLS	5225
CTKRPRW	O88622, Q86W56, Q9QYM2, O02776	5226
DKAKRVSRNKSEKKRR	O15516, Q5RAK8, Q91YB2, Q91YB0, Q8QGQ6, O08785, Q9WVS9, Q6YGZ4	5227
EELRLKEELLKGIYA	Q9QY16, Q9UHL0, Q2TBP1, Q9QY15	5228
EEQLRRRKNSRLNNTG	G5EFF5	5229
EVLKVIRTGKRKKKAWKR MVTKVC	SeqNLS	5230
HHHHHHHHHHHHQPH	Q63934, G3V7L5, Q12837	5231
HKKKHPDASVNFSEFSK	P10103, Q4R844, P12682, B0CM99, A9RA84, Q6YKA4, P09429, P63159, Q08IE6, P63158, Q9YH06, B1MTB0	5232
HKRTKK	Q2R2D5	5233
IINGRKLKLKKSRRRSSQTS NNSFTSRRS	SeqNLS	5234
KAEQERRK	Q8LH59	5235

KEKRKRREELFIEQKKRK	SeqNLS	5236
KKGKDEWFSRGKKP	P30999	5237
KKGPSVQKRKKT	Q6ZN17	5238
KKKTVINDLLHYKKEK	SeqNLS, P32354	5239
KKNGGKGKNKPSAKIKK	SeqNLS	5240
KKPKWDDFKKKKK	Q15397, Q8BKS9, Q562C7	5241
KKRKKD	SeqNLS, Q91Z62, Q1A730, Q969P5, Q2KHT6, Q9CPU7	5242
KKRRKRRRK	SeqNLS	5243
KKRRRRARK	Q9UMS6, D4A702, Q91YE8	5244
KKSKRGR	Q9UBS0	5245
KKSRKRGS	B4FG96	5246
KKSTALSRELGKIMRRR	SeqNLS, P32354	5247
KKSYQDPEIIAHSRPRK	Q9U7C9	5248
KKTGKNRKLKSKRVKTR	Q9Z301, O54943, Q8K3T2	5249
KKVSIAGQSGKLWRWKR	Q6YUL8	5250
KKYENVVIKRSPRKRGRPRK	SeqNLS	5251
KNKKRK	SeqNLS	5252
KPKKKR	SeqNLS	5253
KRAMKDDSHGNSTSPKRRK	Q0E671	5254
KRANSNLVAAYEKAKKK	P23508	5255
KRASEDTTSGSPPKKSSAGPKR	Q9BZZ5, Q5R644	5256
KRFKRRWMVRKMKTKK	SeqNLS	5257
KRGLNSSFETSPKKVK	Q8IV63	5258
KRGNSSIGPNDLSKRKQRKK	SeqNLS	5259
KRIHSVSLSQSQIDPSKKVKRAK	SeqNLS	5260
KRKGKLKNKGSKRKK	O15381	5261
KRRRRRRREKRKR	Q96GM8	5262

KRSNDRTYSPEEEKQRRA	Q91ZF2	5263
KRTVATNGDASGAHRAKKMSK	SeqNLS	5264
KRVYNKGEDEQEHLPKGKKR	SeqNLS	5265
KSGKAPRRRAVSMDNSNK	Q9WVH4, O43524	5266
KVNFLDMSLDDIIIYKELE	Q9P127	5267
KVQHRIAKKTTRRRR	Q9DXE6	5268
LSPSLSPL	Q9Y261, P32182, P35583	5269
MDSLLMNRRKFLYQFKNVRWAKGRRETYLC	Q9GZX7	5270
MPQNEYIELHRKRYGYRLDYHEKKRKKESREAHERSKKAKKMIGLKAKLYHK	SeqNLS	5271
MVQLRPRASR	SeqNLS	5272
NNKLLAKRRKGGASPKDDPMDDIK	Q965G5	5273
NYKRPMDGTYGPPAKRHEGE	O14497, A2BH40	5274
PDTKRAKLDSSETTMVKKK	SeqNLS	5275
PEKRTKI	SeqNLS	5276
PGGRGKKK	Q719N1, Q9UBP0, A2VDN5	5277
PGKMDKGEHRQERRDRPY	Q01844, Q61545	5278
PKKGDKYDKTD	Q45FA5	5279
PKKKSRK	O35914, Q01954	5280
PKKNKPE	Q22663	5281
PKKRAKV	P04295, P89438	5282
PKPKKLKVE	P55263, P55262, P55264, Q64640	5283
PKRGRGR	Q9FYS5, Q43386	5284
PKRRLVDDA	P0C797	5285
PKRRRTY	SeqNLS	5286
PLFKRR	A8X6H4, Q9TXJ0	5287

PLRKAKR	Q86WB0, Q5R8V9	5288
PPAKRKCIF	Q6AZ28, O75928, Q8C5D8	5289
PPARRRRL	Q8NAG6	5290
PPKKKRKV	Q3L6L5, P03070, P14999, P03071	5291
PPNKRMKVKH	Q8BN78	5292
PPRIYPQLPSAPT	P0C799	5293
PQRSPFPKSSVKR	SeqNLS	5294
PRPRKVPR	P0C799	5295
PRRRVQRKR	SeqNLS, Q5R448, Q5TAQ9	5296
PRRVRLK	Q58DJ0, P56477, Q13568	5297
PSRKRPR	Q62315, Q5F363, Q92833	5298
PSSKKRKV	SeqNLS	5299
PTKKRVK	P07664	5300
QRPGPYDRP	SeqNLS	5301
RGKGGKGLGKGGAKRHRK	SeqNLS	5302
RKAGKGGGGHKTTKKRSA KDEKVP	B4FG96	5303
RKIKLKRAK	A1L3G9	5304
RKIKRKRAK	B9X187	5305
RKKEAPGPREELRSRGR	O35126, P54258, Q5IS70, P54259	5306
RKKRKGK	SeqNLS, Q29243, Q62165, Q28685, O18738, Q9TSZ6, Q14118	5307
RKKRRQRRR	P04326, P69697, P69698, P05907, P20879, P04613, P19553, P0C1J9, P20893, P12506, P04612, Q73370, P0C1K0, P05906, P35965, P04609, P04610, P04614, P04608, P05905	5308
RKKSIPLSIKNLKRKHKRKK NKITR	Q9C0C9	5309
RKLVKPKNTKMKTKLRTNP Y	Q14190	5310
RKRLILSDKGQLDWKK	SeqNLS, Q91Z62, Q1A730, Q2KHT6, Q9CPU7	5311

RKRLKSK	Q13309	5312
RKRRVRDNM	Q8QPH4, Q809M7, A8C8X1, Q2VNC5, Q38SQ0, O89749, Q6DNQ9, Q809L9, Q0A429, Q20NV3, P16509, P16505, Q6DNQ5, P16506, Q6XT06, P26118, Q2ICQ2, Q2RCG8, Q0A2D0, Q0A2H9, Q9IQ46, Q809M3, Q6J847, Q6J856, B4URE4, A4GCM7, Q0A440, P26120, P16511,	5313
RKRSPKDKKEKDLDGAGKR RKT	Q7RTP6	5314
RKRTPRVDGQTGENDMNK RRRK	O94851	5315
RLPVRRRRRR	P04499, P12541, P03269, P48313, P03270	5316
RLRFRKPKSK	P69469	5317
RQQRKR	Q14980	5318
RRDLNSSFETSPKKVK	Q8K3G5	5319
RRDRAKLR	Q9SLB8	5320
RRGDGRRR	Q80WE1, Q5R9B4, Q06787, P35922	5321
RRGRKRKAEKQ	Q812D1, Q5XXA9, Q99JF8, Q8MJG1, Q66T72, O75475	5322
RRKKRR	Q0VD86, Q58DS6, Q5R6G2, Q9ERI5, Q6AYK2, Q6NYC1	5323
RRKRSKSEDMDSVESKRRR	Q7TT18	5324
RRKRSR	Q99PU7, D3ZHS6, Q92560, A2VDM8	5325
RRPKGKTLQKRKPK	Q6ZN17	5326
RRRGFERFGPDNMGRKRK	Q63014, Q9DBR0	5327
RRRGKNKVAAQNCRK	SeqNLS	5328
RRRKRR	Q5FVH8, Q6MZT1, Q08DH5, Q8BQP9	5329
RRRQKQKGGASRRR	SeqNLS	5330
RRRREGPRARRRR	P08313, P10231	5331
RRTIRLKLVYDKCDRSCKIQ KKNRNKCQYCRFHKCLSVG MSHNAIRFGRMPRSEKAKL KAE	SeqNLS	5332

RRVPQRKEVSRCRKCRK	Q5RJN4, Q32L09, Q8CAK3, Q9NUL5	5333
RVGGRRQAVECIEDLLNEP GQPLDLSCKRPRP	P03255	5334
RVVKLRIAP	P52639, Q8JMN0	5335
RVVRRR	P70278	5336
SKRKTKISRKTR	Q5RAY1, O00443	5337
SYVKTVPNRTRTYIKL	P21935	5338
TGKNEAKKRKIA	P52739, Q8K3J5, Q5RAU9	5339
TLSPASSPSSVSCPVIPASTD ESPGSALNI	SeqNLS	5340
VSKKQRTGKKIH	P52739, Q8K3J5, Q5RAU9	5341
SPKKKRKVE		5342
KRTAD GSEFE SPKKKRKVE		5343
PAAKRVKLD		5344
PKKKRKV		5345
MDSLLMNRRKFLYQFKNVR WAKGRRETYLC		5346
SPKKKRKVEAS		5347
MAPKKKRKVGIHRGVP		5348
KRTADGSEFEKRTADGSEFE SPKKKAKVE		5349
KRTADGSEFE		5350
KRTADGSEFESPKKKAKVE		5351
AGKRTADGSEFEKRTADGS EFESPKKKAKVE		4001

In some embodiments, the NLS is a bipartite NLS. A bipartite NLS typically comprises two basic amino acid clusters separated by a spacer sequence (which may be, e.g., about 10 amino acids in length). A monopartite NLS typically lacks a spacer. An example of a bipartite NLS is the nucleoplasmin NLS, having the sequence KR[PAATKKAGQA]KKKK (SEQ ID NO: 5015), wherein the spacer is bracketed. Another exemplary bipartite NLS has the sequence PKKKRKVEGADKRTADGSEFESPKKKRKV (SEQ ID NO: 5016). Exemplary NLSs are

described in International Application WO2020051561, which is herein incorporated by reference in its entirety, including for its disclosures regarding nuclear localization sequences.

In certain embodiments, a gene editor system polypeptide (e.g., a gene modifying polypeptide as described herein) further comprises an intracellular localization sequence, e.g., a nuclear localization sequence and/or a nucleolar localization sequence. The nuclear localization sequence and/or nucleolar localization sequence may be amino acid sequences that promote the import of the protein into the nucleus and/or nucleolus, where it can promote integration of heterologous sequence into the genome. In certain embodiments, a gene editor system polypeptide (e.g., (e.g., a gene modifying polypeptide as described herein) further comprises a nucleolar localization sequence. In certain embodiments, the gene modifying polypeptide is encoded on a first RNA, and the template RNA is a second, separate, RNA, and the nucleolar localization signal is encoded on the RNA encoding the gene modifying polypeptide and not on the template RNA. In some embodiments, the nucleolar localization signal is located at the N-terminus, C-terminus, or in an internal region of the polypeptide. In some embodiments, a plurality of the same or different nucleolar localization signals are used. In some embodiments, the nuclear localization signal is less than 5, 10, 25, 50, 75, or 100 amino acids in length. Various polypeptide nucleolar localization signals can be used. For example, Yang et al., *Journal of Biomedical Science* 22, 33 (2015), describe a nuclear localization signal that also functions as a nucleolar localization signal. In some embodiments, the nucleolar localization signal may also be a nuclear localization signal. In some embodiments, the nucleolar localization signal may overlap with a nuclear localization signal. In some embodiments, the nucleolar localization signal may comprise a stretch of basic residues. In some embodiments, the nucleolar localization signal may be rich in arginine and lysine residues. In some embodiments, the nucleolar localization signal may be derived from a protein that is enriched in the nucleolus. In some embodiments, the nucleolar localization signal may be derived from a protein enriched at ribosomal RNA loci. In some embodiments, the nucleolar localization signal may be derived from a protein that binds rRNA. In some embodiments, the nucleolar localization signal may be derived from MSP58. In some embodiments, the nucleolar localization signal may be a monopartite motif. In some embodiments, the nucleolar localization signal may be a bipartite motif. In some embodiments, the nucleolar localization signal may consist of a multiple monopartite or bipartite motifs. In some embodiments, the nucleolar localization signal may consist of a mix of monopartite and

bipartite motifs. In some embodiments, the nucleolar localization signal may be a dual bipartite motif. In some embodiments, the nucleolar localization motif may be a KRASSQALGTIPKRRSSSRFIKRKK (SEQ ID NO: 5017). In some embodiments, the nucleolar localization signal may be derived from nuclear factor-κB-inducing kinase. In some embodiments, the nucleolar localization signal may be an RKKRKKK motif (SEQ ID NO: 5018) (described in Birbach et al., Journal of Cell Science, 117 (3615-3624), 2004).

Evolved Variants of Gene Modifying Polypeptides and Systems

In some embodiments, the invention provides evolved variants of gene modifying polypeptides as described herein. Evolved variants can, in some embodiments, be produced by mutagenizing a reference gene modifying polypeptide, or one of the fragments or domains comprised therein. In some embodiments, one or more of the domains (e.g., the reverse transcriptase domain) is evolved. One or more of such evolved variant domains can, in some embodiments, be evolved alone or together with other domains. An evolved variant domain or domains may, in some embodiments, be combined with unevolved cognate component(s) or evolved variants of the cognate component(s), e.g., which may have been evolved in either a parallel or serial manner.

In some embodiments, the process of mutagenizing a reference gene modifying polypeptide, or fragment or domain thereof, comprises mutagenizing the reference gene modifying polypeptide or fragment or domain thereof. In embodiments, the mutagenesis comprises a continuous evolution method (e.g., PACE) or non-continuous evolution method (e.g., PANCE), e.g., as described herein. In some embodiments, the evolved gene modifying polypeptide, or a fragment or domain thereof, comprises one or more amino acid variations introduced into its amino acid sequence relative to the amino acid sequence of the reference gene modifying polypeptide, or fragment or domain thereof. In embodiments, amino acid sequence variations may include one or more mutated residues (e.g., conservative substitutions, non-conservative substitutions, or a combination thereof) within the amino acid sequence of a reference gene modifying polypeptide, e.g., as a result of a change in the nucleotide sequence encoding the gene modifying polypeptide that results in, e.g., a change in the codon at any particular position in the coding sequence, the deletion of one or more amino acids (e.g., a truncated protein), the insertion of one or more amino acids, or any combination of the foregoing. The evolved variant gene modifying polypeptide may include variants in one or more

components or domains of the gene modifying polypeptide (e.g., variants introduced into a reverse transcriptase domain).

In some aspects, the disclosure provides gene modifying polypeptides, systems, kits, and methods using or comprising an evolved variant of a gene modifying polypeptide, e.g., employs an evolved variant of a gene modifying polypeptide or a gene modifying polypeptide produced or producible by PACE or PANCE. In embodiments, the unevolved reference gene modifying polypeptide is a gene modifying polypeptide as disclosed herein.

The term "phage-assisted continuous evolution (PACE),"as used herein, generally refers to continuous evolution that employs phage as viral vectors. Examples of PACE technology have been described, for example, in International PCT Application No. PCT/US 2009/056194, filed September 8, 2009, published as WO 2010/028347 on March 11, 2010; International PCT Application, PCT/US2011/066747, filed December 22, 2011, published as WO 2012/088381 on June 28, 2012; U.S. Patent No. 9,023,594, issued May 5, 2015; U.S. Patent No. 9,771,574, issued September 26, 2017; U.S. Patent No. 9,394,537, issued July 19, 2016; International PCT Application, PCT/US2015/012022, filed January 20, 2015, published as WO 2015/134121 on September 11, 2015; U.S. Patent No. 10,179,911, issued January 15, 2019; and International PCT Application, PCT/US2016/027795, filed April 15, 2016, published as WO 2016/168631 on October 20, 2016, the entire contents of each of which are incorporated herein by reference.

The term "phage-assisted non-continuous evolution (PANCE)," as used herein, generally refers to non-continuous evolution that employs phage as viral vectors. Examples of PANCE technology have been described, for example, in Suzuki T. et al, Crystal structures reveal an elusive functional domain of pyrrolysyl-tRNA synthetase, Nat Chem Biol. 13(12): 1261-1266 (2017), incorporated herein by reference in its entirety. Briefly, PANCE is a technique for rapid *in vivo* directed evolution using serial flask transfers of evolving selection phage (SP), which contain a gene of interest to be evolved, across fresh host cells (e.g., E. coli cells). Genes inside the host cell may be held constant while genes contained in the SP continuously evolve. Following phage growth, an aliquot of infected cells may be used to transfect a subsequent flask containing host E. coli. This process can be repeated and/or continued until the desired phenotype is evolved, e.g., for as many transfers as desired.

Methods of applying PACE and PANCE to gene modifying polypeptides may be readily appreciated by the skilled artisan by reference to, *inter alia*, the foregoing references. Additional

exemplary methods for directing continuous evolution of genome-modifying proteins or systems, e.g., in a population of host cells, e.g., using phage particles, can be applied to generate evolved variants of gene modifying polypeptides, or fragments or subdomains thereof. Non-limiting examples of such methods are described in International PCT Application, PCT/US2009/056194, filed September 8, 2009, published as WO 2010/028347 on March 11, 2010; International PCT Application, PCT/US2011/066747, filed December 22, 2011, published as WO 2012/088381 on June 28, 2012; U.S. Patent No. 9,023,594, issued May 5, 2015; U.S. Patent No. 9,771,574, issued September 26, 2017; U.S. Patent No. 9,394,537, issued July 19, 2016; International PCT Application, PCT/US2015/012022, filed January 20, 2015, published as WO 2015/134121 on September 11, 2015; U.S. Patent No. 10,179,911, issued January 15, 2019; International Application No. PCT/US2019/37216, filed June 14, 2019, International Patent Publication WO 2019/023680, published January 31, 2019, International PCT Application, PCT/US2016/027795, filed April 15, 2016, published as WO 2016/168631 on October 20, 2016, and International Patent Publication No. PCT/US2019/47996, filed August 23, 2019, each of which is incorporated herein by reference in its entirety.

In some non-limiting illustrative embodiments, a method of evolution of a evolved variant gene modifying polypeptide, of a fragment or domain thereof, comprises: (a) contacting a population of host cells with a population of viral vectors comprising the gene of interest (the starting gene modifying polypeptide or fragment or domain thereof), wherein: (1) the host cell is amenable to infection by the viral vector; (2) the host cell expresses viral genes required for the generation of viral particles; (3) the expression of at least one viral gene required for the production of an infectious viral particle is dependent on a function of the gene of interest; and/or (4) the viral vector allows for expression of the protein in the host cell, and can be replicated and packaged into a viral particle by the host cell. In some embodiments, the method comprises (b) contacting the host cells with a mutagen, using host cells with mutations that elevate mutation rate (e.g., either by carrying a mutation plasmid or some genome modification—e.g., proofing-impaired DNA polymerase, SOS genes, such as UmuC, UmuD', and/or RecA, which mutations, if plasmid-bound, may be under control of an inducible promoter), or a combination thereof. In some embodiments, the method comprises (c) incubating the population of host cells under conditions allowing for viral replication and the production of viral particles, wherein host cells are removed from the host cell population, and fresh, uninfected host cells are introduced into the

population of host cells, thus replenishing the population of host cells and creating a flow of host cells. In some embodiments, the cells are incubated under conditions allowing for the gene of interest to acquire a mutation. In some embodiments, the method further comprises (d) isolating a mutated version of the viral vector, encoding an evolved gene product (e.g., an evolved variant gene modifying polypeptide, or fragment or domain thereof), from the population of host cells.

The skilled artisan will appreciate a variety of features employable within the above-described framework. For example, in some embodiments, the viral vector or the phage is a filamentous phage, for example, an M13 phage, e.g., an M13 selection phage. In certain embodiments, the gene required for the production of infectious viral particles is the M13 gene III (gIII). In embodiments, the phage may lack a functional gIII, but otherwise comprise gI, gII, gIV, gV, gVI, gVII, gVIII, gIX, and a gX. In some embodiments, the generation of infectious VSV particles involves the envelope protein VSV-G. Various embodiments can use different retroviral vectors, for example, Murine Leukemia Virus vectors, or Lentiviral vectors. In embodiments, the retroviral vectors can efficiently be packaged with VSV-G envelope protein, e.g., as a substitute for the native envelope protein of the virus.

In some embodiments, host cells are incubated according to a suitable number of viral life cycles, e.g., at least 10, at least 20, at least 30, at least 40, at least 50, at least 100, at least 200, at least 300, at least 400, at least, 500, at least 600, at least 700, at least 800, at least 900, at least 1000, at least 1250, at least 1500, at least 1750, at least 2000, at least 2500, at least 3000, at least 4000, at least 5000, at least 7500, at least 10000, or more consecutive viral life cycles, which in on illustrative and non-limiting examples of M13 phage is 10-20 minutes per virus life cycle. Similarly, conditions can be modulated to adjust the time a host cell remains in a population of host cells, e.g., about 10, about 11, about 12, about 13, about 14, about 15, about 16, about 17, about 18, about 19, about 20, about 21, about 22, about 23, about 24, about 25, about 30, about 35, about 40, about 45, about 50, about 55, about 60, about 70, about 80, about 90, about 100, about 120, about 150, or about 180 minutes. Host cell populations can be controlled in part by density of the host cells, or, in some embodiments, the host cell density in an inflow, e.g., 10^3 cells/ml, about 10^4 cells/ml, about 10^5 cells/ml, about 5- 10^5 cells/ml, about 10^6 cells/ml, about 5- 10^6 cells/ml, about 10^7 cells/ml, about 5- 10^7 cells/ml, about 10^8 cells/ml, about 5- 10^8 cells/ml, about 10^9 cells/ml, about $5\cdot 10^9$ cells/ml, about 10^{10} cells/ml, or about $5\cdot 10^{10}$ cells/ml.

Inteins

In some embodiments, as described in more detail below, an intein-N (intN) domain may be fused to the N-terminal portion of a first domain of a gene modifying polypeptide described herein, and an intein-C (intC) domain may be fused to the C-terminal portion of a second domain of a gene modifying polypeptide described herein for the joining of the N-terminal portion to the C-terminal portion, thereby joining the first and second domains. In some embodiments, the first and second domains are each independently chosen from a DNA binding domain, an RNA binding domain, an RT domain, and an endonuclease domain.

Inteins can occur as self-splicing protein intron (e.g., peptide), e.g., which ligates flanking N-terminal and C-terminal exteins (e.g., fragments to be joined). An intein may, in some instances, comprise a fragment of a protein that is able to excise itself and join the remaining fragments (the exteins) with a peptide bond in a process known as protein splicing. Inteins are also referred to as "protein introns." The process of an intein excising itself and joining the remaining portions of the protein is herein termed "protein splicing" or "intein-mediated protein splicing."

In some embodiments, an intein of a precursor protein (an intein containing protein prior to intein-mediated protein splicing) comes from two genes. Such intein is referred to herein as a split intein (e.g., split intein-N and split intein-C). Accordingly, an intein-based approach may be used to join a first polypeptide sequence and a second polypeptide sequence together. For example, in cyanobacteria, DnaE, the catalytic subunit a of DNA polymerase III, is encoded by two separate genes, dnaE-n and dnaE-c. An intein-N domain, such as that encoded by the dnaE-n gene, when situated as part of a first polypeptide sequence, may join the first polypeptide sequence with a second polypeptide sequence, wherein the second polypeptide sequence comprises an intein-C domain, such as that encoded by the dnaE-c gene. Accordingly, in some embodiments, a protein can be made by providing nucleic acid encoding the first and second polypeptide sequences (e.g., wherein a first nucleic acid molecule encodes the first polypeptide sequence and a second nucleic acid molecule encodes the second polypeptide sequence), and the nucleic acid is introduced into the cell under conditions that allow for production of the first and second polypeptide sequences, and for joining of the first to the second polypeptide sequence via an intein-based mechanism.

Use of inteins for joining heterologous protein fragments is described, for example, in Wood et al., J. Biol. Chem.289(21); 14512-9 (2014) (incorporated herein by reference in its entirety). For example, when fused to separate protein fragments, the inteins IntN and IntC may recognize each other, splice themselves out, and/or simultaneously ligate the flanking N- and C-terminal exteins of the protein fragments to which they were fused, thereby reconstituting a full-length protein from the two protein fragments.

In some embodiments, a synthetic intein based on the dnaE intein, the Cfa-N (e.g., split intein-N) and Cfa-C (e.g., split intein-C) intein pair, is used. Examples of such inteins have been described, e.g., in Stevens et al., J Am Chem Soc. 2016 Feb. 24; 138(7):2162-5 (incorporated herein by reference in its entirety). Non-limiting examples of intein pairs that may be used in accordance with the present disclosure include: Cfa DnaE intein, Ssp GyrB intein, Ssp DnaX intein, Ter DnaE3 intein, Ter ThyX intein, Rma DnaB intein and Cne Prp8 intein (e.g., as described in U.S. Pat. No. 8,394,604, incorporated herein by reference.

In some embodiments involving a split Cas9, an intein-N domain and an intein-C domain may be fused to the N-terminal portion of the split Cas9 and the C-terminal portion of a split Cas9, respectively, for the joining of the N-terminal portion of the split Cas9 and the C-terminal portion of the split Cas9. For example, in some embodiments, an intein-N is fused to the C-terminus of the N-terminal portion of the split Cas9, i.e., to form a structure of N— [N-terminal portion of the split Cas9]-[intein-N]~ C. In some embodiments, an intein-C is fused to the N-terminus of the C-terminal portion of the split Cas9, i.e., to form a structure of N-[intein-C]~ [C-terminal portion of the split Cas9]-C. The mechanism of intein-mediated protein splicing for joining the proteins the inteins are fused to (e.g., split Cas9) is described in Shah et al., Chem Sci. 2014; 5(l):446-46l, incorporated herein by reference. Methods for designing and using inteins are known in the art and described, for example by WO2020051561, W02014004336, WO2017132580, US20150344549, and US20180127780, each of which is incorporated herein by reference in their entirety.

In some embodiments, a split refers to a division into two or more fragments. In some embodiments, a split Cas9 protein or split Cas9 comprises a Cas9 protein that is provided as an N-terminal fragment and a C-terminal fragment encoded by two separate nucleotide sequences. The polypeptides corresponding to the N-terminal portion and the C-terminal portion of the Cas9 protein may be spliced to form a reconstituted Cas9 protein. In embodiments, the Cas9 protein is

divided into two fragments within a disordered region of the protein, e.g., as described in Nishimasu et al., Cell, Volume 156, Issue 5, pp. 935-949, 2014, or as described in Jiang et al. (2016) Science 351: 867-871 and PDB file: 5F9R (each of which is incorporated herein by reference in its entirety). A disordered region may be determined by one or more protein structure determination techniques known in the art, including, without limitation, X-ray crystallography, NMR spectroscopy, electron microscopy (e.g., cryoEM), and/or *in silico* protein modeling. In some embodiments, the protein is divided into two fragments at any C, T, A, or S, e.g., within a region of SpCas9 between amino acids A292- G364, F445-K483, or E565-T637, or at corresponding positions in any other Cas9, Cas9 variant (e.g., nCas9, dCas9), or other napDNAbp. In some embodiments, protein is divided into two fragments at SpCas9 T310, T313, A456, S469, or C574. In some embodiments, the process of dividing the protein into two fragments is referred to as splitting the protein.

In some embodiments, a protein fragment ranges from about 2-1000 amino acids (e.g., between 2-10, 10-50, 50-100, 100-200, 200-300, 300-400, 400-500, 500-600, 600-700, 700-800, 800-900, or 900-1000 amino acids) in length. In some embodiments, a protein fragment ranges from about 5-500 amino acids (e.g., between 5-10, 10-50, 50-100, 100-200, 200-300, 300-400, or 400-500 amino acids) in length. In some embodiments, a protein fragment ranges from about 20-200 amino acids (e.g., between 20-30, 30-40, 40-50, 50-100, or 100-200 amino acids) in length.

In some embodiments, a portion or fragment of a gene modifying polypeptide is fused to an intein. The nuclease can be fused to the N-terminus or the C-terminus of the intein. In some embodiments, a portion or fragment of a fusion protein is fused to an intein and fused to an AAV capsid protein. The intein, nuclease and capsid protein can be fused together in any arrangement (e.g., nuclease-intein-capsid, intein-nuclease-capsid, capsid-intein-nuclease, etc.). In some embodiments, the N-terminus of an intein is fused to the C-terminus of a fusion protein and the C-terminus of the intein is fused to the N-terminus of an AAV capsid protein.

In some embodiments, an endonuclease domain (e.g., a nickase Cas9 domain) is fused to intein-N and a polypeptide comprising an RT domain is fused to an intein-C.

Exemplary nucleotide and amino acid sequences of intein-N domains and compatible intein-C domains are provided below:

DnaE Intein-N DNA:

TGCCTGTCATACGAAACCGAGATACTGACAGTAGAATATGGCCTTCTGCCAATCGGG
AAGATTGTGGAGAAACGGATAGAATGCACAGTTTACTCTGTCGATAACAATGGTAA
CATTTATACTCAGCCAGTTGCCCAGTGGCACGACCGGGGAGAGCAGGAAGTATTCG
AATACTGTCTGGAGGATGGAAGTCTCATTAGGGCCACTAAGGACCACAAATTTATG
ACAGTCGATGGCCAGATGCTGCCTATAGACGAAATCTTTGAGCGAGAGTTGGACCTC
ATGCGAGTTGACAACCTTCCTAAT (SEQ ID NO: 5029)

DnaE Intein-N Protein:
CLSYETEILTVEYGLLPIGKIVEKRIECTVYSVDNNGNIYTQPVAQWHDRGEQEVFEYCL
EDGSLIRATKDHKFMTVDGQMLPIDEIFERELDLMRVDNLPN (SEQ ID NO: 5030)

DnaE Intein-C DNA:
ATGATCAAGATAGCTACAAGGAAGTATCTTGGCAAACAAAACGTTTATGATATTGG
AGTCGAAAGAGATCACAACTTTGCTCTGAAGAACGGATTCATAGCTTCTAAT (SEQ
ID NO: 5031)

DnaE Intein-C Protein:
MIKIATRKYLGKQNVYDIGVERDHNFALKNGFIASN (SEQ ID NO: 5032)

Cfa-N DNA:
TGCCTGTCTTATGATACCGAGATACTTACCGTTGAATATGGCTTCTTGCCTATTGGAA
AGATTGTCGAAGAGAGAATTGAATGCACAGTATATACTGTAGACAAGAATGGTTTC
GTTTACACACAGCCCATTGCTCAATGGCACAATCGCGGCGAACAAGAAGTATTTGA
GTACTGTCTCGAGGATGGAAGCATCATACGAGCAACTAAAGATCATAAATTCATGA
CCACTGACGGGCAGATGTTGCCAATAGATGAGATATTCGAGCGGGGCTTGGATCTC
AAACAAGTGGATGGATTG CCA (SEQ ID NO: 5033)

Cfa-N Protein:
CLSYDTEILTVEYGFLPIGKIVEERIECTVYTVDKNGFVYTQPIAQWHNRGEQEVFEYCL
EDGSIIRATKDHKFMTTDGQMLPIDEIFERGLDLKQVDGLP (SEQ ID NO: 5034)

Cfa-C DNA:
ATGAAGAGGACTGCCGATGGATCAGAGTTTGAATCTCCCAAGAAGAAGAGGAAAGT
AAAGATAATATCTCGAAAAAGTCTTGGTACCCAAAATGTCTATGATATTGGAGTGGA
GAAAGATCACAACTTCCTTCTCAAGAACGGTCTCGTAGCCAGCAAC (SEQ ID NO:
5035)

Cfa-C Protein:
MKRTADGSEFESPKKKRKVKIISRKSLGTQNVYDIGVEKDHNFLLKNGLVASN (SEQ ID
NO: 5036)

Additional domains

The gene modifying polypeptide can bind a target DNA sequence and template nucleic acid (e.g., template RNA), nick the target site, and write (e.g., reverse transcribe) the template

into DNA, resulting in a modification of the target site. In some embodiments, additional domains may be added to the polypeptide to enhance the efficiency of the process. In some embodiments, the gene modifying polypeptide may contain an additional DNA ligation domain to join reverse transcribed DNA to the DNA of the target site. In some embodiments, the polypeptide may comprise a heterologous RNA-binding domain. In some embodiments, the polypeptide may comprise a domain having 5′ to 3′ exonuclease activity (e.g., wherein the 5′ to 3′ exonuclease activity increases repair of the alteration of the target site, e.g., in favor of alteration over the original genomic sequence). In some embodiments, the polypeptide may comprise a domain having 3′ to 5′ exonuclease activity, e.g., proof-reading activity. In some embodiments, the writing domain, e.g., RT domain, has 3′ to 5′ exonuclease activity, e.g., proof-reading activity.

Template nucleic acids

The gene modifying systems described herein can modify a host target DNA site using a template nucleic acid sequence. In some embodiments, the gene modifying systems described herein transcribe an RNA sequence template into host target DNA sites by target-primed reverse transcription (TPRT). By modifying DNA sequence(s) via reverse transcription of the RNA sequence template directly into the host genome, the gene modifying system can insert an object sequence into a target genome without the need for exogenous DNA sequences to be introduced into the host cell (unlike, for example, CRISPR systems), as well as eliminate an exogenous DNA insertion step. The gene modifying system can also delete a sequence from the target genome or introduce a substitution using an object sequence. Therefore, the gene modifying system provides a platform for the use of customized RNA sequence templates containing object sequences, e.g., sequences comprising heterologous gene coding and/or function information.

In some embodiments, the template nucleic acid comprises one or more sequence (e.g., 2 sequences) that binds the gene modifying polypeptide.

In some embodiments a system or method described herein comprises a single template nucleic acid (e.g., template RNA). In some embodiments a system or method described herein comprises a plurality of template nucleic acids (e.g., template RNAs). For example, a system described herein comprises a first RNA comprising (e.g., from 5′ to 3′) a sequence that binds the gene modifying polypeptide (e.g., the DNA-binding domain and/or the endonuclease domain,

e.g., a gRNA) and a sequence that binds a target site (e.g., a second strand of a site in a target genome), and a second RNA (e.g., a template RNA) comprising (e.g., from 5′ to 3′) optionally a sequence that binds the gene modifying polypeptide (e.g., that specifically binds the RT domain), a heterologous object sequence, and a PBS sequence. In some embodiments, when the system comprises a plurality of nucleic acids, each nucleic acid comprises a conjugating domain. In some embodiments, a conjugating domain enables association of nucleic acid molecules, e.g., by hybridization of complementary sequences. For example, in some embodiments a first RNA comprises a first conjugating domain and a second RNA comprises a second conjugating domain, and the first and second conjugating domains are capable of hybridizing to one another, e.g., under stringent conditions. In some embodiments, the stringent conditions for hybridization include hybridization in 4x sodium chloride/sodium citrate (SSC), at about 65 C, followed by a wash in 1xSSC, at about 65 C.

In some embodiments, the template nucleic acid comprises RNA. In some embodiments, the template nucleic acid comprises DNA (e.g., single stranded or double stranded DNA).

In some embodiments, the template nucleic acid comprises one or more (e.g., 2) homology domains that have homology to the target sequence. In some embodiments, the homology domains are about 10-20, 20-50, or 50-100 nucleotides in length.

In some embodiments, a template RNA can comprise a gRNA sequence, e.g., to direct the gene modifying polypeptide to a target site of interest. In some embodiments, a template RNA comprises (e.g., from 5′ to 3′) (i) optionally a gRNA spacer that binds a target site (e.g., a second strand of a site in a target genome), (ii) optionally a gRNA scaffold that binds a polypeptide described herein (e.g., a gene modifying polypeptide or a Cas polypeptide), (iii) a heterologous object sequence comprising a mutation region (optionally the heterologous object sequence comprises, from 5’ to 3’, a first homology region, a mutation region, and a second homology region), and (iv) a primer binding site (PBS) sequence comprising a 3′ target homology domain.

The template nucleic acid (e.g., template RNA) component of a genome editing system described herein typically is able to bind the gene modifying polypeptide of the system. In some embodiments the template nucleic acid (e.g., template RNA) has a 3′ region that is capable of

binding a gene modifying polypeptide. The binding region, e.g., 3′ region, may be a structured RNA region, e.g., having at least 1, 2 or 3 hairpin loops, capable of binding the gene modifying polypeptide of the system. The binding region may associate the template nucleic acid (e.g., template RNA) with any of the polypeptide modules. In some embodiments, the binding region of the template nucleic acid (e.g., template RNA) may associate with an RNA-binding domain in the polypeptide. In some embodiments, the binding region of the template nucleic acid (e.g., template RNA) may associate with the reverse transcription domain of the gene modifying polypeptide (e.g., specifically bind to the RT domain). In some embodiments, the template nucleic acid (e.g., template RNA) may associate with the DNA binding domain of the polypeptide, e.g., a gRNA associating with a Cas9-derived DNA binding domain. In some embodiments, the binding region may also provide DNA target recognition, e.g., a gRNA hybridizing to the target DNA sequence and binding the polypeptide, e.g., a Cas9 domain. In some embodiments, the template nucleic acid (e.g., template RNA) may associate with multiple components of the polypeptide, e.g., DNA binding domain and reverse transcription domain.

In some embodiments the template RNA has a poly-A tail at the 3′ end. In some embodiments the template RNA does not have a poly-A tail at the 3′ end.

In some embodiments, the template nucleic acid is a template RNA. In some embodiments, the template RNA comprises one or more modified nucleotides. For example, in some embodiments, the template RNA comprises one or more deoxyribonucleotides. In some embodiments, regions of the template RNA are replaced by DNA nucleotides, e.g., to enhance stability of the molecule. For example, the 3′ end of the template may comprise DNA nucleotides, while the rest of the template comprises RNA nucleotides that can be reverse transcribed. For instance, in some embodiments, the heterologous object sequence is primarily or wholly made up of RNA nucleotides (e.g., at least 90%, 95%, 98%, or 99% RNA nucleotides). In some embodiments, the PBS sequence is primarily or wholly made up of DNA nucleotides (e.g., at least 90%, 95%, 98%, or 99% DNA nucleotides). In other embodiments, the heterologous object sequence for writing into the genome may comprise DNA nucleotides. In some embodiments, the DNA nucleotides in the template are copied into the genome by a domain capable of DNA-dependent DNA polymerase activity. In some embodiments, the DNA-dependent DNA polymerase activity is provided by a DNA polymerase domain in the polypeptide. In some embodiments, the DNA-dependent DNA polymerase activity is provided

by a reverse transcriptase domain that is also capable of DNA-dependent DNA polymerization, e.g., second strand synthesis. In some embodiments, the template molecule is composed of only DNA nucleotides.

In some embodiments, a system described herein comprises two nucleic acids which together comprise the sequences of a template RNA described herein. In some embodiments, the two nucleic acids are associated with each other non-covalently, e.g., directly associated with each other (e.g., via base pairing), or indirectly associated as part of a complex comprising one or more additional molecule.

A template RNA described herein may comprise, from 5' to 3': (1) a gRNA spacer; (2) a gRNA scaffold; (3) heterologous object sequence (4) a primer binding site (PBS) sequence. Each of these components is now described in more detail.

gRNA spacer and gRNA scaffold

A template RNA described herein may comprise a gRNA spacer that directs the gene modifying system to a target nucleic acid, and a gRNA scaffold that promotes association of the template RNA with the Cas domain of the gene modifying polypeptide. The systems described herein can also comprise a gRNA that is not part of a template nucleic acid. For example, a gRNA that comprises a gRNA spacer and gRNA scaffold, but not a heterologous object sequence or a PBS sequence, can be used, e.g., to induce second strand nicking, e.g., as described in the section herein entitled "Second Strand Nicking".

In some embodiments, the gRNA is a short synthetic RNA composed of a scaffold sequence that participates in CRISPR-associated protein binding and a user-defined ~20 nucleotide targeting sequence for a genomic target. The structure of a complete gRNA was described by Nishimasu et al. Cell 156, P935-949 (2014). The gRNA (also referred to as sgRNA for single-guide RNA) consists of crRNA- and tracrRNA-derived sequences connected by an artificial tetraloop. The crRNA sequence can be divided into guide (20 nt) and repeat (12 nt) regions, whereas the tracrRNA sequence can be divided into anti-repeat (14 nt) and three tracrRNA stem loops (Nishimasu et al. Cell 156, P935-949 (2014)). In practice, guide RNA sequences are generally designed to have a length of between 17 – 24 nucleotides (e.g., 19, 20, or 21 nucleotides) and be complementary to a targeted nucleic acid sequence. Custom gRNA generators and algorithms are available commercially for use in the design of effective guide

RNAs. In some embodiments, the gRNA comprises two RNA components from the native CRISPR system, e.g. crRNA and tracrRNA. As is well known in the art, the gRNA may also comprise a chimeric, single guide RNA (sgRNA) containing sequence from both a tracrRNA (for binding the nuclease) and at least one crRNA (to guide the nuclease to the sequence targeted for editing/binding). Chemically modified sgRNAs have also been demonstrated to be effective for use with CRISPR-associated proteins; see, for example, Hendel et al. (2015) Nature Biotechnol., 985 – 991. In some embodiments, a gRNA spacer comprises a nucleic acid sequence that is complementary to a DNA sequence associated with a target gene.

In some embodiments, the region of the template nucleic acid, e.g., template RNA, comprising the gRNA adopts an underwound ribbon-like structure of gRNA bound to target DNA (e.g., as described in Mulepati et al. Science 19 Sep 2014:Vol. 345, Issue 6203, pp. 1479-1484). Without wishing to be bound by theory, this non-canonical structure is thought to be facilitated by rotation of every sixth nucleotide out of the RNA-DNA hybrid. Thus, in some embodiments, the region of the template nucleic acid, e.g., template RNA, comprising the gRNA may tolerate increased mismatching with the target site at some interval, e.g., every sixth base. In some embodiments, the region of the template nucleic acid, e.g., template RNA, comprising the gRNA comprising homology to the target site may possess wobble positions at a regular interval, e.g., every sixth base, that do not need to base pair with the target site.

In some embodiments, the template nucleic acid (e.g., template RNA) has at least 15, 16, 17, 18, 19, 20, 21, 22, 23, or 24 bases of at least 80%, 85%, 90%, 95%, 99%, or 100% homology to the target site, e.g., at the 5' end, e.g., comprising a gRNA spacer sequence of length appropriate to the Cas9 domain of the gene modifying polypeptide (Table 8).

In some embodiments, a Cas9 derivative with enhanced activity may be used in the gene modification polypeptide. In some embodiments, a Cas9 derivative may comprise mutations that improve activity of the HNH endonuclease domain, e.g., SpyCas9 R221K, N394K, or mutations that improve R-loop formation, e.g., SpyCas9 L1245V, or comprise a combination of such mutations, e.g., SpyCas9 R221K/N394K, SpyCas9 N394K/L1245V, SpyCas9 R221K/L1245V, or SpyCas9 R221K/N394K/L1245V (see, e.g., Spencer and Zhang Sci Rep 7:16836 (2017), the Cas9 derivatives and comprising mutations of which are incorporated herein by reference). In some embodiments, a Cas9 derivative may comprise one or more types of mutations described herein, e.g., PAM-modifying mutations, protein stabilizing mutations, activity enhancing

mutations, and/or mutations partially or fully inactivating one or two endonuclease domains relative to the parental enzyme (e.g., one or more mutations to abolish endonuclease activity towards one or both strands of a target DNA, e.g., a nickase or catalytically dead enzyme). In some embodiments, a Cas9 enzyme used in a system described herein may comprise mutations that confer nickase activity toward the enzyme (e.g., SpyCas9 N863A or H840A) in addition to mutations improving catalytic efficiency (e.g., SpyCas9 R221K, N394K, and/or L1245V). In some embodiments, a Cas9 enzyme used in a system described herein is a SpyCas9 enzyme or derivative that further comprises an N863A mutation to confer nickase activity in addition to R221K and N394K mutations to improve catalytic efficiency.

Table 12 provides parameters to define components for designing gRNA and/or Template RNAs to apply Cas variants listed in Table 8 for gene modifying. The cut site indicates the validated or predicted protospacer adjacent motif (PAM) requirements, validated or predicted location of cut site (relative to the most upstream base of the PAM site). The gRNA for a given enzyme can be assembled by concatenating the crRNA, Tetraloop, and tracrRNA sequences, and further adding a 5′ spacer of a length within Spacer (min) and Spacer (max) that matches a protospacer at a target site. Further, the predicted location of the ssDNA nick at the target is important for designing a PBS sequence of a Template RNA that can anneal to the sequence immediately 5′ of the nick in order to initiate target primed reverse transcription. In some embodiments, a gRNA scaffold described herein comprises a nucleic acid sequence comprising, in the 5’ to 3’ direction, a crRNA of Table 12, a tetraloop from the same row of Table 12, and a tracrRNA from the same row of Table 12, or a sequence having at least 70%, 80%, 85%, 90%, 95%, or 99% identity thereto. In some embodiments, the gRNA or template RNA comprising the scaffold further comprises a gRNA spacer having a length within the Spacer (min) and Spacer (max) indicated in the same row of Table 12. In some embodiments, the gRNA or template RNA having a sequence according to Table 12 is comprised by a system that further comprises a gene modifying polypeptide, wherein the gene modifying polypeptide comprises a Cas domain described in the same row of Table 12.

Table 12 Parameters to define components for designing gRNA and/or Template RNAs to apply Cas variants listed in Table 8 in gene modifying systems

Variant	PAM(s)	SEQ ID NO:	Cut	Tier	Spacer (min)	Spacer (max)	crRNA	SEQ ID NO:	Tetraloop	SEQ ID NO:	tracrRNA	SEQ ID NO:
Nme2Cas9	NNNNCC	10,001	-3	1	22	24	GTTGTAGC TCCCTTTCT CATTTCG	10,051	GAAA	10,101	CGAAATGAGAACCGTTGCTACAATAAGGC CGTCTGAAAAGATGTGCCGCAACGCTCTG CCCCTTAAAGCTTCTGCTTTAAGGGGCATC GTTTA	10,151
PpnCas9	NNNNRTT	10,002		1	21	24	GTTGTAGC TCCCTTTTT CATTTCGC	10,052	GAAA	10,102	GCGAAATGAAAAACGTTGTTACAATAAGA GATGAATTTCTCGCAAAGCTCTGCCTCTTG AAATTTCGGTTTCAAGAGGCATC	10,152
SauCas9	NNGRR;N NGRRT	10,003	-3	1	21	23	GTTTTAGT ACTCTG	10,053	GAAA	10,103	CAGAATCTACTAAAACAAGGCAAAATGCC GTGTTTATCTCGTCAACTTGTTGGCGAGA	10,153
SauCas9-KKH	NNNRR;N NNRRT	10,004	-3	1	21	21	GTTTTAGT ACTCTG	10,054	GAAA	10,104	CAGAATCTACTAAAACAAGGCAAAATGCC GTGTTTATCTCGTCAACTTGTTGGCGAGA	10,154
SauriCas9	NNGG	10,005	-3	1	21	21	GTTTTAGT ACTCTG	10,055	GAAA	10,105	CAGAATCTACTAAAACAAGGCAAAATGCC GTGTTTATCTCGTCAACTTGTTGGCGAGA	10,155
SauriCas9-KKH	NNRG	10,006	-3	1	21	21	GTTTTAGT ACTCTG	10,056	GAAA	10,106	CAGAATCTACTAAAACAAGGCAAAATGCC GTGTTTATCTCGTCAACTTGTTGGCGAGA	10,156
ScaCas9-Sc++	NNG	10,007	-3	1	20	20	GTTTTAGA GCTA	10,057	GAAA	10,107	TAGCAAGTTAAAATAAGGCTAGTCCGTTA TCAACTTGAAAAAGTGGCACCGAGTCGGT GC	10,157
SpyCas9	NGG	10,008	-3	1	20	20	GTTTTAGA GCTA	10,058	GAAA	10,108	TAGCAAGTTAAAATAAGGCTAGTCCGTTA TCAACTTGAAAAAGTGGCACCGAGTCGGT GC	10,158
SpyCas9_i_v1	NGG		-3	1	20	20	GTTTTAGA GCTA	10,058	GAAA	10,190	TAGCAAGTTAAAATAAGGCTAGTCCGTTA TCAACTTGGACTTCGGTCCAAGTGGCACC GAGTCGGTGC	10,193
SpyCas9_i_v2	NGG		-3	1	20	20	GTTTTAGA GCTA	10,058	GAAA	10,191	TAGCAAGTTAAAATAAGGCTAGTCCGTTA TCAACTTGGAGCTTGCTCCAAGTGGCACC GAGTCGGTGC	10,194

SpyCas9_i_v3	NGG		-3	1	20	20	GTTTTAGA GCTA	10,058	GAAA	10,192	GTTTTAGAGCTAGAAATAGCAAGTTAAAA TAAGGCTAGTCCGTTATCGACTTGAAAAA GTCGCACCGAGTCGGTGC	10,195
SpyCas9-NG	NG (NGG=NG A=NGT>N GC)	10,009	-3	1	20	20	GTTTTAGA GCTA	10,059	GAAA	10,109	TAGCAAGTTAAAATAAGGCTAGTCCGTTA TCAACTTGAAAAAGTGGCACCGAGTCGGT GC	10,159
SpyCas9-SpRY	NRN>NYN	10,010	-3	1	20	20	GTTTTAGA GCTA	10,060	GAAA	10,110	TAGCAAGTTAAAATAAGGCTAGTCCGTTA TCAACTTGAAAAAGTGGCACCGAGTCGGT GC	10,160
St1Cas9	NNAGAA W>NNAG GAW=NN GGAAW	10,011	-3	1	20	20	GTCTTTGTA CTCTG	10,061	GTAC	10,111	CAGAAGCTACAAAGATAAGGCTTCATGCC GAAATCAACACCCTGTCATTTTATGGCAG GGTGTTTT	10,161
BlatCas9	NNNNCN AA>NNNN CNDD>NN NNC	10,012	-3	1	19	23	GCTATAGT TCCTTACT	10,062	GAAA	10,112	GGTAAGTTGCTATAGTAAGGGCAACAGAC CCGAGGCGTTGGGGATCGCCTAGCCCGTG TTTACGGGCTCTCCCCATATTCAAAATAAT GACAGACGAGCACCTTGGAGCATTTATCT CCGAGGTGCT	10,162
cCas9-v16	NNVACT; NNVATG M;NNVAT T;NNVGCT ;NNVGTG; NNVGTT	10,013	-3	2	21	21	GTCTTAGT ACTCTG	10,063	GAAA	10,113	CAGAATCTACTAAGACAAGGCAAAATGCC GTGTTTATCTCGTCAACTTGTTGGCGAGA	10,163
cCas9-v17	NNVRRN	10,014	-3	2	21	21	GTCTTAGT ACTCTG	10,064	GAAA	10,114	CAGAATCTACTAAGACAAGGCAAAATGCC GTGTTTATCTCGTCAACTTGTTGGCGAGA	10,164
cCas9-v21	NNVACT; NNVATG M;NNVAT T;NNVGCT ;NNVGTG; NNVGTT	10,015	-3	2	21	21	GTCTTAGT ACTCTG	10,065	GAAA	10,115	CAGAATCTACTAAGACAAGGCAAAATGCC GTGTTTATCTCGTCAACTTGTTGGCGAGA	10,165
cCas9-v42	NNVRRN	10,016	-3	2	21	21	GTCTTAGT ACTCTG	10,066	GAAA	10,116	CAGAATCTACTAAGACAAGGCAAAATGCC GTGTTTATCTCGTCAACTTGTTGGCGAGA	10,166

CdiCas9	NNRHHHY;NNRAAAY	10,017		2	22	22	ACTGGGGTTCAG	10,067	GAAA	10,117	CTGAACCTCAGTAAGCATTGGCTCGTTTCCAATGTTGATTGCTCCGCCGGTGCTCCTTATTTTTAAGGGCGCCGGC	10,167
CjeCas9	NNNNRYAC	10,018	-3	2	21	23	GTTTTAGTCCCT	10,068	GAAA	10,118	AGGGACTAAAATAAAGAGTTTGCGGGACTCTGCGGGGTTACAATCCCCTAAAACCGC	10,168
GeoCas9	NNNNCRAA	10,019		2	21	23	GTCATAGTTCCCCTGA	10,069	GAAA	10,119	TCAGGGTTACTATGATAAGGGCTTTCTGCCTAAGGCAGACTGACCCGCGGCGTTGGGGATCGCCTGTGCCCGCTTTTGGCGGGCATTCCCCATCCTT	10,169
iSpyMacCas9	NAAN	10,020	-3	2	19	21	GTTTTAGAGCTA	10,070	GAAA	10,120	TAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	10,170
NmeCas9	NNNNGAYT;NNNNGYTT;NNNNGAYA;NNNNGTCT	10,021	-3	2	20	24	GTTGTAGCTCCCTTTCTCATTTCG	10,071	GAAA	10,121	CGAAATGAGAACCGTTGCTACAATAAGGCCGTCTGAAAAGATGTGCCGCAACGCTCTGCCCCTTAAAGCTTCTGCTTTAAGGGGCATCGTTTA	10,171
ScaCas9	NNG	10,022	-3	2	20	20	GTTTTAGAGCTA	10,072	GAAA	10,122	TAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	10,172
ScaCas9-HiFi-Sc++	NNG	10,023	-3	2	20	20	GTTTTAGAGCTA	10,073	GAAA	10,123	TAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	10,173
SpyCas9-3var-NRRH	NRRH	10,024	-3	2	20	20	GTTTAAGAGCTATGCTG	10,074	GAAA	10,124	CAGCATAGCAAGTTTAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	10,174
SpyCas9-3var-NRTH	NRTH	10,025	-3	2	20	20	GTTTAAGAGCTATGCTG	10,075	GAAA	10,125	CAGCATAGCAAGTTTAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	10,175
SpyCas9-3var-NRCH	NRCH	10,026	-3	2	20	20	GTTTAAGAGCTATGCTG	10,076	GAAA	10,126	CAGCATAGCAAGTTTAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	10,176

SpyCas9-HF1	NGG	10,027	-3	2	20	20	GTTTTAGA GCTA	10,077	GAAA	10,127	TAGCAAGTTAAAATAAGGCTAGTCCGTTA TCAACTTGAAAAAGTGGCACCGAGTCGGT GC	10,177
SpyCas9-QQR1	NAAG	10,028	-3	2	20	20	GTTTTAGA GCTA	10,078	GAAA	10,128	TAGCAAGTTAAAATAAGGCTAGTCCGTTA TCAACTTGAAAAAGTGGCACCGAGTCGGT GC	10,178
SpyCas9-SpG	NGN	10,029	-3	2	20	20	GTTTTAGA GCTA	10,079	GAAA	10,129	TAGCAAGTTAAAATAAGGCTAGTCCGTTA TCAACTTGAAAAAGTGGCACCGAGTCGGT GC	10,179
SpyCas9-VQR	NGAN	10,030	-3	2	20	20	GTTTTAGA GCTA	10,080	GAAA	10,130	TAGCAAGTTAAAATAAGGCTAGTCCGTTA TCAACTTGAAAAAGTGGCACCGAGTCGGT GC	10,180
SpyCas9-VRER	NGCG	10,031	-3	2	20	20	GTTTTAGA GCTA	10,081	GAAA	10,131	TAGCAAGTTAAAATAAGGCTAGTCCGTTA TCAACTTGAAAAAGTGGCACCGAGTCGGT GC	10,181
SpyCas9-xCas	NG;GAA;GAT	10,032	-3	2	20	20	GTTTAAGA GCTATGCT G	10,082	GAAA	10,132	CAGCATAGCAAGTTTAAATAAGGCTAGTC CGTTATCAACTTGAAAAAGTGGCACCGAG TCGGTGC	10,182
SpyCas9-xCas-NG	NG	10,033	-3	2	20	20	GTTTAAGA GCTATGCT G	10,083	GAAA	10,133	CAGCATAGCAAGTTTAAATAAGGCTAGTC CGTTATCAACTTGAAAAAGTGGCACCGAG TCGGTGC	10,183
St1Cas9-CNRZ1066	NNACAA	10,034	-3	2	20	20	GTCTTTGTA CTCTG	10,084	GTAC	10,134	CAGAAGCTACAAAGATAAGGCTTCATGCC GAAATCAACACCCTGTCATTTTATGGCAG GGTGTTTT	10,184
St1Cas9-LMG1831	NNGCAA	10,035	-3	2	20	20	GTCTTTGTA CTCTG	10,085	GTAC	10,135	CAGAAGCTACAAAGATAAGGCTTCATGCC GAAATCAACACCCTGTCATTTTATGGCAG GGTGTTTT	10,185
St1Cas9-MTH17CL396	NNAAAA	10,036	-3	2	20	20	GTCTTTGTA CTCTG	10,086	GTAC	10,136	CAGAAGCTACAAAGATAAGGCTTCATGCC GAAATCAACACCCTGTCATTTTATGGCAG GGTGTTTT	10,186
St1Cas9-TH1477	NNGAAA	10,037	-3	2	20	20	GTCTTTGTA CTCTG	10,087	GTAC	10,137	CAGAAGCTACAAAGATAAGGCTTCATGCC GAAATCAACACCCTGTCATTTTATGGCAG GGTGTTTT	10,187

sRGN3.1	NNGG	10,038		1	21	23	GTTTTAGTACTCTG	10,088	GAAA	10,138	CAGAATCTACTGAAACAAGACAATATGTCGTGTTTATCCCATCAATTTATTGGTGGGATTTT	10,188
sRGN3.3	NNGG	10,039		1	21	23	GTTTTAGTACTCTG	10,089	GAAA	10,139	CAGAATCTACTGAAACAAGACAATATGTCGTGTTTATCCCATCAATTTATTGGTGGGATTTT	10,189

Herein, when an RNA sequence (e.g., a template RNA sequence) is said to comprise a particular sequence (e.g., a sequence of Table 12 or a portion thereof) that comprises thymine (T), it is of course understood that the RNA sequence may (and frequently does) comprise uracil (U) in place of T. For instance, the RNA sequence may comprise U at every position shown as T in the sequence in Table 12. More specifically, the present disclosure provides an RNA sequence according to every gRNA scaffold sequence of Table 12, wherein the RNA sequence has a U in place of each T in the sequence in Table 12. Additionally, it is understood that terminal Us and Ts may optionally be added or removed from tracrRNA sequences and may be modified or unmodified when provided as RNA. Without wishing to be bound by example, versions of gRNA scaffold sequences alternative to those exemplified in Table 12 may also function with the different Cas9 enzymes or derivatives thereof exemplified in Table 8, e.g., alternate gRNA scaffold sequences with nucleotide additions, substitutions, or deletions, e.g., sequences with stem-loop structures added or removed. It is contemplated herein that the gRNA scaffold sequences represent a component of gene modifying systems that can be similarly optimized for a given system, Cas-RT fusion polypeptide, indication, target mutation, template RNA, or delivery vehicle.

Heterologous object sequence

A template RNA described herein may comprise a heterologous object sequence that the gene modifying polypeptide can use as a template for reverse transcription, to write a desired sequence into the target nucleic acid. In some embodiments, the heterologous object sequence comprises, from 5' to 3', a post-edit homology region, the mutation region, and a pre-edit homology region. Without wishing to be bound by theory, an RT performing reverse transcription on the template RNA first reverse transcribes the pre-edit homology region, then the mutation region, and then the post-edit homology region, thereby creating a DNA strand comprising the desired mutation with a homology region on either side.

In some embodiments, the heterologous object sequence is at least 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 120, 140, 160, 180, 200, 500, or 1,000 nucleotides (nts) in length, or at least 1, 1.5, 2, 2.5, 3, 3.5, 4, 4.5, 5, 5.5, 6, 6.5, 7, 7.5, 8, 8.5, 9, 9.5, or 10 kilobases in length. In some embodiments, the heterologous object sequence is no more than 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 120, 140, 160, 180, 200, 500, 1,000, or 2000 nucleotides (nts) in length, or no more than 20, 15, 10, 9, 8, 7, 6, 5, 4, or 3 kilobases in length. In some embodiments, the heterologous object sequence is 30-1000, 40-1000, 50-1000, 60-1000, 70-1000, 74-1000, 75-1000, 76-1000, 77-1000, 78-1000, 79-1000, 80-1000, 85-1000, 90-1000, 100-1000, 120-1000, 140-1000, 160-1000, 180-1000, 200-1000, 500-1000, 30-500, 40-500, 50-500, 60-500, 70-500, 74-500, 75-500, 76-500, 77-500, 78-500, 79-500, 80-500, 85-500, 90-500, 100-500, 120-500, 140-500, 160-500, 180-500, 200-500, 30-200, 40-200, 50-200, 60-200, 70-200, 74-200, 75-200, 76-200, 77-200, 78-200, 79-200, 80-200, 85-200, 90-200, 100-200, 120-200, 140-200, 160-200, 180-200, 30-100, 40-100, 50-100, 60-100, 70-100, 74-100, 75-100, 76-100, 77-100, 78-100, 79-100, 80-100, 85-100, or 90-100 nucleotides (nts) in length, or 1-20, 1-15, 1-10, 1-9, 1-8, 1-7, 1-6, 1-5, 1-4, 1-3, 1-2, 2-20, 2-15, 2-10, 2-9, 2-8, 2-7, 2-6, 2-5, 2-4, 2-3, 3-20, 3-15, 3-10, 3-9, 3-8, 3-7, 3-6, 3-5, 3-4, 4-20, 4-15, 4-10, 4-9, 4-8, 4-7, 4-6, 4-5, 5-20, 5-15, 5-10, 5-9, 5-8, 5-7, 5-6, 6-20, 6-15, 6-10, 6-9, 6-8, 6-7, 7-20, 7-15, 7-10, 7-9, 7-8, 8-20, 8-15, 8-10, 8-9, 9-20, 9-15, 9-10, 10-15, 10-20, or 15-20 kilobases in length. In some embodiments, the

heterologous object sequence is 10-100, 10-90, 10-80, 10-70, 10-60, 10-50, 10-40, 10-30, or 10-20 nt in length, e.g., 10-80, 10-50, or 10-20 nt in length, e.g., about10-20 nt in length. In some embodiments, the heterologous object sequence is 8-30, 9-25, 10-20, 11-16, or 12-15 nucleotides in length, e.g., is 11-16 nt in length. Without wishing to be bound by theory, in some embodiments, a larger insertion size, larger region of editing (e.g., the distance between a first edit/substitution and a second edit/substitution in the target region), and/or greater number of desired edits (e.g., mismatches of the heterologous object sequence to the target genome), may result in a longer optimal heterologous object sequence.

In certain embodiments, the template nucleic acid comprises a customized RNA sequence template which can be identified, designed, engineered and constructed to contain sequences altering or specifying host genome function, for example by introducing a heterologous coding region into a genome; affecting or causing exon structure/alternative splicing, e.g., leading to exon skipping of one or more exons; causing disruption of an endogenous gene, e.g., creating a genetic knockout; causing transcriptional activation of an endogenous gene; causing epigenetic regulation of an endogenous DNA; causing up-regulation of one or more operably linked genes, e.g., leading to gene activation or overexpression; causing down-regulation of one or more operably linked genes, e.g., creating a genetic knock-down; etc. In certain embodiments, a customized RNA sequence template can be engineered to contain sequences coding for exons and/or transgenes, provide binding sites for transcription factor activators, repressors, enhancers, etc., and combinations thereof. In some embodiments, a customized template can be engineered to encode a nucleic acid or peptide tag to be expressed in an endogenous RNA transcript or endogenous protein operably linked to the target site. In other embodiments, the coding sequence can be further customized with splice donor sites, splice acceptor sites, or poly-A tails.

The template nucleic acid (e.g., template RNA) of the system typically comprises an object sequence (e.g., a heterologous object sequence) for writing a desired sequence into a target DNA. The object sequence may be coding or non-coding. The template nucleic acid (e.g., template RNA) can be designed to result in insertions, mutations, or deletions at the target DNA locus. In some embodiments, the template nucleic acid (e.g., template RNA) may be designed to cause an insertion in the target DNA. For example, the template nucleic acid (e.g., template RNA) may contain a heterologous sequence, wherein the reverse transcription will result in insertion of the heterologous sequence into the target DNA. In other embodiments, the RNA

template may be designed to introduce a deletion into the target DNA. For example, the template nucleic acid (e.g., template RNA) may match the target DNA upstream and downstream of the desired deletion, wherein the reverse transcription will result in the copying of the upstream and downstream sequences from the template nucleic acid (e.g., template RNA) without the intervening sequence, e.g., causing deletion of the intervening sequence. In other embodiments, the template nucleic acid (e.g., template RNA) may be designed to introduce an edit into the target DNA. For example, the template RNA may match the target DNA sequence with the exception of one or more nucleotides, wherein the reverse transcription will result in the copying of these edits into the target DNA, e.g., resulting in mutations, e.g., transition or transversion mutations.

In some embodiments, writing of an object sequence into a target site results in the substitution of nucleotides, e.g., where the full length of the object sequence corresponds to a matching length of the target site with one or more mismatched bases. In some embodiments, a heterologous object sequence may be designed such that a combination of sequence alterations may occur, e.g., a simultaneous addition and deletion, addition and substitution, or deletion and substitution.

In some embodiments, the heterologous object sequence may contain an open reading frame or a fragment of an open reading frame. In some embodiments the heterologous object sequence has a Kozak sequence. In some embodiments the heterologous object sequence has an internal ribosome entry site. In some embodiments the heterologous object sequence has a self-cleaving peptide such as a T2A or P2A site. In some embodiments the heterologous object sequence has a start codon. In some embodiments the template RNA has a splice acceptor site. In some embodiments the template RNA has a splice donor site. Exemplary splice acceptor and splice donor sites are described in WO2016044416, incorporated herein by reference in its entirety. Exemplary splice acceptor site sequences are known to those of skill in the art. In some embodiments the template RNA has a microRNA binding site downstream of the stop codon. In some embodiments the template RNA has a polyA tail downstream of the stop codon of an open reading frame. In some embodiments the template RNA comprises one or more exons. In some embodiments the template RNA comprises one or more introns. In some embodiments the template RNA comprises a eukaryotic transcriptional terminator. In some embodiments the template RNA comprises an enhanced translation element or a translation enhancing element. In

some embodiments the RNA comprises the human T-cell leukemia virus (HTLV-1) R region. In some embodiments the RNA comprises a posttranscriptional regulatory element that enhances nuclear export, such as that of Hepatitis B Virus (HPRE) or Woodchuck Hepatitis Virus (WPRE).

In some embodiments, the heterologous object sequence may contain a non-coding sequence. For example, the template nucleic acid (e.g., template RNA) may comprise a regulatory element, e.g., a promoter or enhancer sequence or miRNA binding site. In some embodiments, integration of the object sequence at a target site will result in upregulation of an endogenous gene. In some embodiments, integration of the object sequence at a target site will result in downregulation of an endogenous gene. In some embodiments the template nucleic acid (e.g., template RNA) comprises a tissue specific promoter or enhancer, each of which may be unidirectional or bidirectional. In some embodiments the promoter is an RNA polymerase I promoter, RNA polymerase II promoter, or RNA polymerase III promoter. In some embodiments the promoter comprises a TATA element. In some embodiments the promoter comprises a B recognition element. In some embodiments the promoter has one or more binding sites for transcription factors.

In some embodiments, the template nucleic acid (e.g., template RNA) comprises a site that coordinates epigenetic modification. In some embodiments, the template nucleic acid (e.g., template RNA) comprises a chromatin insulator. For example, the template nucleic acid (e.g., template RNA) comprises a CTCF site or a site targeted for DNA methylation.

In some embodiments, the template nucleic acid (e.g., template RNA) comprises a gene expression unit composed of at least one regulatory region operably linked to an effector sequence. The effector sequence may be a sequence that is transcribed into RNA (e.g., a coding sequence or a non-coding sequence such as a sequence encoding a micro RNA).

In some embodiments, the heterologous object sequence of the template nucleic acid (e.g., template RNA) is inserted into a target genome in an endogenous intron. In some embodiments, the heterologous object sequence of the template nucleic acid (e.g., template RNA) is inserted into a target genome and thereby acts as a new exon. In some embodiments, the insertion of the heterologous object sequence into the target genome results in replacement of a natural exon or the skipping of a natural exon.

The template nucleic acid (e.g., template RNA) can be designed to result in insertions, mutations, or deletions at the target DNA locus. In some embodiments, the template nucleic acid (e.g., template RNA) may be designed to cause an insertion in the target DNA. For example, the template nucleic acid (e.g., template RNA) may contain a heterologous object sequence, wherein the reverse transcription will result in insertion of the heterologous object sequence into the target DNA. In other embodiments, the RNA template may be designed to write a deletion into the target DNA. For example, the template nucleic acid (e.g., template RNA) may match the target DNA upstream and downstream of the desired deletion, wherein the reverse transcription will result in the copying of the upstream and downstream sequences from the template nucleic acid (e.g., template RNA) without the intervening sequence, e.g., causing deletion of the intervening sequence. In other embodiments, the template nucleic acid (e.g., template RNA) may be designed to write an edit into the target DNA. For example, the template RNA may match the target DNA sequence with the exception of one or more nucleotides, wherein the reverse transcription will result in the copying of these edits into the target DNA, e.g., resulting in mutations, e.g., transition or transversion mutations.

In some embodiments, the pre-edit homology domain comprises a nucleic acid sequence having 100% sequence identity with a nucleic acid sequence comprised in a target nucleic acid molecule.

In some embodiments, the post-edit homology domain comprises a nucleic acid sequence having 100% sequence identity with a nucleic acid sequence comprised in a target nucleic acid molecule.

PBS sequence

In some embodiments, a template nucleic acid (e.g., template RNA) comprises a PBS sequence. In some embodiments, a PBS sequence is disposed 3′ of the heterologous object sequence and is complementary to a sequence adjacent to a site to be modified by a system described herein, or comprises no more than 1, 2, 3, 4, or 5 mismatches to a sequence complementary to the sequence adjacent to a site to be modified by the system/gene modifying polypeptide. In some embodiments, the PBS sequence binds within 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 nucleotides of a nick site in the target nucleic acid molecule. In some embodiments, binding of the PBS sequence to the target nucleic acid molecule permits initiation of target-primed reverse transcription (TPRT), e.g., with the 3′ homology domain acting as a primer for TPRT. In some

embodiments, the PBS sequence is 3-5, 5-10, 10-30, 10-25, 10-20, 10-19, 10-18, 10-17, 10-16, 10-15, 10-14, 10-13, 10-12, 10-11, 11-30, 11-25, 11-20, 11-19, 11-18, 11-17, 11-16, 11-15, 11-14, 11-13, 11-12, 12-30, 12-25, 12-20, 12-19, 12-18, 12-17, 12-16, 12-15, 12-14, 12-13, 13-30, 13-25, 13-20, 13-19, 13-18, 13-17, 13-16, 13-15, 13-14, 14-30, 14-25, 14-20, 14-19, 14-18, 14-17, 14-16, 14-15, 15-30, 15-25, 15-20, 15-19, 15-18, 15-17, 15-16, 16-30, 16-25, 16-20, 16-19, 16-18, 16-17, 17-30, 17-25, 17-20, 17-19, 17-18, 18-30, 18-25, 18-20, 18-19, 19-30, 19-25, 19-20, 20-30, 20-25, or 25-30 nucleotides in length, e.g., 10-17, 12-16, or 12-14 nucleotides in length. In some embodiments, the PBS sequence is 5-20, 8-16, 8-14, 8-13, 9-13, 9-12, or 10-12 nucleotides in length, e.g., 9-12 nucleotides in length.

The template nucleic acid (e.g., template RNA) may have some homology to the target DNA. In some embodiments, the template nucleic acid (e.g., template RNA) PBS sequence domain may serve as an annealing region to the target DNA, such that the target DNA is positioned to prime the reverse transcription of the template nucleic acid (e.g., template RNA). In some embodiments the template nucleic acid (e.g., template RNA) has at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 175, 200 or more bases of exact homology to the target DNA at the 3′ end of the RNA. In some embodiments the template nucleic acid (e.g., template RNA) has at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 175, 200 or more bases of at least 50%, 60%, 70%, 80%, 85%, 90%, 95%, 97%, 98%, 99% or 100% homology to the target DNA, e.g., at the 5′ end of the template nucleic acid (e.g., template RNA).

Exemplary template sequences

In some embodiments of the systems and methods herein, the template RNA comprises a gRNA spacer comprising the core nucleotides of a gRNA spacer sequence of Table 1. In some embodiments, the gRNA spacer additionally comprises one or more (e.g., 2, 3, or all) consecutive nucleotides starting with the 3’ end of the flanking nucleotides of the gRNA spacer. In some embodiments, the template RNA comprising a sequence of Table 1 is comprised by a system that further comprises a gene modifying polypeptide having an RT domain listed in the same line of Table 1. RT domain amino acid sequences can be found, e.g., in Table 6 herein.

Table 1: Exemplary gRNA spacer Cas pairs

Table 1 provides a gRNA database for correcting the pathogenic EV6 mutation in HBB. List of spacers, PAMs, and Cas variants for generating a nick at an appropriate position to enable installation of a desired genomic edit with a gene modifying system. The spacers in this table are designed to be used with a gene modifying polypeptide comprising a nickase variant of the Cas species indicated in the table. Tables 2, 3, and 4 detail the other components of the system and are organized such that the ID number shown here in Column 1 ("ID") is meant to correspond to the same ID number in the subsequent tables.

ID	PAM sequence	SEQ ID NO	gRNA spacer	SEQ ID NO	Cas species	distance	Overlaps mutation
1	AGAAG	16001	TGGTGCATCTGACTCCTGTGG	16917	SauCas9KKH	0	0
2	AGAAGT	16002	TGGTGCATCTGACTCCTGTGG	16918	SauCas9KKH	0	0
3	AGAAGT	16003	TGGTGCATCTGACTCCTGTGG	16919	cCas9-v17	0	0
4	AGAAGT	16004	TGGTGCATCTGACTCCTGTGG	16920	cCas9-v42	0	0
5	AG	16005	GGTGCATCTGACTCCTGTGG	16921	SpyCas9-NG	0	0
6	AG	16006	GGTGCATCTGACTCCTGTGG	16922	SpyCas9-xCas	0	0
7	AG	16007	GGTGCATCTGACTCCTGTGG	16923	SpyCas9-xCas-NG	0	0
8	AGA	16008	GGTGCATCTGACTCCTGTGG	16924	SpyCas9-SpG	0	0
9	AGA	16009	GGTGCATCTGACTCCTGTGG	16925	SpyCas9-SpRY	0	0
10	AGAAGTCT	16010	ccatGGTGCATCTGACTCCTGTGG	16926	NmeCas9	0	0
11	AGAA	16011	GGTGCATCTGACTCCTGTGG	16927	SpyCas9-3var-NRRH	0	0
12	AGAA	16012	GGTGCATCTGACTCCTGTGG	16928	SpyCas9-VQR	0	0
13	GAGAA	16013	ccATGGTGCATCTGACTCCTGTG	16929	SauCas9	1	0
14	GAGAA	16014	ATGGTGCATCTGACTCCTGTG	16930	SauCas9KKH	1	0
15	AGGAG	16015	gcAGTAACGGCAGACTTCTCCAC	16931	SauCas9	1	0
16	AGGAG	16016	AGTAACGGCAGACTTCTCCAC	16932	SauCas9KKH	1	0
17	AGGAGT	16017	gcAGTAACGGCAGACTTCTCCAC	16933	SauCas9	1	0
18	AGGAGT	16018	AGTAACGGCAGACTTCTCCAC	16934	SauCas9KKH	1	0

19	AGGAGT	16019	AGTAACGGCAGACTTCTCCAC	16935	cCas9-v17	1	0
20	AGGAGT	16020	AGTAACGGCAGACTTCTCCAC	16936	cCas9-v42	1	0
21	GAG	16021	TGGTGCATCTGACTCCTGTG	16937	ScaCas9	1	0
22	GAG	16022	TGGTGCATCTGACTCCTGTG	16938	ScaCas9-HiFi-Sc++	1	0
23	GAG	16023	TGGTGCATCTGACTCCTGTG	16939	ScaCas9-Sc++	1	0
24	GAG	16024	TGGTGCATCTGACTCCTGTG	16940	SpyCas9-SpRY	1	0
25	AGG	16025	GTAACGGCAGACTTCTCCAC	16941	ScaCas9	1	0
26	AGG	16026	GTAACGGCAGACTTCTCCAC	16942	ScaCas9-HiFi-Sc++	1	0
27	AGG	16027	GTAACGGCAGACTTCTCCAC	16943	ScaCas9-Sc++	1	0
28	AGG	16028	GTAACGGCAGACTTCTCCAC	16944	SpyCas9	1	0
29	AGG	16029	GTAACGGCAGACTTCTCCAC	16945	SpyCas9-HF1	1	0
30	AGG	16030	GTAACGGCAGACTTCTCCAC	16946	SpyCas9-SpG	1	0
31	AGG	16031	GTAACGGCAGACTTCTCCAC	16947	SpyCas9-SpRY	1	0
32	AG	16032	GTAACGGCAGACTTCTCCAC	16948	SpyCas9-NG	1	0
33	AG	16033	GTAACGGCAGACTTCTCCAC	16949	SpyCas9-xCas	1	0
34	AG	16034	GTAACGGCAGACTTCTCCAC	16950	SpyCas9-xCas-NG	1	0
35	GAGAAG	16035	ATGGTGCATCTGACTCCTGTG	16951	cCas9-v17	1	0
36	GAGAAG	16036	ATGGTGCATCTGACTCCTGTG	16952	cCas9-v42	1	0
37	GAGA	16037	TGGTGCATCTGACTCCTGTG	16953	SpyCas9-3var-NRRH	1	0
38	AGGA	16038	GTAACGGCAGACTTCTCCAC	16954	SpyCas9-3var-NRRH	1	0
39	CAGGA	16039	ggCAGTAACGGCAGACTTCTCCA	16955	SauCas9	2	0
40	CAGGA	16040	CAGTAACGGCAGACTTCTCCA	16956	SauCas9KKH	2	0
41	GGAGA	16041	CATGGTGCATCTGACTCCTGT	16957	SauCas9KKH	2	0
42	CAGG	16042	CAGTAACGGCAGACTTCTCCA	16958	SauriCas9	2	0
43	CAGG	16043	CAGTAACGGCAGACTTCTCCA	16959	SauriCas9-KKH	2	0
44	GGAG	16044	CATGGTGCATCTGACTCCTGT	16960	SauriCas9-KKH	2	0

45	GGAG	16045	ATGGTGCATCTGACTCCTG T	16961	SpyCas9-VQR	2	0
46	CAG	16046	AGTAACGGCAGACTTCTCC A	16962	ScaCas9	2	0
47	CAG	16047	AGTAACGGCAGACTTCTCC A	16963	ScaCas9-HiFi-Sc++	2	0
48	CAG	16048	AGTAACGGCAGACTTCTCC A	16964	ScaCas9-Sc++	2	0
49	CAG	16049	AGTAACGGCAGACTTCTCC A	16965	SpyCas9-SpRY	2	0
50	GG	16050	ATGGTGCATCTGACTCCTG T	16966	SpyCas9-NG	2	0
51	GG	16051	ATGGTGCATCTGACTCCTG T	16967	SpyCas9-xCas	2	0
52	GG	16052	ATGGTGCATCTGACTCCTG T	16968	SpyCas9-xCas-NG	2	0
53	GGA	16053	ATGGTGCATCTGACTCCTG T	16969	SpyCas9-SpG	2	0
54	GGA	16054	ATGGTGCATCTGACTCCTG T	16970	SpyCas9-SpRY	2	0
55	GGAGAA	16055	CATGGTGCATCTGACTCCT GT	16971	cCas9-v17	2	0
56	GGAGAA	16056	CATGGTGCATCTGACTCCT GT	16972	cCas9-v42	2	0
57	CAGGAG	16057	CAGTAACGGCAGACTTCTC CA	16973	cCas9-v17	2	0
58	CAGGAG	16058	CAGTAACGGCAGACTTCTC CA	16974	cCas9-v42	2	0
59	tGGAG	16059	caCCATGGTGCATCTGACTC CTG	16975	SauCas9	3	1
60	tGGAG	16060	CCATGGTGCATCTGACTCC TG	16976	SauCas9KKH	3	1
61	aCAGG	16061	GCAGTAACGGCAGACTTCT CC	16977	SauCas9KKH	3	1
62	aCAG	16062	GCAGTAACGGCAGACTTCT CC	16978	SauriCas9-KKH	3	1
63	tGG	16063	CATGGTGCATCTGACTCCT G	16979	ScaCas9	3	1
64	tGG	16064	CATGGTGCATCTGACTCCT G	16980	ScaCas9-HiFi-Sc++	3	1
65	tGG	16065	CATGGTGCATCTGACTCCT G	16981	ScaCas9-Sc++	3	1
66	tGG	16066	CATGGTGCATCTGACTCCT G	16982	SpyCas9	3	1
67	tGG	16067	CATGGTGCATCTGACTCCT G	16983	SpyCas9-HF1	3	1
68	tGG	16068	CATGGTGCATCTGACTCCT G	16984	SpyCas9-SpG	3	1
69	tGG	16069	CATGGTGCATCTGACTCCT G	16985	SpyCas9-SpRY	3	1
70	tG	16070	CATGGTGCATCTGACTCCT G	16986	SpyCas9-NG	3	1
71	tG	16071	CATGGTGCATCTGACTCCT G	16987	SpyCas9-xCas	3	1

72	tG	16072	CATGGTGCATCTGACTCCTG	16988	SpyCas9-xCas-NG	3	1
73	aCA	16073	CAGTAACGGCAGACTTCTCC	16989	SpyCas9-SpRY	3	1
74	tGGAGA	16074	CCATGGTGCATCTGACTCCTG	16990	cCas9-v17	3	1
75	tGGAGA	16075	CCATGGTGCATCTGACTCCTG	16991	cCas9-v42	3	1
76	aCAGGA	16076	GCAGTAACGGCAGACTTCTCC	16992	cCas9-v17	3	1
77	aCAGGA	16077	GCAGTAACGGCAGACTTCTCC	16993	cCas9-v42	3	1
78	tGGA	16078	CATGGTGCATCTGACTCCTG	16994	SpyCas9-3var-NRRH	3	1
79	GtGGA	16079	acACCATGGTGCATCTGACTCCT	16995	SauCas9	4	1
80	GtGGA	16080	ACCATGGTGCATCTGACTCCT	16996	SauCas9KKH	4	1
81	CaCAG	16081	GGCAGTAACGGCAGACTTCTC	16997	SauCas9KKH	4	1
82	GtGG	16082	ACCATGGTGCATCTGACTCCT	16998	SauriCas9	4	1
83	GtGG	16083	ACCATGGTGCATCTGACTCCT	16999	SauriCas9-KKH	4	1
84	GtG	16084	CCATGGTGCATCTGACTCCT	17000	ScaCas9	4	1
85	GtG	16085	CCATGGTGCATCTGACTCCT	17001	ScaCas9-HiFi-Sc++	4	1
86	GtG	16086	CCATGGTGCATCTGACTCCT	17002	ScaCas9-Sc++	4	1
87	GtG	16087	CCATGGTGCATCTGACTCCT	17003	SpyCas9-SpRY	4	1
88	CaC	16088	GCAGTAACGGCAGACTTCTC	17004	SpyCas9-SpRY	4	1
89	GtGGAG	16089	ACCATGGTGCATCTGACTCCT	17005	cCas9-v17	4	1
90	GtGGAG	16090	ACCATGGTGCATCTGACTCCT	17006	cCas9-v42	4	1
91	CaCAGG	16091	GGCAGTAACGGCAGACTTCTC	17007	cCas9-v17	4	1
92	CaCAGG	16092	GGCAGTAACGGCAGACTTCTC	17008	cCas9-v42	4	1
93	CaCA	16093	GCAGTAACGGCAGACTTCTC	17009	SpyCas9-3var-NRCH	4	1
94	TGtGG	16094	CACCATGGTGCATCTGACTCC	17010	SauCas9KKH	5	1
95	TG	16095	ACCATGGTGCATCTGACTCC	17011	SpyCas9-NG	5	0
96	TG	16096	ACCATGGTGCATCTGACTCC	17012	SpyCas9-xCas	5	0
97	TG	16097	ACCATGGTGCATCTGACTCC	17013	SpyCas9-xCas-NG	5	0

98	TGt	16098	ACCATGGTGCATCTGACTCC	17014	SpyCas9-SpG	5	1
99	TGt	16099	ACCATGGTGCATCTGACTCC	17015	SpyCas9-SpRY	5	1
100	CCa	16100	GGCAGTAACGGCAGACTTCT	17016	SpyCas9-SpRY	5	1
101	CTG	16101	CACCATGGTGCATCTGACTC	17017	ScaCas9	6	0
102	CTG	16102	CACCATGGTGCATCTGACTC	17018	ScaCas9-HiFi-Sc++	6	0
103	CTG	16103	CACCATGGTGCATCTGACTC	17019	ScaCas9-Sc++	6	0
104	CTG	16104	CACCATGGTGCATCTGACTC	17020	SpyCas9-SpRY	6	0
105	TCC	16105	GGGCAGTAACGGCAGACTTC	17021	SpyCas9-SpRY	6	0
106	TCCaCAGG	16106	acagGGCAGTAACGGCAGACTTC	17022	BlatCas9	6	1
107	TCCaC	16107	acagGGCAGTAACGGCAGACTTC	17023	BlatCas9	6	1
108	CTC	16108	AGGGCAGTAACGGCAGACTT	17024	SpyCas9-SpRY	7	0
109	CCT	16109	ACACCATGGTGCATCTGACT	17025	SpyCas9-SpRY	7	0
110	TCT	16110	CAGGGCAGTAACGGCAGACT	17026	SpyCas9-SpRY	8	0
111	TCC	16111	GACACCATGGTGCATCTGAC	17027	SpyCas9-SpRY	8	0
112	TCTCC	16112	ccacAGGGCAGTAACGGCAGACT	17028	BlatCas9	8	0
113	TTCTCC	16113	ccCCACAGGGCAGTAACGGCAGAC	17029	Nme2Cas9	9	0
114	TTC	16114	ACAGGGCAGTAACGGCAGAC	17030	SpyCas9-SpRY	9	0
115	CTC	16115	AGACACCATGGTGCATCTGA	17031	SpyCas9-SpRY	9	0
116	TTCTC	16116	cccaCAGGGCAGTAACGGCAGAC	17032	BlatCas9	9	0
117	CTT	16117	CACAGGGCAGTAACGGCAGA	17033	SpyCas9-SpRY	10	0
118	ACT	16118	CAGACACCATGGTGCATCTG	17034	SpyCas9-SpRY	10	0
119	ACTCCTGt	16119	aaacAGACACCATGGTGCATCTG	17035	BlatCas9	10	1
120	ACTCC	16120	aaacAGACACCATGGTGCATCTG	17036	BlatCas9	10	0
121	GACTCC	16121	tcAAACAGACACCATGGTGCATCT	17037	Nme2Cas9	11	0
122	GAC	16122	ACAGACACCATGGTGCATCT	17038	SpyCas9-SpRY	11	0
123	ACT	16123	CCACAGGGCAGTAACGGCAG	17039	SpyCas9-SpRY	11	0
124	GACTCCTG	16124	caaaCAGACACCATGGTGCATCT	17040	BlatCas9	11	0

125	ACTTC	16125	gcccCACAGGGCAGTAACGGCAG	17041	BlatCas9	11	0
126	GACTC	16126	caaaCAGACACCATGGTGCATCT	17042	BlatCas9	11	0
127	GACT	16127	ACAGACACCATGGTGCATCT	17043	SpyCas9-3var-NRCH	11	0
128	TG	16128	AACAGACACCATGGTGCATC	17044	SpyCas9-NG	12	0
129	TG	16129	AACAGACACCATGGTGCATC	17045	SpyCas9-xCas	12	0
130	TG	16130	AACAGACACCATGGTGCATC	17046	SpyCas9-xCas-NG	12	0
131	GAC	16131	CCCACAGGGCAGTAACGGCA	17047	SpyCas9-SpRY	12	0
132	TGA	16132	AACAGACACCATGGTGCATC	17048	SpyCas9-SpG	12	0
133	TGA	16133	AACAGACACCATGGTGCATC	17049	SpyCas9-SpRY	12	0
134	TGACTCC	16134	CAAACAGACACCATGGTGCATC	17050	CdiCas9	12	0
135	TGAC	16135	AACAGACACCATGGTGCATC	17051	SpyCas9-3var-NRRH	12	0
136	TGAC	16136	AACAGACACCATGGTGCATC	17052	SpyCas9-VQR	12	0
137	GACT	16137	CCCACAGGGCAGTAACGGCA	17053	SpyCas9-3var-NRCH	12	0
138	CTG	16138	AAACAGACACCATGGTGCAT	17054	ScaCas9	13	0
139	CTG	16139	AAACAGACACCATGGTGCAT	17055	ScaCas9-HiFi-Sc++	13	0
140	CTG	16140	AAACAGACACCATGGTGCAT	17056	ScaCas9-Sc++	13	0
141	CTG	16141	AAACAGACACCATGGTGCAT	17057	SpyCas9-SpRY	13	0
142	AG	16142	CCCCACAGGGCAGTAACGGC	17058	SpyCas9-NG	13	0
143	AG	16143	CCCCACAGGGCAGTAACGGC	17059	SpyCas9-xCas	13	0
144	AG	16144	CCCCACAGGGCAGTAACGGC	17060	SpyCas9-xCas-NG	13	0
145	AGA	16145	CCCCACAGGGCAGTAACGGC	17061	SpyCas9-SpG	13	0
146	AGA	16146	CCCCACAGGGCAGTAACGGC	17062	SpyCas9-SpRY	13	0
147	CTGAC	16147	ctcaAACAGACACCATGGTGCAT	17063	BlatCas9	13	0
148	CTGACT	16148	CAAACAGACACCATGGTGCAT	17064	cCas9-v16	13	0
149	CTGACT	16149	CAAACAGACACCATGGTGCAT	17065	cCas9-v21	13	0

150	AGACTTC	16150	TGCCCCACAGGGCAGTAACGGC	17066	CdiCas9	13	0
151	CTGACTC	16151	TCAAACAGACACCATGGTGCAT	17067	CdiCas9	13	0
152	AGAC	16152	CCCCACAGGGCAGTAACGGC	17068	SpyCas9-3var-NRRH	13	0
153	AGAC	16153	CCCCACAGGGCAGTAACGGC	17069	SpyCas9-VQR	13	0
154	TCTGA	16154	TCAAACAGACACCATGGTGCA	17070	SauCas9KKH	14	0
155	CAG	16155	GCCCCACAGGGCAGTAACGG	17071	ScaCas9	14	0
156	CAG	16156	GCCCCACAGGGCAGTAACGG	17072	ScaCas9-HiFi-Sc++	14	0
157	CAG	16157	GCCCCACAGGGCAGTAACGG	17073	ScaCas9-Sc++	14	0
158	CAG	16158	GCCCCACAGGGCAGTAACGG	17074	SpyCas9-SpRY	14	0
159	TCT	16159	CAAACAGACACCATGGTGCA	17075	SpyCas9-SpRY	14	0
160	CAGAC	16160	cttgCCCCACAGGGCAGTAACGG	17076	BlatCas9	14	0
161	CAGACT	16161	TGCCCCACAGGGCAGTAACGG	17077	cCas9-v16	14	0
162	CAGACT	16162	TGCCCCACAGGGCAGTAACGG	17078	cCas9-v21	14	0
163	CAGACTT	16163	TTGCCCCACAGGGCAGTAACGG	17079	CdiCas9	14	0
164	CAGA	16164	GCCCCACAGGGCAGTAACGG	17080	SpyCas9-3var-NRRH	14	0
165	GCAGA	16165	TTGCCCCACAGGGCAGTAACG	17081	SauCas9KKH	15	0
166	GCAG	16166	TTGCCCCACAGGGCAGTAACG	17082	SauriCas9-KKH	15	0
167	GCA	16167	TGCCCCACAGGGCAGTAACG	17083	SpyCas9-SpRY	15	0
168	ATC	16168	TCAAACAGACACCATGGTGC	17084	SpyCas9-SpRY	15	0
169	GCAGAC	16169	TTGCCCCACAGGGCAGTAACG	17085	cCas9-v17	15	0
170	GCAGAC	16170	TTGCCCCACAGGGCAGTAACG	17086	cCas9-v42	15	0
171	ATCTGACT	16171	aaccTCAAACAGACACCATGGTGC	17087	NmeCas9	15	0
172	GGCAG	16172	CTTGCCCCACAGGGCAGTAAC	17088	SauCas9KKH	16	0
173	GG	16173	TTGCCCCACAGGGCAGTAAC	17089	SpyCas9-NG	16	0
174	GG	16174	TTGCCCCACAGGGCAGTAAC	17090	SpyCas9-xCas	16	0
175	GG	16175	TTGCCCCACAGGGCAGTAAC	17091	SpyCas9-xCas-NG	16	0

176	GGC	16176	TTGCCCCACAGGGCAGTAAC	17092	SpyCas9-SpG	16	0
177	GGC	16177	TTGCCCCACAGGGCAGTAAC	17093	SpyCas9-SpRY	16	0
178	CAT	16178	CTCAAACAGACACCATGGTG	17094	SpyCas9-SpRY	16	0
179	GGCAGA	16179	CTTGCCCCACAGGGCAGTAAC	17095	cCas9-v17	16	0
180	GGCAGA	16180	CTTGCCCCACAGGGCAGTAAC	17096	cCas9-v42	16	0
181	GGCAGACT	16181	caccTTGCCCCACAGGGCAGTAAC	17097	NmeCas9	16	0
182	CATC	16182	CTCAAACAGACACCATGGTG	17098	SpyCas9-3var-NRTH	16	0
183	GGCA	16183	TTGCCCCACAGGGCAGTAAC	17099	SpyCas9-3var-NRCH	16	0
184	CGG	16184	CTTGCCCCACAGGGCAGTAA	17100	ScaCas9	17	0
185	CGG	16185	CTTGCCCCACAGGGCAGTAA	17101	ScaCas9-HiFi-Sc++	17	0
186	CGG	16186	CTTGCCCCACAGGGCAGTAA	17102	ScaCas9-Sc++	17	0
187	CGG	16187	CTTGCCCCACAGGGCAGTAA	17103	SpyCas9	17	0
188	CGG	16188	CTTGCCCCACAGGGCAGTAA	17104	SpyCas9-HF1	17	0
189	CGG	16189	CTTGCCCCACAGGGCAGTAA	17105	SpyCas9-SpG	17	0
190	CGG	16190	CTTGCCCCACAGGGCAGTAA	17106	SpyCas9-SpRY	17	0
191	CG	16191	CTTGCCCCACAGGGCAGTAA	17107	SpyCas9-NG	17	0
192	CG	16192	CTTGCCCCACAGGGCAGTAA	17108	SpyCas9-xCas	17	0
193	CG	16193	CTTGCCCCACAGGGCAGTAA	17109	SpyCas9-xCas-NG	17	0
194	GCA	16194	CCTCAAACAGACACCATGGT	17110	SpyCas9-SpRY	17	0
195	GCATCTGA	16195	caacCTCAAACAGACACCATGGT	17111	BlatCas9	17	0
196	GCATC	16196	caacCTCAAACAGACACCATGGT	17112	BlatCas9	17	0
197	CGGC	16197	CTTGCCCCACAGGGCAGTAA	17113	SpyCas9-3var-NRRH	17	0
198	ACGG	16198	ACCTTGCCCCACAGGGCAGTA	17114	SauriCas9	18	0
199	ACGG	16199	ACCTTGCCCCACAGGGCAGTA	17115	SauriCas9-KKH	18	0
200	ACG	16200	CCTTGCCCCACAGGGCAGTA	17116	ScaCas9	18	0

201	ACG	16201	CCTTGCCCCACAGGGCAGTA	17117	ScaCas9-HiFi-Sc++	18	0
202	ACG	16202	CCTTGCCCCACAGGGCAGTA	17118	ScaCas9-Sc++	18	0
203	ACG	16203	CCTTGCCCCACAGGGCAGTA	17119	SpyCas9-SpRY	18	0
204	TG	16204	ACCTCAAACAGACACCATGG	17120	SpyCas9-NG	18	0
205	TG	16205	ACCTCAAACAGACACCATGG	17121	SpyCas9-xCas	18	0
206	TG	16206	ACCTCAAACAGACACCATGG	17122	SpyCas9-xCas-NG	18	0
207	TGC	16207	ACCTCAAACAGACACCATGG	17123	SpyCas9-SpG	18	0
208	TGC	16208	ACCTCAAACAGACACCATGG	17124	SpyCas9-SpRY	18	0
209	ACGGCAGA	16209	tcacCTTGCCCCACAGGGCAGTA	17125	BlatCas9	18	0
210	ACGGC	16210	tcacCTTGCCCCACAGGGCAGTA	17126	BlatCas9	18	0
211	TGCA	16211	ACCTCAAACAGACACCATGG	17127	SpyCas9-3var-NRCH	18	0
212	AACGG	16212	CACCTTGCCCCACAGGGCAGT	17128	SauCas9KKH	19	0
213	GTG	16213	AACCTCAAACAGACACCATG	17129	ScaCas9	19	0
214	GTG	16214	AACCTCAAACAGACACCATG	17130	ScaCas9-HiFi-Sc++	19	0
215	GTG	16215	AACCTCAAACAGACACCATG	17131	ScaCas9-Sc++	19	0
216	GTG	16216	AACCTCAAACAGACACCATG	17132	SpyCas9-SpRY	19	0
217	AAC	16217	ACCTTGCCCCACAGGGCAGT	17133	SpyCas9-SpRY	19	0
218	AACGGC	16218	CACCTTGCCCCACAGGGCAGT	17134	cCas9-v17	19	0
219	AACGGC	16219	CACCTTGCCCCACAGGGCAGT	17135	cCas9-v42	19	0
220	GTGCATC	16220	GCAACCTCAAACAGACACCATG	17136	CdiCas9	19	0
221	GG	16221	CAACCTCAAACAGACACCAT	17137	SpyCas9-NG	20	0
222	GG	16222	CAACCTCAAACAGACACCAT	17138	SpyCas9-xCas	20	0
223	GG	16223	CAACCTCAAACAGACACCAT	17139	SpyCas9-xCas-NG	20	0
224	TAA	16224	CACCTTGCCCCACAGGGCAG	17140	SpyCas9-SpRY	20	0
225	GGT	16225	CAACCTCAAACAGACACCAT	17141	SpyCas9-SpG	20	0
226	GGT	16226	CAACCTCAAACAGACACCAT	17142	SpyCas9-SpRY	20	0

227	GGTGC	16227	tagcAACCTCAAACAGACACCAT	17143	BlatCas9	20	0
228	TAAC	16228	CACCTTGCCCCACAGGGCAG	17144	SpyCas9-3var-NRRH	20	0
229	TAAC	16229	tcACCTTGCCCCACAGGGCAG	17145	iSpyMacCas9	20	0
230	TGG	16230	GCAACCTCAAACAGACACCA	17146	ScaCas9	21	0
231	TGG	16231	GCAACCTCAAACAGACACCA	17147	ScaCas9-HiFi-Sc++	21	0
232	TGG	16232	GCAACCTCAAACAGACACCA	17148	ScaCas9-Sc++	21	0
233	TGG	16233	GCAACCTCAAACAGACACCA	17149	SpyCas9	21	0
234	TGG	16234	GCAACCTCAAACAGACACCA	17150	SpyCas9-HF1	21	0
235	TGG	16235	GCAACCTCAAACAGACACCA	17151	SpyCas9-SpG	21	0
236	TGG	16236	GCAACCTCAAACAGACACCA	17152	SpyCas9-SpRY	21	0
237	TG	16237	GCAACCTCAAACAGACACCA	17153	SpyCas9-NG	21	0
238	TG	16238	GCAACCTCAAACAGACACCA	17154	SpyCas9-xCas	21	0
239	TG	16239	GCAACCTCAAACAGACACCA	17155	SpyCas9-xCas-NG	21	0
240	GTA	16240	TCACCTTGCCCCACAGGGCA	17156	SpyCas9-SpRY	21	0
241	GTAAC	16241	cgttCACCTTGCCCCACAGGGCA	17157	BlatCas9	21	0
242	TGGT	16242	GCAACCTCAAACAGACACCA	17158	SpyCas9-3var-NRRH	21	0
243	AGTAA	16243	GTTCACCTTGCCCCACAGGGC	17159	SauCas9KKH	22	0
244	ATGG	16244	TAGCAACCTCAAACAGACACC	17160	SauriCas9	22	0
245	ATGG	16245	TAGCAACCTCAAACAGACACC	17161	SauriCas9-KKH	22	0
246	ATG	16246	AGCAACCTCAAACAGACACC	17162	ScaCas9	22	0
247	ATG	16247	AGCAACCTCAAACAGACACC	17163	ScaCas9-HiFi-Sc++	22	0
248	ATG	16248	AGCAACCTCAAACAGACACC	17164	ScaCas9-Sc++	22	0
249	ATG	16249	AGCAACCTCAAACAGACACC	17165	SpyCas9-SpRY	22	0
250	AG	16250	TTCACCTTGCCCCACAGGGC	17166	SpyCas9-NG	22	0
251	AG	16251	TTCACCTTGCCCCACAGGGC	17167	SpyCas9-xCas	22	0
252	AG	16252	TTCACCTTGCCCCACAGGGC	17168	SpyCas9-xCas-NG	22	0

253	AGT	16253	TTCACCTTGCCCCACAGGGC	17169	SpyCas9-SpG	22	0
254	AGT	16254	TTCACCTTGCCCCACAGGGC	17170	SpyCas9-SpRY	22	0
255	ATGGTG	16255	TAGCAACCTCAAACAGACACC	17171	cCas9-v16	22	0
256	ATGGTG	16256	TAGCAACCTCAAACAGACACC	17172	cCas9-v21	22	0
257	AGTA	16257	TTCACCTTGCCCCACAGGGC	17173	SpyCas9-3var-NRTH	22	0
258	CATGG	16258	CTAGCAACCTCAAACAGACAC	17174	SauCas9KKH	23	0
259	CATGGT	16259	CTAGCAACCTCAAACAGACAC	17175	SauCas9KKH	23	0
260	CAG	16260	GTTCACCTTGCCCCACAGGG	17176	ScaCas9	23	0
261	CAG	16261	GTTCACCTTGCCCCACAGGG	17177	ScaCas9-HiFi-Sc++	23	0
262	CAG	16262	GTTCACCTTGCCCCACAGGG	17178	ScaCas9-Sc++	23	0
263	CAG	16263	GTTCACCTTGCCCCACAGGG	17179	SpyCas9-SpRY	23	0
264	CAT	16264	TAGCAACCTCAAACAGACAC	17180	SpyCas9-SpRY	23	0
265	CAGTAAC	16265	ACGTTCACCTTGCCCCACAGGG	17181	CdiCas9	23	0
266	CAGT	16266	GTTCACCTTGCCCCACAGGG	17182	SpyCas9-3var-NRRH	23	0
267	GCAG	16267	ACGTTCACCTTGCCCCACAGG	17183	SauriCas9-KKH	24	0
268	GCA	16268	CGTTCACCTTGCCCCACAGG	17184	SpyCas9-SpRY	24	0
269	CCA	16269	CTAGCAACCTCAAACAGACA	17185	SpyCas9-SpRY	24	0
270	GGCAG	16270	CACGTTCACCTTGCCCCACAG	17186	SauCas9KKH	25	0
271	GGCAGT	16271	CACGTTCACCTTGCCCCACAG	17187	SauCas9KKH	25	0
272	GGCAGT	16272	CACGTTCACCTTGCCCCACAG	17188	cCas9-v17	25	0
273	GGCAGT	16273	CACGTTCACCTTGCCCCACAG	17189	cCas9-v42	25	0
274	GG	16274	ACGTTCACCTTGCCCCACAG	17190	SpyCas9-NG	25	0
275	GG	16275	ACGTTCACCTTGCCCCACAG	17191	SpyCas9-xCas	25	0
276	GG	16276	ACGTTCACCTTGCCCCACAG	17192	SpyCas9-xCas-NG	25	0
277	GGC	16277	ACGTTCACCTTGCCCCACAG	17193	SpyCas9-SpG	25	0
278	GGC	16278	ACGTTCACCTTGCCCCACAG	17194	SpyCas9-SpRY	25	0

279	ACC	16279	ACTAGCAACCTCAAACAGAC	17195	SpyCas9-SpRY	25	0
280	GGCA	16280	ACGTTCACCTTGCCCCACAG	17196	SpyCas9-3var-NRCH	25	0
281	GGG	16281	CACGTTCACCTTGCCCCACA	17197	ScaCas9	26	0
282	GGG	16282	CACGTTCACCTTGCCCCACA	17198	ScaCas9-HiFi-Sc++	26	0
283	GGG	16283	CACGTTCACCTTGCCCCACA	17199	ScaCas9-Sc++	26	0
284	GGG	16284	CACGTTCACCTTGCCCCACA	17200	SpyCas9	26	0
285	GGG	16285	CACGTTCACCTTGCCCCACA	17201	SpyCas9-HF1	26	0
286	GGG	16286	CACGTTCACCTTGCCCCACA	17202	SpyCas9-SpG	26	0
287	GGG	16287	CACGTTCACCTTGCCCCACA	17203	SpyCas9-SpRY	26	0
288	GG	16288	CACGTTCACCTTGCCCCACA	17204	SpyCas9-NG	26	0
289	GG	16289	CACGTTCACCTTGCCCCACA	17205	SpyCas9-xCas	26	0
290	GG	16290	CACGTTCACCTTGCCCCACA	17206	SpyCas9-xCas-NG	26	0
291	CAC	16291	CACTAGCAACCTCAAACAGA	17207	SpyCas9-SpRY	26	0
292	GGGC	16292	CACGTTCACCTTGCCCCACA	17208	SpyCas9-3var-NRRH	26	0
293	CACC	16293	CACTAGCAACCTCAAACAGA	17209	SpyCas9-3var-NRCH	26	0
294	AGGG	16294	TCCACGTTCACCTTGCCCCAC	17210	SauriCas9	27	0
295	AGGG	16295	TCCACGTTCACCTTGCCCCAC	17211	SauriCas9-KKH	27	0
296	AGG	16296	CCACGTTCACCTTGCCCCAC	17212	ScaCas9	27	0
297	AGG	16297	CCACGTTCACCTTGCCCCAC	17213	ScaCas9-HiFi-Sc++	27	0
298	AGG	16298	CCACGTTCACCTTGCCCCAC	17214	ScaCas9-Sc++	27	0
299	AGG	16299	CCACGTTCACCTTGCCCCAC	17215	SpyCas9	27	0
300	AGG	16300	CCACGTTCACCTTGCCCCAC	17216	SpyCas9-HF1	27	0
301	AGG	16301	CCACGTTCACCTTGCCCCAC	17217	SpyCas9-SpG	27	0
302	AGG	16302	CCACGTTCACCTTGCCCCAC	17218	SpyCas9-SpRY	27	0
303	AG	16303	CCACGTTCACCTTGCCCCAC	17219	SpyCas9-NG	27	0

304	AG	16304	CCACGTTCACCTTGCCCCAC	17220	SpyCas9-xCas	27	0
305	AG	16305	CCACGTTCACCTTGCCCCAC	17221	SpyCas9-xCas-NG	27	0
306	ACA	16306	TCACTAGCAACCTCAAACAG	17222	SpyCas9-SpRY	27	0
307	AGGGCAGT	16307	catcCACGTTCACCTTGCCCCAC	17223	BlatCas9	27	0
308	ACACCATG	16308	tgttCACTAGCAACCTCAAACAG	17224	BlatCas9	27	0
309	AGGGC	16309	catcCACGTTCACCTTGCCCCAC	17225	BlatCas9	27	0
310	ACACC	16310	tgttCACTAGCAACCTCAAACAG	17226	BlatCas9	27	0
311	ACACCAT	16311	GTTCACTAGCAACCTCAAACAG	17227	CdiCas9	27	0
312	GACACC	16312	tgTGTTCACTAGCAACCTCAAACA	17228	Nme2Cas9	28	0
313	CAGGG	16313	tcATCCACGTTCACCTTGCCCCA	17229	SauCas9	28	0
314	CAGGG	16314	ATCCACGTTCACCTTGCCCCA	17230	SauCas9KKH	28	0
315	CAGG	16315	ATCCACGTTCACCTTGCCCCA	17231	SauriCas9	28	0
316	CAGG	16316	ATCCACGTTCACCTTGCCCCA	17232	SauriCas9-KKH	28	0
317	CAG	16317	TCCACGTTCACCTTGCCCCA	17233	ScaCas9	28	0
318	CAG	16318	TCCACGTTCACCTTGCCCCA	17234	ScaCas9-HiFi-Sc++	28	0
319	CAG	16319	TCCACGTTCACCTTGCCCCA	17235	ScaCas9-Sc++	28	0
320	CAG	16320	TCCACGTTCACCTTGCCCCA	17236	SpyCas9-SpRY	28	0
321	GAC	16321	TTCACTAGCAACCTCAAACA	17237	SpyCas9-SpRY	28	0
322	GACACCAT	16322	gtgtTCACTAGCAACCTCAAACA	17238	BlatCas9	28	0
323	GACAC	16323	gtgtTCACTAGCAACCTCAAACA	17239	BlatCas9	28	0
324	CAGGGC	16324	ATCCACGTTCACCTTGCCCCA	17240	cCas9-v17	28	0
325	CAGGGC	16325	ATCCACGTTCACCTTGCCCCA	17241	cCas9-v42	28	0
326	GACA	16326	TTCACTAGCAACCTCAAACA	17242	SpyCas9-3var-NRCH	28	0
327	ACAGG	16327	CATCCACGTTCACCTTGCCCC	17243	SauCas9KKH	29	0
328	ACAG	16328	CATCCACGTTCACCTTGCCCC	17244	SauriCas9-KKH	29	0
329	AG	16329	GTTCACTAGCAACCTCAAAC	17245	SpyCas9-NG	29	0

330	AG	16330	GTTCACTAGCAACCTCAAAC	17246	SpyCas9-xCas	29	0
331	AG	16331	GTTCACTAGCAACCTCAAAC	17247	SpyCas9-xCas-NG	29	0
332	AGA	16332	GTTCACTAGCAACCTCAAAC	17248	SpyCas9-SpG	29	0
333	AGA	16333	GTTCACTAGCAACCTCAAAC	17249	SpyCas9-SpRY	29	0
334	ACA	16334	ATCCACGTTCACCTTGCCCC	17250	SpyCas9-SpRY	29	0
335	ACAGGG	16335	CATCCACGTTCACCTTGCCCC	17251	cCas9-v17	29	0
336	ACAGGG	16336	CATCCACGTTCACCTTGCCCC	17252	cCas9-v42	29	0
337	AGACACC	16337	GTGTTCACTAGCAACCTCAAAC	17253	CdiCas9	29	0
338	AGAC	16338	GTTCACTAGCAACCTCAAAC	17254	SpyCas9-3var-NRRH	29	0
339	AGAC	16339	GTTCACTAGCAACCTCAAAC	17255	SpyCas9-VQR	29	0
340	CACAG	16340	TCATCCACGTTCACCTTGCCC	17256	SauCas9KKH	30	0
341	CAG	16341	TGTTCACTAGCAACCTCAAA	17257	ScaCas9	30	0
342	CAG	16342	TGTTCACTAGCAACCTCAAA	17258	ScaCas9-HiFi-Sc++	30	0
343	CAG	16343	TGTTCACTAGCAACCTCAAA	17259	ScaCas9-Sc++	30	0
344	CAG	16344	TGTTCACTAGCAACCTCAAA	17260	SpyCas9-SpRY	30	0
345	CAC	16345	CATCCACGTTCACCTTGCCC	17261	SpyCas9-SpRY	30	0
346	CAGAC	16346	ctgtGTTCACTAGCAACCTCAAA	17262	BlatCas9	30	0
347	CACAGG	16347	TCATCCACGTTCACCTTGCCC	17263	cCas9-v17	30	0
348	CACAGG	16348	TCATCCACGTTCACCTTGCCC	17264	cCas9-v42	30	0
349	CAGACAC	16349	TGTGTTCACTAGCAACCTCAAA	17265	CdiCas9	30	0
350	CAGA	16350	TGTTCACTAGCAACCTCAAA	17266	SpyCas9-3var-NRRH	30	0
351	CACA	16351	CATCCACGTTCACCTTGCCC	17267	SpyCas9-3var-NRCH	30	0
352	ACAGA	16352	TGTGTTCACTAGCAACCTCAA	17268	SauCas9KKH	31	0
353	ACAG	16353	TGTGTTCACTAGCAACCTCAA	17269	SauriCas9-KKH	31	0
354	CCA	16354	TCATCCACGTTCACCTTGCC	17270	SpyCas9-SpRY	31	0

355	ACA	16355	GTGTTCACTAGCAACCTCA A	17271	SpyCas9-SpRY	31	0
356	ACAGAC	16356	TGTGTTCACTAGCAACCTC AA	17272	cCas9-v17	31	0
357	ACAGAC	16357	TGTGTTCACTAGCAACCTC AA	17273	cCas9-v42	31	0
358	ACAGAC AC	16358	acTGTGTTCACTAGCAACCT CAA	17274	CjeCas9	31	0
359	AACAG	16359	CTGTGTTCACTAGCAACCT CA	17275	SauCas9KKH	32	0
360	AAC	16360	TGTGTTCACTAGCAACCTC A	17276	SpyCas9-SpRY	32	0
361	CCC	16361	TTCATCCACGTTCACCTTGC	17277	SpyCas9-SpRY	32	0
362	CCCACA GG	16362	aactTCATCCACGTTCACCTT GC	17278	BlatCas9	32	0
363	CCCAC	16363	aactTCATCCACGTTCACCTT GC	17279	BlatCas9	32	0
364	AACAGA	16364	CTGTGTTCACTAGCAACCT CA	17280	cCas9-v17	32	0
365	AACAGA	16365	CTGTGTTCACTAGCAACCT CA	17281	cCas9-v42	32	0
366	AACAGA CA	16366	caacTGTGTTCACTAGCAACC TCA	17282	NmeCas9	32	0
367	AACA	16367	TGTGTTCACTAGCAACCTC A	17283	SpyCas9-3var-NRCH	32	0
368	AAA	16368	CTGTGTTCACTAGCAACCT C	17284	SpyCas9-SpRY	33	0
369	CCC	16369	CTTCATCCACGTTCACCTTG	17285	SpyCas9-SpRY	33	0
370	AAAC	16370	CTGTGTTCACTAGCAACCT C	17286	SpyCas9-3var-NRRH	33	0
371	AAAC	16371	acTGTGTTCACTAGCAACCT C	17287	iSpyMacCas9	33	0
372	CAA	16372	ACTGTGTTCACTAGCAACC T	17288	SpyCas9-SpRY	34	0
373	GCC	16373	ACTTCATCCACGTTCACCTT	17289	SpyCas9-SpRY	34	0
374	CAAACA GA	16374	acaaCTGTGTTCACTAGCAAC CT	17290	BlatCas9	34	0
375	GCCCC	16375	ccaaCTTCATCCACGTTCACC TT	17291	BlatCas9	34	0
376	CAAAC	16376	acaaCTGTGTTCACTAGCAAC CT	17292	BlatCas9	34	0
377	CAAA	16377	ACTGTGTTCACTAGCAACC T	17293	SpyCas9-3var-NRRH	34	0
378	CAAA	16378	aaCTGTGTTCACTAGCAACC T	17294	iSpyMacCas9	34	0
379	TGCCCC	16379	caCCAACTTCATCCACGTTC ACCT	17295	Nme2Cas9	35	0

380	TCAAA	16380	CAACTGTGTTCACTAGCAACC	17296	SauCas9KKH	35	0
381	TG	16381	AACTTCATCCACGTTCACCT	17297	SpyCas9-NG	35	0
382	TG	16382	AACTTCATCCACGTTCACCT	17298	SpyCas9-xCas	35	0
383	TG	16383	AACTTCATCCACGTTCACCT	17299	SpyCas9-xCas-NG	35	0
384	TGC	16384	AACTTCATCCACGTTCACCT	17300	SpyCas9-SpG	35	0
385	TGC	16385	AACTTCATCCACGTTCACCT	17301	SpyCas9-SpRY	35	0
386	TCA	16386	AACTGTGTTCACTAGCAACC	17302	SpyCas9-SpRY	35	0
387	TGCCC	16387	accaACTTCATCCACGTTCACCT	17303	BlatCas9	35	0
388	TCAAAC	16388	CAACTGTGTTCACTAGCAACC	17304	cCas9-v17	35	0
389	TCAAAC	16389	CAACTGTGTTCACTAGCAACC	17305	cCas9-v42	35	0
390	TGCC	16390	AACTTCATCCACGTTCACCT	17306	SpyCas9-3var-NRCH	35	0
391	TTGCCC	16391	ccACCAACTTCATCCACGTTCACC	17307	Nme2Cas9	36	0
392	CTCAA	16392	ACAACTGTGTTCACTAGCAAC	17308	SauCas9KKH	36	0
393	TTG	16393	CAACTTCATCCACGTTCACC	17309	ScaCas9	36	0
394	TTG	16394	CAACTTCATCCACGTTCACC	17310	ScaCas9-HiFi-Sc++	36	0
395	TTG	16395	CAACTTCATCCACGTTCACC	17311	ScaCas9-Sc++	36	0
396	TTG	16396	CAACTTCATCCACGTTCACC	17312	SpyCas9-SpRY	36	0
397	CTC	16397	CAACTGTGTTCACTAGCAAC	17313	SpyCas9-SpRY	36	0
398	TTGCC	16398	caccAACTTCATCCACGTTCACC	17314	BlatCas9	36	0
399	CTCAAA	16399	ACAACTGTGTTCACTAGCAAC	17315	cCas9-v17	36	0
400	CTCAAA	16400	ACAACTGTGTTCACTAGCAAC	17316	cCas9-v42	36	0
401	TTGCCCC	16401	ACCAACTTCATCCACGTTCACC	17317	CdiCas9	36	0
402	CTTGCC	16402	acCACCAACTTCATCCACGTTCAC	17318	Nme2Cas9	37	0
403	CTT	16403	CCAACTTCATCCACGTTCAC	17319	SpyCas9-SpRY	37	0
404	CCT	16404	ACAACTGTGTTCACTAGCAA	17320	SpyCas9-SpRY	37	0
405	CTTGC	16405	ccacCAACTTCATCCACGTTCAC	17321	BlatCas9	37	0

406	CCT	16406	ACCAACTTCATCCACGTTCA	17322	SpyCas9-SpRY	38	0
407	ACC	16407	CACAACTGTGTTCACTAGCA	17323	SpyCas9-SpRY	38	0
408	ACCTCAAA	16408	tgacACAACTGTGTTCACTAGCA	17324	BlatCas9	38	0
409	ACCTCAAA	16409	tgacACAACTGTGTTCACTAGCA	17325	BlatCas9	38	0
410	ACCTCAAA	16410	tgACACAACTGTGTTCACTAGCA	17326	GeoCas9	38	0
411	ACCTC	16411	tgacACAACTGTGTTCACTAGCA	17327	BlatCas9	38	0
412	AAC	16412	ACACAACTGTGTTCACTAGC	17328	SpyCas9-SpRY	39	0
413	ACC	16413	CACCAACTTCATCCACGTTC	17329	SpyCas9-SpRY	39	0
414	AACC	16414	ACACAACTGTGTTCACTAGC	17330	SpyCas9-3var-NRCH	39	0
415	CAC	16415	CCACCAACTTCATCCACGTT	17331	SpyCas9-SpRY	40	0
416	CAA	16416	GACACAACTGTGTTCACTAG	17332	SpyCas9-SpRY	40	0
417	CAACC	16417	tctgACACAACTGTGTTCACTAG	17333	BlatCas9	40	0
418	CAACCTC	16418	CTGACACAACTGTGTTCACTAG	17334	CdiCas9	40	0
419	CAAC	16419	GACACAACTGTGTTCACTAG	17335	SpyCas9-3var-NRRH	40	0
420	CAAC	16420	tgACACAACTGTGTTCACTAG	17336	iSpyMacCas9	40	0
421	CACC	16421	CCACCAACTTCATCCACGTT	17337	SpyCas9-3var-NRCH	40	0
422	GCAACC	16422	ctTCTGACACAACTGTGTTCACTA	17338	Nme2Cas9	41	0
423	TCA	16423	ACCACCAACTTCATCCACGT	17339	SpyCas9-SpRY	41	0
424	GCA	16424	TGACACAACTGTGTTCACTA	17340	SpyCas9-SpRY	41	0
425	TCACCTTG	16425	ctcaCCACCAACTTCATCCACGT	17341	BlatCas9	41	0
426	TCACC	16426	ctcaCCACCAACTTCATCCACGT	17342	BlatCas9	41	0
427	GCAAC	16427	ttctGACACAACTGTGTTCACTA	17343	BlatCas9	41	0
428	TCACCTT	16428	TCACCACCAACTTCATCCACGT	17344	CdiCas9	41	0
429	GCAACCT	16429	TCTGACACAACTGTGTTCACTA	17345	CdiCas9	41	0
430	TTCACC	16430	gcCTCACCACCAACTTCATCCACG	17346	Nme2Cas9	42	0

431	AGCAA	16431	TCTGACACAACTGTGTTCACT	17347	SauCas9KKH	42	0
432	AG	16432	CTGACACAACTGTGTTCACT	17348	SpyCas9-NG	42	0
433	AG	16433	CTGACACAACTGTGTTCACT	17349	SpyCas9-xCas	42	0
434	AG	16434	CTGACACAACTGTGTTCACT	17350	SpyCas9-xCas-NG	42	0
435	AGC	16435	CTGACACAACTGTGTTCACT	17351	SpyCas9-SpG	42	0
436	AGC	16436	CTGACACAACTGTGTTCACT	17352	SpyCas9-SpRY	42	0
437	TTC	16437	CACCACCAACTTCATCCACG	17353	SpyCas9-SpRY	42	0
438	TTCACCTT	16438	cctcACCACCAACTTCATCCACG	17354	BlatCas9	42	0
439	TTCAC	16439	cctcACCACCAACTTCATCCACG	17355	BlatCas9	42	0
440	AGCAAC	16440	TCTGACACAACTGTGTTCACT	17356	cCas9-v17	42	0
441	AGCAAC	16441	TCTGACACAACTGTGTTCACT	17357	cCas9-v42	42	0
442	AGCA	16442	CTGACACAACTGTGTTCACT	17358	SpyCas9-3var-NRCH	42	0
443	TAG	16443	TCTGACACAACTGTGTTCAC	17359	ScaCas9	43	0
444	TAG	16444	TCTGACACAACTGTGTTCAC	17360	ScaCas9-HiFi-Sc++	43	0
445	TAG	16445	TCTGACACAACTGTGTTCAC	17361	ScaCas9-Sc++	43	0
446	TAG	16446	TCTGACACAACTGTGTTCAC	17362	SpyCas9-SpRY	43	0
447	GTT	16447	TCACCACCAACTTCATCCAC	17363	SpyCas9-SpRY	43	0
448	TAGCAAC	16448	CTTCTGACACAACTGTGTTCAC	17364	CdiCas9	43	0
449	TAGC	16449	TCTGACACAACTGTGTTCAC	17365	SpyCas9-3var-NRRH	43	0
450	TAGCAA	16450	TCTGACACAACTGTGTTCAC	17366	St1Cas9-LMG1831	43	0
451	CTAG	16451	CTTCTGACACAACTGTGTTCA	17367	SauriCas9-KKH	44	0
452	CG	16452	CTCACCACCAACTTCATCCA	17368	SpyCas9-NG	44	0
453	CG	16453	CTCACCACCAACTTCATCCA	17369	SpyCas9-xCas	44	0
454	CG	16454	CTCACCACCAACTTCATCCA	17370	SpyCas9-xCas-NG	44	0
455	CGT	16455	CTCACCACCAACTTCATCCA	17371	SpyCas9-SpG	44	0
456	CGT	16456	CTCACCACCAACTTCATCCA	17372	SpyCas9-SpRY	44	0

457	CTA	16457	TTCTGACACAACTGTGTTCA	17373	SpyCas9-SpRY	44	0
458	CGTTC	16458	ggccTCACCACCAACTTCATCCA	17374	BlatCas9	44	0
459	CTAGC	16459	tgctTCTGACACAACTGTGTTCA	17375	BlatCas9	44	0
460	CGTT	16460	CTCACCACCAACTTCATCCA	17376	SpyCas9-3var-NRTH	44	0
461	ACTAG	16461	GCTTCTGACACAACTGTGTTC	17377	SauCas9KKH	45	0
462	ACG	16462	CCTCACCACCAACTTCATCC	17378	ScaCas9	45	0
463	ACG	16463	CCTCACCACCAACTTCATCC	17379	ScaCas9-HiFi-Sc++	45	0
464	ACG	16464	CCTCACCACCAACTTCATCC	17380	ScaCas9-Sc++	45	0
465	ACG	16465	CCTCACCACCAACTTCATCC	17381	SpyCas9-SpRY	45	0
466	ACT	16466	CTTCTGACACAACTGTGTTC	17382	SpyCas9-SpRY	45	0
467	CAC	16467	GCCTCACCACCAACTTCATC	17383	SpyCas9-SpRY	46	0
468	CAC	16468	GCTTCTGACACAACTGTGTT	17384	SpyCas9-SpRY	46	0
469	CACGTT	16469	GGCCTCACCACCAACTTCATC	17385	cCas9-v16	46	0
470	CACGTT	16470	GGCCTCACCACCAACTTCATC	17386	cCas9-v21	46	0
471	CACT	16471	GCTTCTGACACAACTGTGTT	17387	SpyCas9-3var-NRCH	46	0
472	CCACGTT	16472	ccaGGGCCTCACCACCAACTTCAT	17388	PpnCas9	47	0
473	CCA	16473	GGCCTCACCACCAACTTCAT	17389	SpyCas9-SpRY	47	0
474	TCA	16474	TGCTTCTGACACAACTGTGT	17390	SpyCas9-SpRY	47	0
475	TCC	16475	GGGCCTCACCACCAACTTCA	17391	SpyCas9-SpRY	48	0
476	TTC	16476	TTGCTTCTGACACAACTGTG	17392	SpyCas9-SpRY	48	0
477	TCCACGTT	16477	ccagGGCCTCACCACCAACTTCA	17393	BlatCas9	48	0
478	TTCACTAG	16478	cattTGCTTCTGACACAACTGTG	17394	BlatCas9	48	0
479	TCCAC	16479	ccagGGCCTCACCACCAACTTCA	17395	BlatCas9	48	0
480	TTCAC	16480	cattTGCTTCTGACACAACTGTG	17396	BlatCas9	48	0
481	TTCACT	16481	TTTGCTTCTGACACAACTGTG	17397	cCas9-v16	48	0
482	TTCACT	16482	TTTGCTTCTGACACAACTGTG	17398	cCas9-v21	48	0

483	ATC	16483	AGGGCCTCACCACCAACTTC	17399	SpyCas9-SpRY	49	0
484	GTT	16484	TTTGCTTCTGACACAACTGT	17400	SpyCas9-SpRY	49	0
485	TG	16485	ATTTGCTTCTGACACAACTG	17401	SpyCas9-NG	50	0
486	TG	16486	ATTTGCTTCTGACACAACTG	17402	SpyCas9-xCas	50	0
487	TG	16487	ATTTGCTTCTGACACAACTG	17403	SpyCas9-xCas-NG	50	0
488	CAT	16488	CAGGGCCTCACCACCAACTT	17404	SpyCas9-SpRY	50	0
489	TGT	16489	ATTTGCTTCTGACACAACTG	17405	SpyCas9-SpG	50	0
490	TGT	16490	ATTTGCTTCTGACACAACTG	17406	SpyCas9-SpRY	50	0
491	CATCC	16491	gcccAGGGCCTCACCACCAACTT	17407	BlatCas9	50	0
492	TGTTC	16492	tacaTTTGCTTCTGACACAACTG	17408	BlatCas9	50	0
493	CATC	16493	CAGGGCCTCACCACCAACTT	17409	SpyCas9-3var-NRTH	50	0
494	TGTT	16494	ATTTGCTTCTGACACAACTG	17410	SpyCas9-3var-NRTH	50	0
495	TCATCC	16495	ctGCCCAGGGCCTCACCACCAACT	17411	Nme2Cas9	51	0
496	GTG	16496	CATTTGCTTCTGACACAACT	17412	ScaCas9	51	0
497	GTG	16497	CATTTGCTTCTGACACAACT	17413	ScaCas9-HiFi-Sc++	51	0
498	GTG	16498	CATTTGCTTCTGACACAACT	17414	ScaCas9-Sc++	51	0
499	GTG	16499	CATTTGCTTCTGACACAACT	17415	SpyCas9-SpRY	51	0
500	TCA	16500	CCAGGGCCTCACCACCAACT	17416	SpyCas9-SpRY	51	0
501	TCATC	16501	tgccCAGGGCCTCACCACCAACT	17417	BlatCas9	51	0
502	TG	16502	ACATTTGCTTCTGACACAAC	17418	SpyCas9-NG	52	0
503	TG	16503	ACATTTGCTTCTGACACAAC	17419	SpyCas9-xCas	52	0
504	TG	16504	ACATTTGCTTCTGACACAAC	17420	SpyCas9-xCas-NG	52	0
505	TGT	16505	ACATTTGCTTCTGACACAAC	17421	SpyCas9-SpG	52	0
506	TGT	16506	ACATTTGCTTCTGACACAAC	17422	SpyCas9-SpRY	52	0
507	TTC	16507	CCCAGGGCCTCACCACCAAC	17423	SpyCas9-SpRY	52	0
508	CTGTGTT	16508	tgcTTACATTTGCTTCTGACACAA	17424	PpnCas9	53	0

509	CTG	16509	TACATTTGCTTCTGACACAA	17425	ScaCas9	53	0
510	CTG	16510	TACATTTGCTTCTGACACAA	17426	ScaCas9-HiFi-Sc++	53	0
511	CTG	16511	TACATTTGCTTCTGACACAA	17427	ScaCas9-Sc++	53	0
512	CTG	16512	TACATTTGCTTCTGACACAA	17428	SpyCas9-SpRY	53	0
513	CTT	16513	GCCCAGGGCCTCACCACCAA	17429	SpyCas9-SpRY	53	0
514	ACT	16514	TGCCCAGGGCCTCACCACCA	17430	SpyCas9-SpRY	54	0
515	ACT	16515	TTACATTTGCTTCTGACACA	17431	SpyCas9-SpRY	54	0
516	ACTTC	16516	acctGCCCAGGGCCTCACCACCA	17432	BlatCas9	54	0
517	AAC	16517	CTGCCCAGGGCCTCACCACC	17433	SpyCas9-SpRY	55	0
518	AAC	16518	CTTACATTTGCTTCTGACAC	17434	SpyCas9-SpRY	55	0
519	AACT	16519	CTGCCCAGGGCCTCACCACC	17435	SpyCas9-3var-NRCH	55	0
520	AACT	16520	CTTACATTTGCTTCTGACAC	17436	SpyCas9-3var-NRCH	55	0
521	CAA	16521	CCTGCCCAGGGCCTCACCAC	17437	SpyCas9-SpRY	56	0
522	CAA	16522	GCTTACATTTGCTTCTGACA	17438	SpyCas9-SpRY	56	0
523	CAACTTC	16523	AACCTGCCCAGGGCCTCACCAC	17439	CdiCas9	56	0
524	CAAC	16524	CCTGCCCAGGGCCTCACCAC	17440	SpyCas9-3var-NRRH	56	0
525	CAAC	16525	acCTGCCCAGGGCCTCACCAC	17441	iSpyMacCas9	56	0
526	CAAC	16526	GCTTACATTTGCTTCTGACA	17442	SpyCas9-3var-NRRH	56	0
527	CAAC	16527	tgCTTACATTTGCTTCTGACA	17443	iSpyMacCas9	56	0
528	CCA	16528	ACCTGCCCAGGGCCTCACCA	17444	SpyCas9-SpRY	57	0
529	ACA	16529	TGCTTACATTTGCTTCTGAC	17445	SpyCas9-SpRY	57	0
530	ACAACTGT	16530	tattGCTTACATTTGCTTCTGAC	17446	BlatCas9	57	0
531	CCAAC	16531	ccaaCCTGCCCAGGGCCTCACCA	17447	BlatCas9	57	0
532	ACAAC	16532	tattGCTTACATTTGCTTCTGAC	17448	BlatCas9	57	0
533	CCAACT	16533	AACCTGCCCAGGGCCTCACCA	17449	cCas9-v16	57	0

534	CCAACT	16534	AACCTGCCCAGGGCCTCACCA	17450	cCas9-v21	57	0
535	ACAACT	16535	TTGCTTACATTTGCTTCTGAC	17451	cCas9-v16	57	0
536	ACAACT	16536	TTGCTTACATTTGCTTCTGAC	17452	cCas9-v21	57	0
537	CCAACTT	16537	CAACCTGCCCAGGGCCTCACCA	17453	CdiCas9	57	0
538	ACCAA	16538	CAACCTGCCCAGGGCCTCACC	17454	SauCas9KKH	58	0
539	CACAA	16539	ATTGCTTACATTTGCTTCTGA	17455	SauCas9KKH	58	0
540	CAC	16540	TTGCTTACATTTGCTTCTGA	17456	SpyCas9-SpRY	58	0
541	ACC	16541	AACCTGCCCAGGGCCTCACC	17457	SpyCas9-SpRY	58	0
542	ACCAAC	16542	CAACCTGCCCAGGGCCTCACC	17458	cCas9-v17	58	0
543	ACCAAC	16543	CAACCTGCCCAGGGCCTCACC	17459	cCas9-v42	58	0
544	CACAAC	16544	ATTGCTTACATTTGCTTCTGA	17460	cCas9-v17	58	0
545	CACAAC	16545	ATTGCTTACATTTGCTTCTGA	17461	cCas9-v42	58	0
546	CACA	16546	TTGCTTACATTTGCTTCTGA	17462	SpyCas9-3var-NRCH	58	0
547	CAC	16547	CAACCTGCCCAGGGCCTCAC	17463	SpyCas9-SpRY	59	0
548	ACA	16548	ATTGCTTACATTTGCTTCTG	17464	SpyCas9-SpRY	59	0
549	ACACAAC	16549	CTATTGCTTACATTTGCTTCTG	17465	CdiCas9	59	0
550	CACC	16550	CAACCTGCCCAGGGCCTCAC	17466	SpyCas9-3var-NRCH	59	0
551	ACACAA	16551	ATTGCTTACATTTGCTTCTG	17467	St1Cas9-CNRZ1066	59	0
552	GAC	16552	TATTGCTTACATTTGCTTCT	17468	SpyCas9-SpRY	60	0
553	CCA	16553	CCAACCTGCCCAGGGCCTCA	17469	SpyCas9-SpRY	60	0
554	CCACC	16554	atacCAACCTGCCCAGGGCCTCA	17470	BlatCas9	60	0
555	GACAC	16555	atctATTGCTTACATTTGCTTCT	17471	BlatCas9	60	0
556	GACA	16556	TATTGCTTACATTTGCTTCT	17472	SpyCas9-3var-NRCH	60	0
557	ACCACC	16557	tgATACCAACCTGCCCAGGGCCTC	17473	Nme2Cas9	61	0
558	TG	16558	CTATTGCTTACATTTGCTTC	17474	SpyCas9-NG	61	0

559	TG	16559	CTATTGCTTACATTTGCTTC	17475	SpyCas9-xCas	61	0
560	TG	16560	CTATTGCTTACATTTGCTTC	17476	SpyCas9-xCas-NG	61	0
561	TGA	16561	CTATTGCTTACATTTGCTTC	17477	SpyCas9-SpG	61	0
562	TGA	16562	CTATTGCTTACATTTGCTTC	17478	SpyCas9-SpRY	61	0
563	ACC	16563	ACCAACCTGCCCAGGGCCTC	17479	SpyCas9-SpRY	61	0
564	ACCACCAA	16564	gataCCAACCTGCCCAGGGCCTC	17480	BlatCas9	61	0
565	ACCACCAA	16565	gataCCAACCTGCCCAGGGCCTC	17481	BlatCas9	61	0
566	ACCAC	16566	gataCCAACCTGCCCAGGGCCTC	17482	BlatCas9	61	0
567	TGAC	16567	CTATTGCTTACATTTGCTTC	17483	SpyCas9-3var-NRRH	61	0
568	TGAC	16568	CTATTGCTTACATTTGCTTC	17484	SpyCas9-VQR	61	0
569	CTG	16569	TCTATTGCTTACATTTGCTT	17485	ScaCas9	62	0
570	CTG	16570	TCTATTGCTTACATTTGCTT	17486	ScaCas9-HiFi-Sc++	62	0
571	CTG	16571	TCTATTGCTTACATTTGCTT	17487	ScaCas9-Sc++	62	0
572	CTG	16572	TCTATTGCTTACATTTGCTT	17488	SpyCas9-SpRY	62	0
573	CAC	16573	TACCAACCTGCCCAGGGCCT	17489	SpyCas9-SpRY	62	0
574	CTGAC	16574	ccatCTATTGCTTACATTTGCTT	17490	BlatCas9	62	0
575	CTGACAC	16575	CATCTATTGCTTACATTTGCTT	17491	CdiCas9	62	0
576	CACC	16576	TACCAACCTGCCCAGGGCCT	17492	SpyCas9-3var-NRCH	62	0
577	TCTGA	16577	CATCTATTGCTTACATTTGCT	17493	SauCas9KKH	63	0
578	TCA	16578	ATACCAACCTGCCCAGGGCC	17494	SpyCas9-SpRY	63	0
579	TCT	16579	ATCTATTGCTTACATTTGCT	17495	SpyCas9-SpRY	63	0
580	TCACC	16580	ttgaTACCAACCTGCCCAGGGCC	17496	BlatCas9	63	0
581	TCACCAC	16581	TGATACCAACCTGCCCAGGGCC	17497	CdiCas9	63	0
582	TCTGACAC	16582	gcCATCTATTGCTTACATTTGCT	17498	CjeCas9	63	0
583	CTCACC	16583	ccTTGATACCAACCTGCCCAGGGC	17499	Nme2Cas9	64	0
584	CTC	16584	GATACCAACCTGCCCAGGGC	17500	SpyCas9-SpRY	64	0

585	TTC	16585	CATCTATTGCTTACATTTGC	17501	SpyCas9-SpRY	64	0
586	CTCAC	16586	cttgATACCAACCTGCCCAGGGC	17502	BlatCas9	64	0
587	TTCTGACA	16587	gagcCATCTATTGCTTACATTTGC	17503	NmeCas9	64	0
588	CCT	16588	TGATACCAACCTGCCCAGGG	17504	SpyCas9-SpRY	65	0
589	CTT	16589	CCATCTATTGCTTACATTTG	17505	SpyCas9-SpRY	65	0
590	GCC	16590	TTGATACCAACCTGCCCAGG	17506	SpyCas9-SpRY	66	0
591	GCT	16591	GCCATCTATTGCTTACATTT	17507	SpyCas9-SpRY	66	0
592	GCTTCTGA	16592	agagCCATCTATTGCTTACATTT	17508	BlatCas9	66	0
593	GCCTC	16593	acctTGATACCAACCTGCCCAGG	17509	BlatCas9	66	0
594	GCTTC	16594	agagCCATCTATTGCTTACATTT	17510	BlatCas9	66	0
595	GG	16595	CTTGATACCAACCTGCCCAG	17511	SpyCas9-NG	67	0
596	GG	16596	CTTGATACCAACCTGCCCAG	17512	SpyCas9-xCas	67	0
597	GG	16597	CTTGATACCAACCTGCCCAG	17513	SpyCas9-xCas-NG	67	0
598	TG	16598	AGCCATCTATTGCTTACATT	17514	SpyCas9-NG	67	0
599	TG	16599	AGCCATCTATTGCTTACATT	17515	SpyCas9-xCas	67	0
600	TG	16600	AGCCATCTATTGCTTACATT	17516	SpyCas9-xCas-NG	67	0
601	GGC	16601	CTTGATACCAACCTGCCCAG	17517	SpyCas9-SpG	67	0
602	GGC	16602	CTTGATACCAACCTGCCCAG	17518	SpyCas9-SpRY	67	0
603	TGC	16603	AGCCATCTATTGCTTACATT	17519	SpyCas9-SpG	67	0
604	TGC	16604	AGCCATCTATTGCTTACATT	17520	SpyCas9-SpRY	67	0
605	GGCC	16605	CTTGATACCAACCTGCCCAG	17521	SpyCas9-3var-NRCH	67	0
606	TGCT	16606	AGCCATCTATTGCTTACATT	17522	SpyCas9-3var-NRCH	67	0
607	GGG	16607	CCTTGATACCAACCTGCCCA	17523	ScaCas9	68	0
608	GGG	16608	CCTTGATACCAACCTGCCCA	17524	ScaCas9-HiFi-Sc++	68	0
609	GGG	16609	CCTTGATACCAACCTGCCCA	17525	ScaCas9-Sc++	68	0
610	GGG	16610	CCTTGATACCAACCTGCCCA	17526	SpyCas9	68	0

611	GGG	16611	CCTTGATACCAACCTGCCCA	17527	SpyCas9-HF1	68	0
612	GGG	16612	CCTTGATACCAACCTGCCCA	17528	SpyCas9-SpG	68	0
613	GGG	16613	CCTTGATACCAACCTGCCCA	17529	SpyCas9-SpRY	68	0
614	TTG	16614	GAGCCATCTATTGCTTACAT	17530	ScaCas9	68	0
615	TTG	16615	GAGCCATCTATTGCTTACAT	17531	ScaCas9-HiFi-Sc++	68	0
616	TTG	16616	GAGCCATCTATTGCTTACAT	17532	ScaCas9-Sc++	68	0
617	TTG	16617	GAGCCATCTATTGCTTACAT	17533	SpyCas9-SpRY	68	0
618	GG	16618	CCTTGATACCAACCTGCCCA	17534	SpyCas9-NG	68	0
619	GG	16619	CCTTGATACCAACCTGCCCA	17535	SpyCas9-xCas	68	0
620	GG	16620	CCTTGATACCAACCTGCCCA	17536	SpyCas9-xCas-NG	68	0
621	GGGCC	16621	taacCTTGATACCAACCTGCCCA	17537	BlatCas9	68	0
622	GGGCCTC	16622	AACCTTGATACCAACCTGCCCA	17538	CdiCas9	68	0
623	TTGCTTC	16623	CAGAGCCATCTATTGCTTACAT	17539	CdiCas9	68	0
624	GGGC	16624	CCTTGATACCAACCTGCCCA	17540	SpyCas9-3var-NRRH	68	0
625	AGGGCC	16625	tgTAACCTTGATACCAACCTGCCC	17541	Nme2Cas9	69	0
626	AGGG	16626	AACCTTGATACCAACCTGCCC	17542	SauriCas9	69	0
627	AGGG	16627	AACCTTGATACCAACCTGCCC	17543	SauriCas9-KKH	69	0
628	AGG	16628	ACCTTGATACCAACCTGCCC	17544	ScaCas9	69	0
629	AGG	16629	ACCTTGATACCAACCTGCCC	17545	ScaCas9-HiFi-Sc++	69	0
630	AGG	16630	ACCTTGATACCAACCTGCCC	17546	ScaCas9-Sc++	69	0
631	AGG	16631	ACCTTGATACCAACCTGCCC	17547	SpyCas9	69	0
632	AGG	16632	ACCTTGATACCAACCTGCCC	17548	SpyCas9-HF1	69	0
633	AGG	16633	ACCTTGATACCAACCTGCCC	17549	SpyCas9-SpG	69	0
634	AGG	16634	ACCTTGATACCAACCTGCCC	17550	SpyCas9-SpRY	69	0
635	AG	16635	ACCTTGATACCAACCTGCCC	17551	SpyCas9-NG	69	0
636	AG	16636	ACCTTGATACCAACCTGCCC	17552	SpyCas9-xCas	69	0

637	AG	16637	ACCTTGATACCAACCTGCCC	17553	SpyCas9-xCas-NG	69	0
638	TTT	16638	AGAGCCATCTATTGCTTACA	17554	SpyCas9-SpRY	69	0
639	AGGGC	16639	gtaaCCTTGATACCAACCTGCCC	17555	BlatCas9	69	0
640	TTTGC	16640	ggcaGAGCCATCTATTGCTTACA	17556	BlatCas9	69	0
641	CAGGG	16641	tgTAACCTTGATACCAACCTGCC	17557	SauCas9	70	0
642	CAGGG	16642	TAACCTTGATACCAACCTGCC	17558	SauCas9KKH	70	0
643	CAGG	16643	TAACCTTGATACCAACCTGCC	17559	SauriCas9	70	0
644	CAGG	16644	TAACCTTGATACCAACCTGCC	17560	SauriCas9-KKH	70	0
645	CAG	16645	AACCTTGATACCAACCTGCC	17561	ScaCas9	70	0
646	CAG	16646	AACCTTGATACCAACCTGCC	17562	ScaCas9-HiFi-Sc++	70	0
647	CAG	16647	AACCTTGATACCAACCTGCC	17563	ScaCas9-Sc++	70	0
648	CAG	16648	AACCTTGATACCAACCTGCC	17564	SpyCas9-SpRY	70	0
649	ATT	16649	CAGAGCCATCTATTGCTTAC	17565	SpyCas9-SpRY	70	0
650	CAGGGC	16650	TAACCTTGATACCAACCTGCC	17566	cCas9-v17	70	0
651	CAGGGC	16651	TAACCTTGATACCAACCTGCC	17567	cCas9-v42	70	0
652	ATTTGCTT	16652	agggCAGAGCCATCTATTGCTTAC	17568	NmeCas9	70	0
653	CCAGG	16653	GTAACCTTGATACCAACCTGC	17569	SauCas9KKH	71	0
654	CCAG	16654	GTAACCTTGATACCAACCTGC	17570	SauriCas9-KKH	71	0
655	CAT	16655	GCAGAGCCATCTATTGCTTA	17571	SpyCas9-SpRY	71	0
656	CCA	16656	TAACCTTGATACCAACCTGC	17572	SpyCas9-SpRY	71	0
657	CCAGGG	16657	GTAACCTTGATACCAACCTGC	17573	cCas9-v17	71	0
658	CCAGGG	16658	GTAACCTTGATACCAACCTGC	17574	cCas9-v42	71	0
659	CATT	16659	GCAGAGCCATCTATTGCTTA	17575	SpyCas9-3var-NRTH	71	0
660	CCCAG	16660	TGTAACCTTGATACCAACCTG	17576	SauCas9KKH	72	0
661	CCC	16661	GTAACCTTGATACCAACCTG	17577	SpyCas9-SpRY	72	0
662	ACA	16662	GGCAGAGCCATCTATTGCTT	17578	SpyCas9-SpRY	72	0

663	CCCAGG	16663	TGTAACCTTGATACCAACC TG	17579	cCas9-v17	72	0
664	CCCAGG	16664	TGTAACCTTGATACCAACC TG	17580	cCas9-v42	72	0
665	TAC	16665	GGGCAGAGCCATCTATTGC T	17581	SpyCas9-SpRY	73	0
666	GCC	16666	TGTAACCTTGATACCAACC T	17582	SpyCas9-SpRY	73	0
667	TACATT	16667	AGGGCAGAGCCATCTATTG CT	17583	cCas9-v16	73	0
668	TACATT	16668	AGGGCAGAGCCATCTATTG CT	17584	cCas9-v21	73	0
669	TACA	16669	GGGCAGAGCCATCTATTGC T	17585	SpyCas9-3var-NRCH	73	0
670	TTACATT	16670	TCAGGGCAGAGCCATCTAT TGC	17586	CdiCas9	74	0
671	TTACATT	16671	agtCAGGGCAGAGCCATCTA TTGC	17587	PpnCas9	74	0
672	TG	16672	TTGTAACCTTGATACCAAC C	17588	SpyCas9-NG	74	0
673	TG	16673	TTGTAACCTTGATACCAAC C	17589	SpyCas9-xCas	74	0
674	TG	16674	TTGTAACCTTGATACCAAC C	17590	SpyCas9-xCas-NG	74	0
675	TGC	16675	TTGTAACCTTGATACCAAC C	17591	SpyCas9-SpG	74	0
676	TGC	16676	TTGTAACCTTGATACCAAC C	17592	SpyCas9-SpRY	74	0
677	TTA	16677	AGGGCAGAGCCATCTATTG C	17593	SpyCas9-SpRY	74	0
678	TGCCCAGG	16678	gtctTGTAACCTTGATACCAA CC	17594	BlatCas9	74	0
679	TGCCC	16679	gtctTGTAACCTTGATACCAA CC	17595	BlatCas9	74	0
680	TGCC	16680	TTGTAACCTTGATACCAAC C	17596	SpyCas9-3var-NRCH	74	0
681	CTGCCC	16681	ctGTCTTGTAACCTTGATAC CAAC	17597	Nme2Cas9	75	0
682	CTG	16682	CTTGTAACCTTGATACCAA C	17598	ScaCas9	75	0
683	CTG	16683	CTTGTAACCTTGATACCAA C	17599	ScaCas9-HiFi-Sc++	75	0
684	CTG	16684	CTTGTAACCTTGATACCAA C	17600	ScaCas9-Sc++	75	0
685	CTG	16685	CTTGTAACCTTGATACCAA C	17601	SpyCas9-SpRY	75	0
686	CTT	16686	CAGGGCAGAGCCATCTATT G	17602	SpyCas9-SpRY	75	0
687	CTGCCCAG	16687	tgtcTTGTAACCTTGATACCA AC	17603	BlatCas9	75	0
688	CTTACATT	16688	agtcAGGGCAGAGCCATCTA TTG	17604	BlatCas9	75	0

689	CTGCC	16689	tgtcTTGTAACCTTGATACCAAC	17605	BlatCas9	75	0
690	CTTAC	16690	agtcAGGGCAGAGCCATCTATTG	17606	BlatCas9	75	0
691	CCTGCC	16691	ccTGTCTTGTAACCTTGATACCAA	17607	Nme2Cas9	76	0
692	CCT	16692	TCTTGTAACCTTGATACCAA	17608	SpyCas9-SpRY	76	0
693	GCT	16693	TCAGGGCAGAGCCATCTATT	17609	SpyCas9-SpRY	76	0
694	CCTGC	16694	ctgtCTTGTAACCTTGATACCAA	17610	BlatCas9	76	0
695	TG	16695	GTCAGGGCAGAGCCATCTAT	17611	SpyCas9-NG	77	0
696	TG	16696	GTCAGGGCAGAGCCATCTAT	17612	SpyCas9-xCas	77	0
697	TG	16697	GTCAGGGCAGAGCCATCTAT	17613	SpyCas9-xCas-NG	77	0
698	TGC	16698	GTCAGGGCAGAGCCATCTAT	17614	SpyCas9-SpG	77	0
699	TGC	16699	GTCAGGGCAGAGCCATCTAT	17615	SpyCas9-SpRY	77	0
700	ACC	16700	GTCTTGTAACCTTGATACCA	17616	SpyCas9-SpRY	77	0
701	TGCT	16701	GTCAGGGCAGAGCCATCTAT	17617	SpyCas9-3var-NRCH	77	0
702	TTG	16702	AGTCAGGGCAGAGCCATCTA	17618	ScaCas9	78	0
703	TTG	16703	AGTCAGGGCAGAGCCATCTA	17619	ScaCas9-HiFi-Sc++	78	0
704	TTG	16704	AGTCAGGGCAGAGCCATCTA	17620	ScaCas9-Sc++	78	0
705	TTG	16705	AGTCAGGGCAGAGCCATCTA	17621	SpyCas9-SpRY	78	0
706	AAC	16706	TGTCTTGTAACCTTGATACC	17622	SpyCas9-SpRY	78	0
707	AACC	16707	TGTCTTGTAACCTTGATACC	17623	SpyCas9-3var-NRCH	78	0
708	CAA	16708	CTGTCTTGTAACCTTGATAC	17624	SpyCas9-SpRY	79	0
709	ATT	16709	AAGTCAGGGCAGAGCCATCT	17625	SpyCas9-SpRY	79	0
710	ATTGCTTA	16710	taaaAGTCAGGGCAGAGCCATCT	17626	BlatCas9	79	0
711	CAACC	16711	aaccTGTCTTGTAACCTTGATAC	17627	BlatCas9	79	0
712	ATTGC	16712	taaaAGTCAGGGCAGAGCCATCT	17628	BlatCas9	79	0
713	CAAC	16713	CTGTCTTGTAACCTTGATAC	17629	SpyCas9-3var-NRRH	79	0

714	CAAC	16714	ccTGTCTTGTAACCTTGATAC	17630	iSpyMacCas9	79	0
715	CCAACC	16715	taAACCTGTCTTGTAACCTTGATA	17631	Nme2Cas9	80	0
716	TAT	16716	AAAGTCAGGGCAGAGCCATC	17632	SpyCas9-SpRY	80	0
717	CCA	16717	CCTGTCTTGTAACCTTGATA	17633	SpyCas9-SpRY	80	0
718	CCAACCTG	16718	aaacCTGTCTTGTAACCTTGATA	17634	BlatCas9	80	0
719	CCAAC	16719	aaacCTGTCTTGTAACCTTGATA	17635	BlatCas9	80	0
720	CCAACCT	16720	AACCTGTCTTGTAACCTTGATA	17636	CdiCas9	80	0
721	TATTGCTT	16721	cataAAAGTCAGGGCAGAGCCATC	17637	NmeCas9	80	0
722	TATT	16722	AAAGTCAGGGCAGAGCCATC	17638	SpyCas9-3var-NRTH	80	0
723	ACCAA	16723	AACCTGTCTTGTAACCTTGAT	17639	SauCas9KKH	81	0
724	ACC	16724	ACCTGTCTTGTAACCTTGAT	17640	SpyCas9-SpRY	81	0
725	CTA	16725	AAAAGTCAGGGCAGAGCCAT	17641	SpyCas9-SpRY	81	0
726	ACCAAC	16726	AACCTGTCTTGTAACCTTGAT	17642	cCas9-v17	81	0
727	ACCAAC	16727	AACCTGTCTTGTAACCTTGAT	17643	cCas9-v42	81	0
728	TAC	16728	AACCTGTCTTGTAACCTTGA	17644	SpyCas9-SpRY	82	0
729	TCT	16729	TAAAAGTCAGGGCAGAGCCA	17645	SpyCas9-SpRY	82	0
730	TACC	16730	AACCTGTCTTGTAACCTTGA	17646	SpyCas9-3var-NRCH	82	0
731	ATCTATT	16731	gggCATAAAAGTCAGGGCAGAGCC	17647	PpnCas9	83	0
732	ATA	16732	AAACCTGTCTTGTAACCTTG	17648	SpyCas9-SpRY	83	0
733	ATC	16733	ATAAAAGTCAGGGCAGAGCC	17649	SpyCas9-SpRY	83	0
734	ATACC	16734	cttaAACCTGTCTTGTAACCTTG	17650	BlatCas9	83	0
735	GATACC	16735	tcCTTAAACCTGTCTTGTAACCTT	17651	Nme2Cas9	84	0
736	GAT	16736	TAAACCTGTCTTGTAACCTT	17652	SpyCas9-SpRY	84	0
737	GAT	16737	TAAACCTGTCTTGTAACCTT	17653	SpyCas9-xCas	84	0
738	CAT	16738	CATAAAAGTCAGGGCAGAGC	17654	SpyCas9-SpRY	84	0
739	GATACCAA	16739	ccttAAACCTGTCTTGTAACCTT	17655	BlatCas9	84	0

740	GATACCAA	16740	ccttAAACCTGTCTTGTAACCTT	17656	BlatCas9	84	0
741	GATAC	16741	ccttAAACCTGTCTTGTAACCTT	17657	BlatCas9	84	0
742	GATA	16742	TAAACCTGTCTTGTAACCTT	17658	SpyCas9-3var-NRTH	84	0
743	CATC	16743	CATAAAAGTCAGGGCAGAGC	17659	SpyCas9-3var-NRTH	84	0
744	TG	16744	TTAAACCTGTCTTGTAACCT	17660	SpyCas9-NG	85	0
745	TG	16745	TTAAACCTGTCTTGTAACCT	17661	SpyCas9-xCas	85	0
746	TG	16746	TTAAACCTGTCTTGTAACCT	17662	SpyCas9-xCas-NG	85	0
747	TGA	16747	TTAAACCTGTCTTGTAACCT	17663	SpyCas9-SpG	85	0
748	TGA	16748	TTAAACCTGTCTTGTAACCT	17664	SpyCas9-SpRY	85	0
749	CCA	16749	GCATAAAAGTCAGGGCAGAG	17665	SpyCas9-SpRY	85	0
750	CCATCTAT	16750	tgggCATAAAAGTCAGGGCAGAG	17666	BlatCas9	85	0
751	CCATC	16751	tgggCATAAAAGTCAGGGCAGAG	17667	BlatCas9	85	0
752	TGATACC	16752	CCTTAAACCTGTCTTGTAACCT	17668	CdiCas9	85	0
753	TGAT	16753	TTAAACCTGTCTTGTAACCT	17669	SpyCas9-3var-NRRH	85	0
754	TGAT	16754	TTAAACCTGTCTTGTAACCT	17670	SpyCas9-VQR	85	0
755	TTG	16755	CTTAAACCTGTCTTGTAACC	17671	ScaCas9	86	0
756	TTG	16756	CTTAAACCTGTCTTGTAACC	17672	ScaCas9-HiFi-Sc++	86	0
757	TTG	16757	CTTAAACCTGTCTTGTAACC	17673	ScaCas9-Sc++	86	0
758	TTG	16758	CTTAAACCTGTCTTGTAACC	17674	SpyCas9-SpRY	86	0
759	GCC	16759	GGCATAAAAGTCAGGGCAGA	17675	SpyCas9-SpRY	86	0
760	TTGATAC	16760	TCCTTAAACCTGTCTTGTAACC	17676	CdiCas9	86	0
761	CTTGA	16761	TCCTTAAACCTGTCTTGTAAC	17677	SauCas9KKH	87	0
762	CTTGAT	16762	TCCTTAAACCTGTCTTGTAAC	17678	SauCas9KKH	87	0
763	AG	16763	GGGCATAAAAGTCAGGGCAG	17679	SpyCas9-NG	87	0
764	AG	16764	GGGCATAAAAGTCAGGGCAG	17680	SpyCas9-xCas	87	0

765	AG	16765	GGGCATAAAAGTCAGGGCAG	17681	SpyCas9-xCas-NG	87	0
766	AGC	16766	GGGCATAAAAGTCAGGGCAG	17682	SpyCas9-SpG	87	0
767	AGC	16767	GGGCATAAAAGTCAGGGCAG	17683	SpyCas9-SpRY	87	0
768	CTT	16768	CCTTAAACCTGTCTTGTAAC	17684	SpyCas9-SpRY	87	0
769	CTTGATAC	16769	tcTCCTTAAACCTGTCTTGTAAC	17685	CjeCas9	87	0
770	AGCC	16770	GGGCATAAAAGTCAGGGCAG	17686	SpyCas9-3var-NRCH	87	0
771	GAG	16771	TGGGCATAAAAGTCAGGGCA	17687	ScaCas9	88	0
772	GAG	16772	TGGGCATAAAAGTCAGGGCA	17688	ScaCas9-HiFi-Sc++	88	0
773	GAG	16773	TGGGCATAAAAGTCAGGGCA	17689	ScaCas9-Sc++	88	0
774	GAG	16774	TGGGCATAAAAGTCAGGGCA	17690	SpyCas9-SpRY	88	0
775	CCT	16775	TCCTTAAACCTGTCTTGTAA	17691	SpyCas9-SpRY	88	0
776	GAGCC	16776	ggctGGGCATAAAAGTCAGGGCA	17692	BlatCas9	88	0
777	GAGCCAT	16777	GCTGGGCATAAAAGTCAGGGCA	17693	CdiCas9	88	0
778	CCTTGATA	16778	ggtcTCCTTAAACCTGTCTTGTAA	17694	NmeCas9	88	0
779	GAGC	16779	TGGGCATAAAAGTCAGGGCA	17695	SpyCas9-3var-NRRH	88	0
780	AGAGCC	16780	agGGCTGGGCATAAAAGTCAGGGC	17696	Nme2Cas9	89	0
781	AGAG	16781	GCTGGGCATAAAAGTCAGGGC	17697	SauriCas9-KKH	89	0
782	AGAG	16782	CTGGGCATAAAAGTCAGGGC	17698	SpyCas9-VQR	89	0
783	AG	16783	CTGGGCATAAAAGTCAGGGC	17699	SpyCas9-NG	89	0
784	AG	16784	CTGGGCATAAAAGTCAGGGC	17700	SpyCas9-xCas	89	0
785	AG	16785	CTGGGCATAAAAGTCAGGGC	17701	SpyCas9-xCas-NG	89	0
786	AGA	16786	CTGGGCATAAAAGTCAGGGC	17702	SpyCas9-SpG	89	0
787	AGA	16787	CTGGGCATAAAAGTCAGGGC	17703	SpyCas9-SpRY	89	0
788	ACC	16788	CTCCTTAAACCTGTCTTGTA	17704	SpyCas9-SpRY	89	0
789	AGAGCCAT	16789	gggcTGGGCATAAAAGTCAGGGC	17705	BlatCas9	89	0
790	AGAGC	16790	gggcTGGGCATAAAAGTCAGGGC	17706	BlatCas9	89	0

791	CAGAG	16791	agGGCTGGGCATAAAAGTCAGGG	17707	SauCas9	90	0
792	CAGAG	16792	GGCTGGGCATAAAAGTCAGGG	17708	SauCas9KKH	90	0
793	CAG	16793	GCTGGGCATAAAAGTCAGGG	17709	ScaCas9	90	0
794	CAG	16794	GCTGGGCATAAAAGTCAGGG	17710	ScaCas9-HiFi-Sc++	90	0
795	CAG	16795	GCTGGGCATAAAAGTCAGGG	17711	ScaCas9-Sc++	90	0
796	CAG	16796	GCTGGGCATAAAAGTCAGGG	17712	SpyCas9-SpRY	90	0
797	AAC	16797	TCTCCTTAAACCTGTCTTGT	17713	SpyCas9-SpRY	90	0
798	CAGAGC	16798	GGCTGGGCATAAAAGTCAGGG	17714	cCas9-v17	90	0
799	CAGAGC	16799	GGCTGGGCATAAAAGTCAGGG	17715	cCas9-v42	90	0
800	CAGA	16800	GCTGGGCATAAAAGTCAGGG	17716	SpyCas9-3var-NRRH	90	0
801	AACC	16801	TCTCCTTAAACCTGTCTTGT	17717	SpyCas9-3var-NRCH	90	0
802	GCAGA	16802	GGGCTGGGCATAAAAGTCAGG	17718	SauCas9KKH	91	0
803	GCAG	16803	GGGCTGGGCATAAAAGTCAGG	17719	SauriCas9-KKH	91	0
804	TAA	16804	GTCTCCTTAAACCTGTCTTG	17720	SpyCas9-SpRY	91	0
805	GCA	16805	GGCTGGGCATAAAAGTCAGG	17721	SpyCas9-SpRY	91	0
806	TAACCTTG	16806	ttggTCTCCTTAAACCTGTCTTG	17722	BlatCas9	91	0
807	TAACC	16807	ttggTCTCCTTAAACCTGTCTTG	17723	BlatCas9	91	0
808	GCAGAG	16808	GGGCTGGGCATAAAAGTCAGG	17724	cCas9-v17	91	0
809	GCAGAG	16809	GGGCTGGGCATAAAAGTCAGG	17725	cCas9-v42	91	0
810	TAACCTT	16810	TGGTCTCCTTAAACCTGTCTTG	17726	CdiCas9	91	0
811	TAAC	16811	GTCTCCTTAAACCTGTCTTG	17727	SpyCas9-3var-NRRH	91	0
812	TAAC	16812	ggTCTCCTTAAACCTGTCTTG	17728	iSpyMacCas9	91	0
813	GTAACC	16813	taTTGGTCTCCTTAAACCTGTCTT	17729	Nme2Cas9	92	0
814	GGCAG	16814	AGGGCTGGGCATAAAAGTCAG	17730	SauCas9KKH	92	0
815	GG	16815	GGGCTGGGCATAAAAGTCAG	17731	SpyCas9-NG	92	0

816	GG	16816	GGGCTGGGCATAAAAGTCAG	17732	SpyCas9-xCas	92	0
817	GG	16817	GGGCTGGGCATAAAAGTCAG	17733	SpyCas9-xCas-NG	92	0
818	GGC	16818	GGGCTGGGCATAAAAGTCAG	17734	SpyCas9-SpG	92	0
819	GGC	16819	GGGCTGGGCATAAAAGTCAG	17735	SpyCas9-SpRY	92	0
820	GTA	16820	GGTCTCCTTAAACCTGTCTT	17736	SpyCas9-SpRY	92	0
821	GTAACCTT	16821	attgGTCTCCTTAAACCTGTCTT	17737	BlatCas9	92	0
822	GTAAC	16822	attgGTCTCCTTAAACCTGTCTT	17738	BlatCas9	92	0
823	GGCAGA	16823	AGGGCTGGGCATAAAAGTCAG	17739	cCas9-v17	92	0
824	GGCAGA	16824	AGGGCTGGGCATAAAAGTCAG	17740	cCas9-v42	92	0
825	GTAACCT	16825	TTGGTCTCCTTAAACCTGTCTT	17741	CdiCas9	92	0
826	GGCA	16826	GGGCTGGGCATAAAAGTCAG	17742	SpyCas9-3var-NRCH	92	0
827	TGTAA	16827	TTGGTCTCCTTAAACCTGTCT	17743	SauCas9KKH	93	0
828	GGG	16828	AGGGCTGGGCATAAAAGTCA	17744	ScaCas9	93	0
829	GGG	16829	AGGGCTGGGCATAAAAGTCA	17745	ScaCas9-HiFi-Sc++	93	0
830	GGG	16830	AGGGCTGGGCATAAAAGTCA	17746	ScaCas9-Sc++	93	0
831	GGG	16831	AGGGCTGGGCATAAAAGTCA	17747	SpyCas9	93	0
832	GGG	16832	AGGGCTGGGCATAAAAGTCA	17748	SpyCas9-HF1	93	0
833	GGG	16833	AGGGCTGGGCATAAAAGTCA	17749	SpyCas9-SpG	93	0
834	GGG	16834	AGGGCTGGGCATAAAAGTCA	17750	SpyCas9-SpRY	93	0
835	TG	16835	TGGTCTCCTTAAACCTGTCT	17751	SpyCas9-NG	93	0
836	TG	16836	TGGTCTCCTTAAACCTGTCT	17752	SpyCas9-xCas	93	0
837	TG	16837	TGGTCTCCTTAAACCTGTCT	17753	SpyCas9-xCas-NG	93	0
838	GG	16838	AGGGCTGGGCATAAAAGTCA	17754	SpyCas9-NG	93	0
839	GG	16839	AGGGCTGGGCATAAAAGTCA	17755	SpyCas9-xCas	93	0
840	GG	16840	AGGGCTGGGCATAAAAGTCA	17756	SpyCas9-xCas-NG	93	0
841	TGT	16841	TGGTCTCCTTAAACCTGTCT	17757	SpyCas9-SpG	93	0

842	TGT	16842	TGGTCTCCTTAAACCTGTCT	17758	SpyCas9-SpRY	93	0
843	GGGC	16843	AGGGCTGGGCATAAAAGTCA	17759	SpyCas9-3var-NRRH	93	0
844	TGTA	16844	TGGTCTCCTTAAACCTGTCT	17760	SpyCas9-3var-NRTH	93	0
845	AGGG	16845	CCAGGGCTGGGCATAAAAGTC	17761	SauriCas9	94	0
846	AGGG	16846	CCAGGGCTGGGCATAAAAGTC	17762	SauriCas9-KKH	94	0
847	TTG	16847	TTGGTCTCCTTAAACCTGTC	17763	ScaCas9	94	0
848	TTG	16848	TTGGTCTCCTTAAACCTGTC	17764	ScaCas9-HiFi-Sc++	94	0
849	TTG	16849	TTGGTCTCCTTAAACCTGTC	17765	ScaCas9-Sc++	94	0
850	TTG	16850	TTGGTCTCCTTAAACCTGTC	17766	SpyCas9-SpRY	94	0
851	AGG	16851	CAGGGCTGGGCATAAAAGTC	17767	ScaCas9	94	0
852	AGG	16852	CAGGGCTGGGCATAAAAGTC	17768	ScaCas9-HiFi-Sc++	94	0
853	AGG	16853	CAGGGCTGGGCATAAAAGTC	17769	ScaCas9-Sc++	94	0
854	AGG	16854	CAGGGCTGGGCATAAAAGTC	17770	SpyCas9	94	0
855	AGG	16855	CAGGGCTGGGCATAAAAGTC	17771	SpyCas9-HF1	94	0
856	AGG	16856	CAGGGCTGGGCATAAAAGTC	17772	SpyCas9-SpG	94	0
857	AGG	16857	CAGGGCTGGGCATAAAAGTC	17773	SpyCas9-SpRY	94	0
858	AG	16858	CAGGGCTGGGCATAAAAGTC	17774	SpyCas9-NG	94	0
859	AG	16859	CAGGGCTGGGCATAAAAGTC	17775	SpyCas9-xCas	94	0
860	AG	16860	CAGGGCTGGGCATAAAAGTC	17776	SpyCas9-xCas-NG	94	0
861	AGGGCAGA	16861	agccAGGGCTGGGCATAAAAGTC	17777	BlatCas9	94	0
862	AGGGC	16862	agccAGGGCTGGGCATAAAAGTC	17778	BlatCas9	94	0
863	TTGTAAC	16863	TATTGGTCTCCTTAAACCTGTC	17779	CdiCas9	94	0
864	CAGGG	16864	gaGCCAGGGCTGGGCATAAAAGT	17780	SauCas9	95	0
865	CAGGG	16865	GCCAGGGCTGGGCATAAAAGT	17781	SauCas9KKH	95	0
866	CAGG	16866	GCCAGGGCTGGGCATAAAAGT	17782	SauriCas9	95	0
867	CAGG	16867	GCCAGGGCTGGGCATAAAAGT	17783	SauriCas9-KKH	95	0

868	CAG	16868	CCAGGGCTGGGCATAAAAGT	17784	ScaCas9	95	0
869	CAG	16869	CCAGGGCTGGGCATAAAAGT	17785	ScaCas9-HiFi-Sc++	95	0
870	CAG	16870	CCAGGGCTGGGCATAAAAGT	17786	ScaCas9-Sc++	95	0
871	CAG	16871	CCAGGGCTGGGCATAAAAGT	17787	SpyCas9-SpRY	95	0
872	CTT	16872	ATTGGTCTCCTTAAACCTGT	17788	SpyCas9-SpRY	95	0
873	CAGGGC	16873	GCCAGGGCTGGGCATAAAAGT	17789	cCas9-v17	95	0
874	CAGGGC	16874	GCCAGGGCTGGGCATAAAAGT	17790	cCas9-v42	95	0
875	TCAGG	16875	AGCCAGGGCTGGGCATAAAAG	17791	SauCas9KKH	96	0
876	TCAG	16876	AGCCAGGGCTGGGCATAAAAG	17792	SauriCas9-KKH	96	0
877	TCT	16877	TATTGGTCTCCTTAAACCTG	17793	SpyCas9-SpRY	96	0
878	TCA	16878	GCCAGGGCTGGGCATAAAAG	17794	SpyCas9-SpRY	96	0
879	TCAGGG	16879	AGCCAGGGCTGGGCATAAAAG	17795	cCas9-v17	96	0
880	TCAGGG	16880	AGCCAGGGCTGGGCATAAAAG	17796	cCas9-v42	96	0
881	GTCAG	16881	GAGCCAGGGCTGGGCATAAAA	17797	SauCas9KKH	97	0
882	GTC	16882	CTATTGGTCTCCTTAAACCT	17798	SpyCas9-SpRY	97	0
883	GTC	16883	AGCCAGGGCTGGGCATAAAA	17799	SpyCas9-SpRY	97	0
884	GTCAGG	16884	GAGCCAGGGCTGGGCATAAAA	17800	cCas9-v17	97	0
885	GTCAGG	16885	GAGCCAGGGCTGGGCATAAAA	17801	cCas9-v42	97	0
886	TG	16886	TCTATTGGTCTCCTTAAACC	17802	SpyCas9-NG	98	0
887	TG	16887	TCTATTGGTCTCCTTAAACC	17803	SpyCas9-xCas	98	0
888	TG	16888	TCTATTGGTCTCCTTAAACC	17804	SpyCas9-xCas-NG	98	0
889	AG	16889	GAGCCAGGGCTGGGCATAAA	17805	SpyCas9-NG	98	0
890	AG	16890	GAGCCAGGGCTGGGCATAAA	17806	SpyCas9-xCas	98	0
891	AG	16891	GAGCCAGGGCTGGGCATAAA	17807	SpyCas9-xCas-NG	98	0
892	TGT	16892	TCTATTGGTCTCCTTAAACC	17808	SpyCas9-SpG	98	0
893	TGT	16893	TCTATTGGTCTCCTTAAACC	17809	SpyCas9-SpRY	98	0
894	AGT	16894	GAGCCAGGGCTGGGCATAAA	17810	SpyCas9-SpG	98	0

895	AGT	16895	GAGCCAGGGCTGGGCATAAA	17811	SpyCas9-SpRY	98	0
896	TGTC	16896	TCTATTGGTCTCCTTAAACC	17812	SpyCas9-3var-NRTH	98	0
897	AGTC	16897	GAGCCAGGGCTGGGCATAAA	17813	SpyCas9-3var-NRTH	98	0
898	CTG	16898	TTCTATTGGTCTCCTTAAAC	17814	ScaCas9	99	0
899	CTG	16899	TTCTATTGGTCTCCTTAAAC	17815	ScaCas9-HiFi-Sc++	99	0
900	CTG	16900	TTCTATTGGTCTCCTTAAAC	17816	ScaCas9-Sc++	99	0
901	CTG	16901	TTCTATTGGTCTCCTTAAAC	17817	SpyCas9-SpRY	99	0
902	AAG	16902	GGAGCCAGGGCTGGGCATAA	17818	ScaCas9	99	0
903	AAG	16903	GGAGCCAGGGCTGGGCATAA	17819	ScaCas9-HiFi-Sc++	99	0
904	AAG	16904	GGAGCCAGGGCTGGGCATAA	17820	ScaCas9-Sc++	99	0
905	AAG	16905	GGAGCCAGGGCTGGGCATAA	17821	SpyCas9-SpRY	99	0
906	CTGTCTTG	16906	agttTCTATTGGTCTCCTTAAAC	17822	BlatCas9	99	0
907	AAGTCAGG	16907	gcagGAGCCAGGGCTGGGCATAA	17823	BlatCas9	99	0
908	CTGTC	16908	agttTCTATTGGTCTCCTTAAAC	17824	BlatCas9	99	0
909	AAGTC	16909	gcagGAGCCAGGGCTGGGCATAA	17825	BlatCas9	99	0
910	CTGTCTT	16910	GTTTCTATTGGTCTCCTTAAAC	17826	CdiCas9	99	0
911	AAGT	16911	GGAGCCAGGGCTGGGCATAA	17827	SpyCas9-3var-NRRH	99	0
912	AAAG	16912	CAGGAGCCAGGGCTGGGCATA	17828	SauriCas9-KKH	100	0
913	AAAG	16913	AGGAGCCAGGGCTGGGCATA	17829	SpyCas9-QQR1	100	0
914	AAAG	16914	caGGAGCCAGGGCTGGGCATA	17830	iSpyMacCas9	100	0
915	AAA	16915	AGGAGCCAGGGCTGGGCATA	17831	SpyCas9-SpRY	100	0
916	CCT	16916	TTTCTATTGGTCTCCTTAAA	17832	SpyCas9-SpRY	100	0

In the exemplary template sequences provided herein, capital letters indicate "core nucleotides" while lower case letters indicate "flanking nucleotides." Herein, when an RNA sequence (e.g., a template RNA sequence) is said to comprise a particular sequence (e.g., a sequence of Table 1 or

a portion thereof) that comprises thymine (T), it is of course understood that the RNA sequence may (and frequently does) comprise uracil (U) in place of T. For instance, the RNA sequence may comprise U at every position shown as T in the sequence in Table 1. More specifically, the present disclosure provides an RNA sequence according to every gRNA spacer sequence shown in Table 1, wherein the RNA sequence has a U in place of each T in the sequence in Table 1.

In some embodiments of the systems and methods herein, the heterologous object sequence comprises the core nucleotides of an RT template sequence from Table 3. In some embodiments, the heterologous object sequence additionally comprises one or more (e.g., 2, 3, 4, 5, 10, 20, 30, 40, or all) consecutive nucleotides starting with the 3' end of the flanking nucleotides of the RT template sequence. In some embodiments, the heterologous object sequence comprises the core nucleotides of the RT template sequence of Table 3 that corresponds to the gRNA spacer sequence. In the context of the sequence tables, a first component "corresponds to" a second component when both components have the same ID number in the referenced table. For example, for a gRNA spacer of ID #1, the *corresponding* RT template would be the RT template also having ID #1. In some embodiments, the heterologous object sequence additionally comprises one or more consecutive nucleotides starting with the 3' end of the flanking nucleotides of the RT template sequence.

In some embodiments, the primer binding site (PBS) sequence has a sequence comprising the core nucleotides of a PBS sequence from the same row of Table 3 as the RT template sequence. In some embodiments, the PBS sequence additionally comprises one or more (e.g., 1, 2, 3, 4, 5, 6, 7, or all) consecutive nucleotides starting with the 5' end of the flanking nucleotides of the primer region.

Table 3: Exemplary RT sequence (heterologous object sequence) and PBS sequence pairs

Table 3 provides exemplified PBS sequences and heterologous object sequences (reverse transcription template regions) of a template RNA for correcting the pathogenic EV6 mutation in HBB. The gRNA spacers from Table 1 were filtered, e.g., filtered by occurrence within 15 nt of the desired editing location and use of a Tier 1 Cas enzyme. PBS sequences and heterologous object sequences (reverse transcription template regions) were designed relative to the nick site directed by the cognate gRNA from Table 1, as described in this application. For exemplification, these regions were designed to be 8-17 nt (priming) and 1-50 nt extended beyond the location of the edit (RT). Without wishing to be limited by example, given

variability of length, sequences are provided that use the maximum length parameters and comprise all templates of shorter length within the given parameters. Sequences are shown with uppercase letters indicating core sequence and lowercase letters indicating flanking sequence that may be truncated within the described length parameters.

ID	RT Template Sequence	SEQ ID NO	PBS Sequence	SEQ ID NO
1	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCT	17833	CAGGAGTCagatgcacc	18010
2	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCT	17834	CAGGAGTCagatgcacc	18011
5	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCT	17835	CAGGAGTCagatgcacc	18012
9	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCT	17836	CAGGAGTCagatgcacc	18013
13	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCTC	17837	AGGAGTCAgatgcacca	18014
14	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCTC	17838	AGGAGTCAgatgcacca	18015
15	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAG	17839	GAGAAGTCtgccgttac	18016
16	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAG	17840	GAGAAGTCtgccgttac	18017
17	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAG	17841	GAGAAGTCtgccgttac	18018
18	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAG	17842	GAGAAGTCtgccgttac	18019
23	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCTC	17843	AGGAGTCAgatgcacca	18020
24	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCTC	17844	AGGAGTCAgatgcacca	18021
27	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAG	17845	GAGAAGTCtgccgttac	18022
28	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAG	17846	GAGAAGTCtgccgttac	18023
31	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAG	17847	GAGAAGTCtgccgttac	18024
32	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAG	17848	GAGAAGTCtgccgttac	18025
39	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGG	17849	AGAAGTCTgccgttact	18026
40	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGG	17850	AGAAGTCTgccgttact	18027
41	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCTCA	17851	GGAGTCAGatgccacat	18028
42	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGG	17852	AGAAGTCTgccgttact	18029
43	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGG	17853	AGAAGTCTgccgttact	18030
44	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCTCA	17854	GGAGTCAGatgccacat	18031

48	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGG	17855	AGAAGTCTgccgt tact	18032
49	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGG	17856	AGAAGTCTgccgt tact	18033
50	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCTCA	17857	GGAGTCAGatgca ccat	18034
54	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCTCA	17858	GGAGTCAGatgca ccat	18035
59	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCTCAG	17859	GAGTCAGAtgcac catg	18036
60	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCTCAG	17860	GAGTCAGAtgcac catg	18037
61	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGGA	17861	GAAGTCTGccgtta ctg	18038
62	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGGA	17862	GAAGTCTGccgtta ctg	18039
65	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCTCAG	17863	GAGTCAGAtgcac catg	18040
66	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCTCAG	17864	GAGTCAGAtgcac catg	18041
69	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCTCAG	17865	GAGTCAGAtgcac catg	18042
70	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCTCAG	17866	GAGTCAGAtgcac catg	18043
73	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGGA	17867	GAAGTCTGccgtta ctg	18044
79	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCTCAGG	17868	AGTCAGATgcacc atgg	18045
80	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCTCAGG	17869	AGTCAGATgcacc atgg	18046
81	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGGAG	17870	AAGTCTGCcgttac tgc	18047
82	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCTCAGG	17871	AGTCAGATgcacc atgg	18048
83	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCTCAGG	17872	AGTCAGATgcacc atgg	18049
86	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCTCAGG	17873	AGTCAGATgcacc atgg	18050
87	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCTCAGG	17874	AGTCAGATgcacc atgg	18051
88	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGGAG	17875	AAGTCTGCcgttac tgc	18052
94	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCTCAGGA	17876	GTCAGATGcacca tggt	18053
95	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCTCAGGA	17877	GTCAGATGcacca tggt	18054
99	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCTCAGGA	17878	GTCAGATGcacca tggt	18055
100	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGGAGA	17879	AGTCTGCCgttact gcc	18056
103	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCTCAGGAG	17880	TCAGATGCaccat ggtg	18057
104	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCTCAGGAG	17881	TCAGATGCaccat ggtg	18058

105	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGGAGAA	17882	GTCTGCCGttactgccc	18059
106	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGGAGAA	17883	GTCTGCCGttactgccc	18060
107	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGGAGAA	17884	GTCTGCCGttactgccc	18061
108	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGGAGAAG	17885	TCTGCCGTtactgccct	18062
109	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCTCAGGAGT	17886	CAGATGCAccatggtgt	18063
110	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGGAGAAGT	17887	CTGCCGTTactgccctg	18064
111	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCTCAGGAGTC	17888	AGATGCACcatggtgtc	18065
112	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGGAGAAGT	17889	CTGCCGTTactgccctg	18066
113	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGGAGAAGTC	17890	TGCCGTTActgccctgt	18067
114	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGGAGAAGTC	17891	TGCCGTTActgccctgt	18068
115	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCTCAGGAGTCA	17892	GATGCACCatggtgtct	18069
116	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGGAGAAGTC	17893	TGCCGTTActgccctgt	18070
117	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGGAGAAGTCT	17894	GCCGTTACtgccctgtg	18071
118	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCTCAGGAGTCAG	17895	ATGCACCAtggtgtctg	18072
119	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCTCAGGAGTCAG	17896	ATGCACCAtggtgtctg	18073
120	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCTCAGGAGTCAG	17897	ATGCACCAtggtgtctg	18074
121	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCTCAGGAGTCAGA	17898	TGCACCATggtgtctgt	18075
122	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCTCAGGAGTCAGA	17899	TGCACCATggtgtctgt	18076
123	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGGAGAAGTCTG	17900	CCGTTACTgccctgtgg	18077
124	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCTCAGGAGTCAGA	17901	TGCACCATggtgtctgt	18078
125	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGGAGAAGTCTG	17902	CCGTTACTgccctgtgg	18079
126	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCTCAGGAGTCAGA	17903	TGCACCATggtgtctgt	18080
128	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCTCAGGAGTCAGAT	17904	GCACCATGgtgtctgtt	18081
131	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGGAGAAGTCTGC	17905	CGTTACTGccctgtggg	18082
133	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCTCAGGAGTCAGAT	17906	GCACCATGgtgtctgtt	18083
140	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCTCAGGAGTCAGATG	17907	CACCATGGtgtctgttt	18084
141	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCTCAGGAGTCAGATG	17908	CACCATGGtgtctgttt	18085

142	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGGAGAAGTCTGCC	17909	GTTACTGCcctgtgggg	18086
146	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGGAGAAGTCTGCC	17910	GTTACTGCcctgtgggg	18087
147	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCTCAGGAGTCAGATG	17911	CACCATGGtgtctgttt	18088
154	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCTCAGGAGTCAGATGC	17912	ACCATGGTgtctgttg	18089
157	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGGAGAAGTCTGCCG	17913	TTACTGCCctgtgggc	18090
158	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGGAGAAGTCTGCCG	17914	TTACTGCCctgtgggc	18091
159	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCTCAGGAGTCAGATGC	17915	ACCATGGTgtctgttg	18092
160	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGGAGAAGTCTGCCG	17916	TTACTGCCctgtgggc	18093
165	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGGAGAAGTCTGCCGT	17917	TACTGCCCtgtgggca	18094
166	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGGAGAAGTCTGCCGT	17918	TACTGCCCtgtgggca	18095
167	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGGAGAAGTCTGCCGT	17919	TACTGCCCtgtgggca	18096
168	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCTCAGGAGTCAGATGCA	17920	CCATGGTGtctgtttga	18097
172	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGGAGAAGTCTGCCGTT	17921	ACTGCCCTgtgggcaa	18098
173	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGGAGAAGTCTGCCGTT	17922	ACTGCCCTgtgggcaa	18099
177	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGGAGAAGTCTGCCGTT	17923	ACTGCCCTgtgggcaa	18100
178	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCTCAGGAGTCAGATGCAC	17924	CATGGTGTctgtttgag	18101
186	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGGAGAAGTCTGCCGTTA	17925	CTGCCCTGtggggcaag	18102
187	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGGAGAAGTCTGCCGTTA	17926	CTGCCCTGtggggcaag	18103
190	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGGAGAAGTCTGCCGTTA	17927	CTGCCCTGtggggcaag	18104
191	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGGAGAAGTCTGCCGTTA	17928	CTGCCCTGtggggcaag	18105
194	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCTCAGGAGTCAGATGCACC	17929	ATGGTGTCtgtttgagg	18106
195	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCTCAGGAGTCAGATGCACC	17930	ATGGTGTCtgtttgagg	18107
196	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCTCAGGAGTCAGATGCACC	17931	ATGGTGTCtgtttgagg	18108
198	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGGAGAAGTCTGCCGTTAC	17932	TGCCCTGTggggcaagg	18109
199	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGGAGAAGTCTGCCGTTAC	17933	TGCCCTGTggggcaagg	18110
202	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGGAGAAGTCTGCCGTTAC	17934	TGCCCTGTggggcaagg	18111
203	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGGAGAAGTCTGCCGTTAC	17935	TGCCCTGTggggcaagg	18112

204	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCTCAGGAGTCAGATGCACCA	17936	TGGTGTCTgtttgaggt	18113
208	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCTCAGGAGTCAGATGCACCA	17937	TGGTGTCTgtttgaggt	18114
209	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGGAGAAGTCTGCCGTTAC	17938	TGCCCTGTggggcaagg	18115
210	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGGAGAAGTCTGCCGTTAC	17939	TGCCCTGTggggcaagg	18116
212	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGGAGAAGTCTGCCGTTACT	17940	GCCCTGTGgggcaaggt	18117
215	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCTCAGGAGTCAGATGCACCAT	17941	GGTGTCTGtttgaggtt	18118
216	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCTCAGGAGTCAGATGCACCAT	17942	GGTGTCTGtttgaggtt	18119
217	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGGAGAAGTCTGCCGTTACT	17943	GCCCTGTGgggcaaggt	18120
221	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCTCAGGAGTCAGATGCACCATG	17944	GTGTCTGTttgaggttg	18121
224	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGGAGAAGTCTGCCGTTACTG	17945	CCCTGTGGggcaaggtg	18122
226	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCTCAGGAGTCAGATGCACCATG	17946	GTGTCTGTttgaggttg	18123
227	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCTCAGGAGTCAGATGCACCATG	17947	GTGTCTGTttgaggttg	18124
232	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCTCAGGAGTCAGATGCACCATGG	17948	TGTCTGTTtgaggttgc	18125
233	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCTCAGGAGTCAGATGCACCATGG	17949	TGTCTGTTtgaggttgc	18126
236	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCTCAGGAGTCAGATGCACCATGG	17950	TGTCTGTTtgaggttgc	18127
237	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCTCAGGAGTCAGATGCACCATGG	17951	TGTCTGTTtgaggttgc	18128
240	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGGAGAAGTCTGCCGTTACTGC	17952	CCTGTGGGgcaaggtga	18129
241	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGGAGAAGTCTGCCGTTACTGC	17953	CCTGTGGGgcaaggtga	18130
243	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGGAGAAGTCTGCCGTTACTGCC	17954	CTGTGGGGcaaggtgaa	18131
244	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCTCAGGAGTCAGATGCACCATGGT	17955	GTCTGTTTgaggttgct	18132
245	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCTCAGGAGTCAGATGCACCATGGT	17956	GTCTGTTTgaggttgct	18133
248	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCTCAGGAGTCAGATGCACCATGGT	17957	GTCTGTTTgaggttgct	18134
249	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCTCAGGAGTCAGATGCACCATGGT	17958	GTCTGTTTgaggttgct	18135
250	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGGAGAAGTCTGCCGTTACTGCC	17959	CTGTGGGGcaaggtgaa	18136
254	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGGAGAAGTCTGCCGTTACTGCC	17960	CTGTGGGGcaaggtgaa	18137
258	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCTCAGGAGTCAGATGCACCATGGTG	17961	TCTGTTTGaggttgcta	18138
259	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCTCAGGAGTCAGATGCACCATGGTG	17962	TCTGTTTGaggttgcta	18139

262	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGGAGAAGTCTGCCGTTACTGCCC	17963	TGTGGGGCaaggtgaac	18140
263	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGGAGAAGTCTGCCGTTACTGCCC	17964	TGTGGGGCaaggtgaac	18141
264	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCTCAGGAGTCAGATGCACCATGGTG	17965	TCTGTTTGaggttgcta	18142
267	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGGAGAAGTCTGCCGTTACTGCCCT	17966	GTGGGGCAaggtgaacg	18143
268	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGGAGAAGTCTGCCGTTACTGCCCT	17967	GTGGGGCAaggtgaacg	18144
269	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCTCAGGAGTCAGATGCACCATGGTGT	17968	CTGTTTGAggttgctag	18145
270	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGGAGAAGTCTGCCGTTACTGCCCTG	17969	TGGGGCAAggtgaacgt	18146
271	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGGAGAAGTCTGCCGTTACTGCCCTG	17970	TGGGGCAAggtgaacgt	18147
274	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGGAGAAGTCTGCCGTTACTGCCCTG	17971	TGGGGCAAggtgaacgt	18148
278	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGGAGAAGTCTGCCGTTACTGCCCTG	17972	TGGGGCAAggtgaacgt	18149
279	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCTCAGGAGTCAGATGCACCATGGTGTC	17973	TGTTTGAGgttgctagt	18150
283	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGGAGAAGTCTGCCGTTACTGCCCTGT	17974	GGGGCAAGgtgaacgtg	18151
284	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGGAGAAGTCTGCCGTTACTGCCCTGT	17975	GGGGCAAGgtgaacgtg	18152
287	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGGAGAAGTCTGCCGTTACTGCCCTGT	17976	GGGGCAAGgtgaacgtg	18153
288	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGGAGAAGTCTGCCGTTACTGCCCTGT	17977	GGGGCAAGgtgaacgtg	18154
291	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCTCAGGAGTCAGATGCACCATGGTGTCT	17978	GTTTGAGGttgctagtg	18155
294	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGGAGAAGTCTGCCGTTACTGCCCTGTG	17979	GGGCAAGGtgaacgtgg	18156
295	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGGAGAAGTCTGCCGTTACTGCCCTGTG	17980	GGGCAAGGtgaacgtgg	18157
298	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGGAGAAGTCTGCCGTTACTGCCCTGTG	17981	GGGCAAGGtgaacgtgg	18158
299	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGGAGAAGTCTGCCGTTACTGCCCTGTG	17982	GGGCAAGGtgaacgtgg	18159
302	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGGAGAAGTCTGCCGTTACTGCCCTGTG	17983	GGGCAAGGtgaacgtgg	18160
303	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGGAGAAGTCTGCCGTTACTGCCCTGTG	17984	GGGCAAGGtgaacgtgg	18161
306	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCTCAGGAGTCAGATGCACCATGGTGTCTG	17985	TTTGAGGTtgctagtga	18162
307	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGGAGAAGTCTGCCGTTACTGCCCTGTG	17986	GGGCAAGGtgaacgtgg	18163
308	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCTCAGGAGTCAGATGCACCATGGTGTCTG	17987	TTTGAGGTtgctagtga	18164
309	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGGAGAAGTCTGCCGTTACTGCCCTGTG	17988	GGGCAAGGtgaacgtgg	18165
310	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCTCAGGAGTCAGATGCACCATGGTGTCTG	17989	TTTGAGGTtgctagtga	18166

312	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCTCAGGAG TCAGATGCACCATGGTGTCTGT	17990	TTGAGGTTgctagtgaa	18167
313	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGGAGAA GTCTGCCGTTACTGCCCTGTGG	17991	GGCAAGGTgaacgtgga	18168
314	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGGAGAA GTCTGCCGTTACTGCCCTGTGG	17992	GGCAAGGTgaacgtgga	18169
315	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGGAGAA GTCTGCCGTTACTGCCCTGTGG	17993	GGCAAGGTgaacgtgga	18170
316	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGGAGAA GTCTGCCGTTACTGCCCTGTGG	17994	GGCAAGGTgaacgtgga	18171
319	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGGAGAA GTCTGCCGTTACTGCCCTGTGG	17995	GGCAAGGTgaacgtgga	18172
320	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGGAGAA GTCTGCCGTTACTGCCCTGTGG	17996	GGCAAGGTgaacgtgga	18173
321	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCTCAGGAG TCAGATGCACCATGGTGTCTGT	17997	TTGAGGTTgctagtgaa	18174
322	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCTCAGGAG TCAGATGCACCATGGTGTCTGT	17998	TTGAGGTTgctagtgaa	18175
323	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCTCAGGAG TCAGATGCACCATGGTGTCTGT	17999	TTGAGGTTgctagtgaa	18176
327	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGGAGAA GTCTGCCGTTACTGCCCTGTGGG	18000	GCAAGGTGaacggtgat	18177
328	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGGAGAA GTCTGCCGTTACTGCCCTGTGGG	18001	GCAAGGTGaacggtgat	18178
329	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCTCAGGAG TCAGATGCACCATGGTGTCTGTT	18002	TGAGGTTGctagtgaac	18179
333	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCTCAGGAG TCAGATGCACCATGGTGTCTGTT	18003	TGAGGTTGctagtgaac	18180
334	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGGAGAA GTCTGCCGTTACTGCCCTGTGGG	18004	GCAAGGTGaacggtgat	18181
340	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGGAGAA GTCTGCCGTTACTGCCCTGTGGGG	18005	CAAGGTGAacgtggatg	18182
343	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCTCAGGAG TCAGATGCACCATGGTGTCTGTTT	18006	GAGGTTGCtagtgaaca	18183
344	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCTCAGGAG TCAGATGCACCATGGTGTCTGTTT	18007	GAGGTTGCtagtgaaca	18184
345	ctgtgttcactagcaacctcaaacagacaccatggtgcatctgactcctGAGGAGAA GTCTGCCGTTACTGCCCTGTGGGG	18008	CAAGGTGAacgtggatg	18185
346	cttcatccacgttcaccttgccccacagggcagtaacggcagacttctcCTCAGGAG TCAGATGCACCATGGTGTCTGTTT	18009	GAGGTTGCtagtgaaca	18186

Capital letters indicate "core nucleotides" while lower case letters indicate "flanking nucleotides." Herein, when an RNA sequence (e.g., a template RNA sequence) is said to comprise a particular sequence (e.g., a sequence of Table 3 or a portion thereof) that comprises thymine (T), it is of course understood that the RNA sequence may (and frequently does) comprise uracil (U) in place of T. For instance, the RNA sequence may comprise U at every position shown as T in the sequence in Table 3. More specifically, the present disclosure provides an RNA sequence according to every heterologous object sequence and PBS sequence

shown in Table 3, wherein the RNA sequence has a U in place of each T in the sequence of Table 3.

In some embodiments of the systems and methods herein, the template RNA comprises a gRNA scaffold (e.g., that binds a gene modifying polypeptide, e.g., a Cas polypeptide) that comprises a sequence of a gRNA scaffold of Table 12. In some embodiments, the gRNA scaffold comprises a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity to a gRNA scaffold of Table 12. In some embodiments, the gRNA scaffold comprises a sequence of a scaffold region of Table 12 that corresponds to the RT template sequence, the spacer sequence, or both, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto.

In some embodiments of the systems and methods herein, the system further comprises a second strand-targeting gRNA that directs a nick to the second strand of the human HBB gene. In some embodiments, the second strand-targeting gRNA comprises a left gRNA spacer sequence or a right gRNA spacer sequence from Table 2. In some embodiments, the gRNA spacer additionally comprises one or more (e.g., 2, 3, or all) consecutive nucleotides starting with the 3' end of the flanking nucleotides of the left gRNA spacer sequence or right gRNA spacer sequence. In some embodiments, the second strand-targeting gRNA comprises a sequence comprising the core nucleotides of a second nick gRNA sequence from Table 4, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto. In some embodiments, the second nick gRNA sequence additionally comprises one or more consecutive nucleotides starting with the 3' end of the flanking nucleotides of the second nick gRNA sequence. In some embodiments, the second nick gRNA comprises a gRNA scaffold sequence that is orthogonal to the Cas domain of the gene modifying polypeptide. In some embodiments, the second nick gRNA comprises a gRNA scaffold sequence of Table 12.

Table 2: Exemplary left gRNA spacer and right gRNA spacer pairs

Table 2 provides exemplified second-nick gRNA species for optional use for correcting the pathogenic E6V mutation in HBB. The gRNA spacers from Table 1 were filtered, e.g., filtered by occurrence within 15 nt of the desired editing location and use of a Tier 1 Cas enzyme. Second-nick gRNAs were generated by searching the opposite strand of DNA in the regions -40 to -140 ("left") and +40 to +140 ("right"),

relative to the first nick site defined by the first gRNA, for the PAM utilized by the corresponding Cas variant. One exemplary spacer is shown for each side of the target nick site.

ID	Left gRNA spacer	SEQ ID NO	Left PAM	SEQ ID NO	Right gRNA spacer	SEQ ID NO	Right PAM	SEQ ID NO
1	GCCCAGTTTCTATTGGTCTCC	18187	TTAAA	18364	GGCTCTGCCCTGACTTTTATG	18541	CCCAG	18718
2	GCCCAGTTTCTATTGGTCTCC	18188	TTAAA	18365	GGCTCTGCCCTGACTTTTATG	18542	CCCAG	18719
5	TCTATTGGTCTCCTTAAACC	18189	TG	18366	CTGCCCTGACTTTTATGCCC	18543	AG	18720
9	TTCTATTGGTCTCCTTAAAC	18190	CTG	18367	TCTGCCCTGACTTTTATGCC	18544	CAG	18721
13	tgTAACCTTGATACCAACCTGCC	18191	CAGGG	18368	ccTGGCTCCTGCCCTCCCTGCTC	18545	CTGGG	18722
14	TTGGTCTCCTTAAACCTGTCT	18192	TGTAA	18369	GGCTCTGCCCTGACTTTTATG	18546	CCCAG	18723
15	atCAAGGTTACAAGACAGGTTTA	18193	AGGAG	18370	gaGCCAGGGCTGGGCATAAAAGT	18547	CAGGG	18724
16	TTACAAGACAGGTTTAAGGAG	18194	ACCAA	18371	GAGCCAGGGCTGGGCATAAAA	18548	GTCAG	18725
17	atCAAGGTTACAAGACAGGTTTA	18195	AGGAG	18372	gaGCCAGGGCTGGGCATAAAAGT	18549	CAGGG	18726
18	TTACAAGACAGGTTTAAGGAG	18196	ACCAA	18373	GAGCCAGGGCTGGGCATAAAA	18550	GTCAG	18727
23	TTCTATTGGTCTCCTTAAAC	18197	CTG	18374	TCTGCCCTGACTTTTATGCC	18551	CAG	18728
24	TCTATTGGTCTCCTTAAACC	18198	TGT	18375	CTGCCCTGACTTTTATGCCC	18552	AGC	18729
27	GGTTACAAGACAGGTTTAAG	18199	GAG	18376	GGAGCCAGGGCTGGGCATAA	18553	AAG	18730
28	AAGGTTACAAGACAGGTTTA	18200	AGG	18377	CAGGGCTGGGCATAAAAGTC	18554	AGG	18731
31	GTTACAAGACAGGTTTAAGG	18201	AGA	18378	GAGCCAGGGCTGGGCATAAA	18555	AGT	18732
32	GTTACAAGACAGGTTTAAGG	18202	AG	18379	GAGCCAGGGCTGGGCATAAA	18556	AG	18733
39	atCAAGGTTACAAGACAGGTTTA	18203	AGGAG	18380	gaGCCAGGGCTGGGCATAAAAGT	18557	CAGGG	18734
40	TTACAAGACAGGTTTAAGGAG	18204	ACCAA	18381	GAGCCAGGGCTGGGCATAAAA	18558	GTCAG	18735
41	TTGGTCTCCTTAAACCTGTCT	18205	TGTAA	18382	GCCCTGACTTTTATGCCCAGC	18559	CCTGG	18736
42	TCAAGGTTACAAGACAGGTTT	18206	AAGG	18383	GCCAGGGCTGGGCATAAAAGT	18560	CAGG	18737
43	AAGGTTACAAGACAGGTTTAA	18207	GGAG	18384	AGCCAGGGCTGGGCATAAAAG	18561	TCAG	18738
44	TCTCCACATGCCCAGTTTCTA	18208	TTGG	18385	CCCTGACTTTTATGCCCAGCC	18562	CTGG	18739
48	GGTTACAAGACAGGTTTAAG	18209	GAG	18386	CCAGGGCTGGGCATAAAAGT	18563	CAG	18740

49	TTACAAGACAGGTTTAAGGA	18210	GAC	18387	AGCCAGGGCTGGGCATAAAA	18564	GTC	18741
50	TCTATTGGTCTCCTTAAACC	18211	TG	18388	CTGCCCTGACTTTTATGCCC	18565	AG	18742
54	CTATTGGTCTCCTTAAACCT	18212	GTC	18389	TGCCCTGACTTTTATGCCCA	18566	GCC	18743
59	tgTAACCTTGATACCAACCTGCC	18213	CAGGG	18390	ccTGGCTCCTGCCCTCCCTGCTC	18567	CTGGG	18744
60	TTGGTCTCCTTAAACCTGTCT	18214	TGTAA	18391	GCCCTGACTTTTATGCCCAGC	18568	CCTGG	18745
61	TTACAAGACAGGTTTAAGGAG	18215	ACCAA	18392	AGCCAGGGCTGGGCATAAAAG	18569	TCAGG	18746
62	AAGACAGGTTTAAGGAGACCA	18216	ATAG	18393	AGCCAGGGCTGGGCATAAAAG	18570	TCAG	18747
65	TTGGTCTCCTTAAACCTGTC	18217	TTG	18394	CCTGACTTTTATGCCCAGCC	18571	CTG	18748
66	TCCACATGCCCAGTTTCTAT	18218	TGG	18395	CTGACTTTTATGCCCAGCCC	18572	TGG	18749
69	TATTGGTCTCCTTAAACCTG	18219	TCT	18396	GCCCTGACTTTTATGCCCAG	18573	CCC	18750
70	TCTATTGGTCTCCTTAAACC	18220	TG	18397	CTGCCCTGACTTTTATGCCC	18574	AG	18751
73	TACAAGACAGGTTTAAGGAG	18221	ACC	18398	GCCAGGGCTGGGCATAAAAG	18575	TCA	18752
79	tgTAACCTTGATACCAACCTGCC	18222	CAGGG	18399	ccTGGCTCCTGCCCTCCCTGCTC	18576	CTGGG	18753
80	TTGGTCTCCTTAAACCTGTCT	18223	TGTAA	18400	GCCCTGACTTTTATGCCCAGC	18577	CCTGG	18754
81	TTACAAGACAGGTTTAAGGAG	18224	ACCAA	18401	GCCAGGGCTGGGCATAAAAGT	18578	CAGGG	18755
82	TCTCCACATGCCCAGTTTCTA	18225	TTGG	18402	CCCTGACTTTTATGCCCAGCC	18579	CTGG	18756
83	TCTCCACATGCCCAGTTTCTA	18226	TTGG	18403	CCCTGACTTTTATGCCCAGCC	18580	CTGG	18757
86	TTGGTCTCCTTAAACCTGTC	18227	TTG	18404	CCTGACTTTTATGCCCAGCC	18581	CTG	18758
87	ATTGGTCTCCTTAAACCTGT	18228	CTT	18405	CCCTGACTTTTATGCCCAGC	18582	CCT	18759
88	ACAAGACAGGTTTAAGGAGA	18229	CCA	18406	CCAGGGCTGGGCATAAAAGT	18583	CAG	18760
94	TTGGTCTCCTTAAACCTGTCT	18230	TGTAA	18407	GCCCTGACTTTTATGCCCAGC	18584	CCTGG	18761
95	TGGTCTCCTTAAACCTGTCT	18231	TG	18408	CTGACTTTTATGCCCAGCCC	18585	TG	18762
99	TTGGTCTCCTTAAACCTGTC	18232	TTG	18409	CCTGACTTTTATGCCCAGCC	18586	CTG	18763
100	CAAGACAGGTTTAAGGAGAC	18233	CAA	18410	CAGGGCTGGGCATAAAAGTC	18587	AGG	18764
103	TTGGTCTCCTTAAACCTGTC	18234	TTG	18411	CTGACTTTTATGCCCAGCCC	18588	TGG	18765
104	TGGTCTCCTTAAACCTGTCT	18235	TGT	18412	CTGACTTTTATGCCCAGCCC	18589	TGG	18766
105	AAGACAGGTTTAAGGAGACC	18236	AAT	18413	AGGGCTGGGCATAAAAGTCA	18590	GGG	18767

106	agacAGGTTTAAGGAGACCAATA	18237	GAAACTGG	18414	agccAGGGCTGGGCATAAAAGTC	18591	AGGGCAGA	18768
107	agacAGGTTTAAGGAGACCAATA	18238	GAAACTGG	18415	agccAGGGCTGGGCATAAAAGTC	18592	AGGGCAGA	18769
108	AGACAGGTTTAAGGAGACCA	18239	ATA	18416	GGGCTGGGCATAAAAGTCAG	18593	GGC	18770
109	GGTCTCCTTAAACCTGTCTT	18240	GTA	18417	TGACTTTTATGCCCAGCCCT	18594	GGC	18771
110	GACAGGTTTAAGGAGACCAA	18241	TAG	18418	GGCTGGGCATAAAAGTCAGG	18595	GCA	18772
111	GTCTCCTTAAACCTGTCTTG	18242	TAA	18419	GACTTTTATGCCCAGCCCTG	18596	GCT	18773
112	agacAGGTTTAAGGAGACCAATA	18243	GAAACTGG	18420	gggcTGGGCATAAAAGTCAGGGC	18597	AGAGC	18774
113	tcAAGGTTACAAGACAGGTTTAAG	18244	GAGACC	18421	agGGCTGGGCATAAAAGTCAGGGC	18598	AGAGCC	18775
114	ACAGGTTTAAGGAGACCAAT	18245	AGA	18422	GCTGGGCATAAAAGTCAGGG	18599	CAG	18776
115	TCTCCTTAAACCTGTCTTGT	18246	AAC	18423	ACTTTTATGCCCAGCCCTGG	18600	CTC	18777
116	agacAGGTTTAAGGAGACCAATA	18247	GAAACTGG	18424	gggcTGGGCATAAAAGTCAGGGC	18601	AGAGC	18778
117	CAGGTTTAAGGAGACCAATA	18248	GAA	18425	CTGGGCATAAAAGTCAGGGC	18602	AGA	18779
118	CTCCTTAAACCTGTCTTGTA	18249	ACC	18426	CTTTTATGCCCAGCCCTGGC	18603	TCC	18780
119	ttggTCTCCTTAAACCTGTCTTG	18250	TAACCTTG	18427	gactTTTATGCCCAGCCCTGGCT	18604	CCTGC	18781
120	ttggTCTCCTTAAACCTGTCTTG	18251	TAACCTTG	18428	gactTTTATGCCCAGCCCTGGCT	18605	CCTGC	18782
121	taTTGGTCTCCTTAAACCTGTCTT	18252	GTAACC	18429	tgACTTTTATGCCCAGCCCTGGCT	18606	CCTGCC	18783
122	TCCTTAAACCTGTCTTGTAA	18253	CCT	18430	TTTTATGCCCAGCCCTGGCT	18607	CCT	18784
123	AGGTTTAAGGAGACCAATAG	18254	AAA	18431	TGGGCATAAAAGTCAGGGCA	18608	GAG	18785
124	ttggTCTCCTTAAACCTGTCTTG	18255	TAACCTTG	18432	gactTTTATGCCCAGCCCTGGCT	18609	CCTGC	18786
125	agacAGGTTTAAGGAGACCAATA	18256	GAAACTGG	18433	ggctGGGCATAAAAGTCAGGGCA	18610	GAGCC	18787
126	ttggTCTCCTTAAACCTGTCTTG	18257	TAACCTTG	18434	gactTTTATGCCCAGCCCTGGCT	18611	CCTGC	18788
128	TTAAACCTGTCTTGTAACCT	18258	TG	18435	TTATGCCCAGCCCTGGCTCC	18612	TG	18789
131	GGTTTAAGGAGACCAATAGA	18259	AAC	18436	GGGCATAAAAGTCAGGGCAG	18613	AGC	18790
133	CCTTAAACCTGTCTTGTAAC	18260	CTT	18437	TTTATGCCCAGCCCTGGCTC	18614	CTG	18791
140	CTTAAACCTGTCTTGTAACC	18261	TTG	18438	TTTATGCCCAGCCCTGGCTC	18615	CTG	18792
141	CTTAAACCTGTCTTGTAACC	18262	TTG	18439	TTATGCCCAGCCCTGGCTCC	18616	TGC	18793
142	TTAAGGAGACCAATAGAAAC	18263	TG	18440	GGGCATAAAAGTCAGGGCAG	18617	AG	18794

146	GTTTAAGGAGACC AATAGAA	1826 4	ACT	1844 1	GGCATAAAAGTCA GGGCAGA	1861 8	GCC	1879 5
147	ccttAAACCTGTCTT GTAACCTT	1826 5	GATA CCAA	1844 2	ctttTATGCCCAGCCC TGGCTCC	1861 9	TGCCC	1879 6
154	TCCTTAAACCTGTC TTGTAAC	1826 6	CTTGA T	1844 3	GCCCTGACTTTTAT GCCCAGC	1862 0	CCTGG	1879 7
157	TTTAAGGAGACCA ATAGAAA	1826 7	CTG	1844 4	TGGGCATAAAAGTC AGGGCA	1862 1	GAG	1879 8
158	TTTAAGGAGACCA ATAGAAA	1826 8	CTG	1844 5	GCATAAAAGTCAG GGCAGAG	1862 2	CCA	1879 9
159	TTAAACCTGTCTTG TAACCT	1826 9	TGA	1844 6	TATGCCCAGCCCTG GCTCCT	1862 3	GCC	1880 0
160	ggttTAAGGAGACCA ATAGAAAC	1827 0	TGGG C	1844 7	tgggCATAAAAGTCA GGGCAGAG	1862 4	CCATC	1880 1
165	GTTTAAGGAGACC AATAGAAA	1827 1	CTGG G	1844 8	GGCTGGGCATAAA AGTCAGGG	1862 5	CAGA G	1880 2
166	TTTAAGGAGACCA ATAGAAAC	1827 2	TGGG	1844 9	GCTGGGCATAAAA GTCAGGGC	1862 6	AGAG	1880 3
167	TTAAGGAGACCAA TAGAAAC	1827 3	TGG	1845 0	CATAAAAGTCAGG GCAGAGC	1862 7	CAT	1880 4
168	TAAACCTGTCTTGT AACCTT	1827 4	GAT	1845 1	ATGCCCAGCCCTGG CTCCTG	1862 8	CCC	1880 5
172	GTTTAAGGAGACC AATAGAAA	1827 5	CTGG G	1845 2	GGCTGGGCATAAA AGTCAGGG	1862 9	CAGA G	1880 6
173	TAAGGAGACCAAT AGAAACT	1827 6	GG	1845 3	GGGCATAAAAGTC AGGGCAG	1863 0	AG	1880 7
177	TAAGGAGACCAAT AGAAACT	1827 7	GGG	1845 4	ATAAAAGTCAGGG CAGAGCC	1863 1	ATC	1880 8
178	AAACCTGTCTTGTA ACCTTG	1827 8	ATA	1845 5	TGCCCAGCCCTGGC TCCTGC	1863 2	CCT	1880 9
186	TAAGGAGACCAAT AGAAACT	1827 9	GGG	1845 6	AGTCAGGGCAGAG CCATCTA	1863 3	TTG	1881 0
187	TAAGGAGACCAAT AGAAACT	1828 0	GGG	1845 7	AGGGCTGGGCATA AAAGTCA	1863 4	GGG	1881 1
190	AAGGAGACCAATA GAAACTG	1828 1	GGC	1845 8	TAAAAGTCAGGGC AGAGCCA	1863 5	TCT	1881 2
191	AAGGAGACCAATA GAAACTG	1828 2	GG	1845 9	GTCAGGGCAGAGC CATCTAT	1863 6	TG	1881 3
194	AACCTGTCTTGTAA CCTTGA	1828 3	TAC	1846 0	GCCCAGCCCTGGCT CCTGCC	1863 7	CTC	1881 4
195	cttaAACCTGTCTTGT AACCTTG	1828 4	ATACC	1846 1	tatgCCCAGCCCTGGC TCCTGCC	1863 8	CTCCC	1881 5
196	cttaAACCTGTCTTGT AACCTTG	1828 5	ATACC	1846 2	tatgCCCAGCCCTGGC TCCTGCC	1863 9	CTCCC	1881 6
198	TTTAAGGAGACCA ATAGAAAC	1828 6	TGGG	1846 3	CCAGGGCTGGGCAT AAAAGTC	1864 0	AGGG	1881 7
199	TTTAAGGAGACCA ATAGAAAC	1828 7	TGGG	1846 4	GCTGGGCATAAAA GTCAGGGC	1864 1	AGAG	1881 8
202	TAAGGAGACCAAT AGAAACT	1828 8	GGG	1846 5	AGTCAGGGCAGAG CCATCTA	1864 2	TTG	1881 9
203	AGGAGACCAATAG AAACTGG	1828 9	GCA	1846 6	AAAAGTCAGGGCA GAGCCAT	1864 3	CTA	1882 0
204	TTAAACCTGTCTTG TAACCT	1829 0	TG	1846 7	GCCCTGGCTCCTGC CCTCCC	1864 4	TG	1882 1

208	ACCTGTCTTGTAACCTTGAT	18291	ACC	18468	CCCAGCCCTGGCTCCTGCCC	18645	TCC	18822
209	ggttTAAGGAGACCAATAGAAAC	18292	TGGGC	18469	taaaAGTCAGGGCAGAGCCATCT	18646	ATTGC	18823
210	ggttTAAGGAGACCAATAGAAAC	18293	TGGGC	18470	taaaAGTCAGGGCAGAGCCATCT	18647	ATTGC	18824
212	GAGACCAATAGAAACTGGGCA	18294	TGTGG	18471	GGCTGGGCATAAAAGTCAGGG	18648	CAGAG	18825
215	CTTGTAACCTTGATACCAAC	18295	CTG	18472	AGCCCTGGCTCCTGCCCTCC	18649	CTG	18826
216	CCTGTCTTGTAACCTTGATA	18296	CCA	18473	CCAGCCCTGGCTCCTGCCCT	18650	CCC	18827
217	GGAGACCAATAGAAACTGGG	18297	CAT	18474	AAAGTCAGGGCAGAGCCATC	18651	TAT	18828
221	TTGTAACCTTGATACCAACC	18298	TG	18475	GCCCTGGCTCCTGCCCTCCC	18652	TG	18829
224	GAGACCAATAGAAACTGGGC	18299	ATG	18476	AAGTCAGGGCAGAGCCATCT	18653	ATT	18830
226	CTGTCTTGTAACCTTGATAC	18300	CAA	18477	CAGCCCTGGCTCCTGCCCTC	18654	CCT	18831
227	aaccTGTCTTGTAACCTTGATAC	18301	CAACC	18478	gcccAGCCCTGGCTCCTGCCCTC	18655	CCTGC	18832
232	CTTGTAACCTTGATACCAAC	18302	CTG	18479	AGCCCTGGCTCCTGCCCTCC	18656	CTG	18833
233	ACCTTGATACCAACCTGCCC	18303	AGG	18480	GCTCCTGCCCTCCCTGCTCC	18657	TGG	18834
236	TGTCTTGTAACCTTGATACC	18304	AAC	18481	AGCCCTGGCTCCTGCCCTCC	18658	CTG	18835
237	TTGTAACCTTGATACCAACC	18305	TG	18482	GCCCTGGCTCCTGCCCTCCC	18659	TG	18836
240	AGACCAATAGAAACTGGGCA	18306	TGT	18483	AGTCAGGGCAGAGCCATCTA	18660	TTG	18837
241	gaccAATAGAAACTGGGCATGTG	18307	GAGACAGA	18484	taaaAGTCAGGGCAGAGCCATCT	18661	ATTGC	18838
243	AGACCAATAGAAACTGGGCAT	18308	GTGGA	18485	GGCTGGGCATAAAAGTCAGGG	18662	CAGAG	18839
244	TAACCTTGATACCAACCTGCC	18309	CAGG	18486	TGGCTCCTGCCCTCCCTGCTC	18663	CTGG	18840
245	GTAACCTTGATACCAACCTGC	18310	CCAG	18487	TGGCTCCTGCCCTCCCTGCTC	18664	CTGG	18841
248	CTTGTAACCTTGATACCAAC	18311	CTG	18488	AGCCCTGGCTCCTGCCCTCC	18665	CTG	18842
249	GTCTTGTAACCTTGATACCA	18312	ACC	18489	GCCCTGGCTCCTGCCCTCCC	18666	TGC	18843
250	AGACCAATAGAAACTGGGCA	18313	TG	18490	GTCAGGGCAGAGCCATCTAT	18667	TG	18844
254	GACCAATAGAAACTGGGCAT	18314	GTG	18491	GTCAGGGCAGAGCCATCTAT	18668	TGC	18845
258	TGTAACCTTGATACCAACCTG	18315	CCCAG	18492	CTGGCTCCTGCCCTCCCTGCT	18669	CCTGG	18846
259	TGTAACCTTGATACCAACCTG	18316	CCCAG	18493	CTGGCTCCTGCCCTCCCTGCT	18670	CCTGG	18847
262	ACCAATAGAAACTGGGCATG	18317	TGG	18494	AGTCAGGGCAGAGCCATCTA	18671	TTG	18848

263	ACCAATAGAAACT GGGCATG	18318	TGG	18495	TCAGGGCAGAGCC ATCTATT	18672	GCT	18849
264	TCTTGTAACCTTGA TACCAA	18319	CCT	18496	CCCTGGCTCCTGCC CTCCCT	18673	GCT	18850
267	ACCAATAGAAACT GGGCATGT	18320	GGAG	18497	GCTGGGCATAAAA GTCAGGGC	18674	AGAG	18851
268	CCAATAGAAACTG GGCATGT	18321	GGA	18498	CAGGGCAGAGCCA TCTATTG	18675	CTT	18852
269	CTTGTAACCTTGAT ACCAAC	18322	CTG	18499	CCTGGCTCCTGCCC TCCCTG	18676	CTC	18853
270	ACCAATAGAAACT GGGCATGT	18323	GGAG A	18500	CATCTATTGCTTAC ATTTGCT	18677	TCTGA	18854
271	ACCAATAGAAACT GGGCATGT	18324	GGAG A	18501	CATCTATTGCTTAC ATTTGCT	18678	TCTGA	18855
274	CCAATAGAAACTG GGCATGT	18325	GG	18502	GTCAGGGCAGAGC CATCTAT	18679	TG	18856
278	CAATAGAAACTGG GCATGTG	18326	GAG	18503	AGGGCAGAGCCAT CTATTGC	18680	TTA	18857
279	TTGTAACCTTGATA CCAACC	18327	TGC	18504	CTGGCTCCTGCCCT CCCTGC	18681	TCC	18858
283	CAATAGAAACTGG GCATGTG	18328	GAG	18505	GAGCCATCTATTGC TTACAT	18682	TTG	18859
284	ACCAATAGAAACT GGGCATG	18329	TGG	18506	AGGGCTGGGCATA AAAGTCA	18683	GGG	18860
287	AATAGAAACTGGG CATGTGG	18330	AGA	18507	GGGCAGAGCCATCT ATTGCT	18684	TAC	18861
288	AATAGAAACTGGG CATGTGG	18331	AG	18508	GTCAGGGCAGAGC CATCTAT	18685	TG	18862
291	TGTAACCTTGATAC CAACCT	18332	GCC	18509	TGGCTCCTGCCCTC CCTGCT	18686	CCT	18863
294	AGACCAATAGAAA CTGGGCAT	18333	GTGG	18510	CCAGGGCTGGGCAT AAAAGTC	18687	AGGG	18864
295	ATAGAAACTGGGC ATGTGGAG	18334	ACAG	18511	GCTGGGCATAAAA GTCAGGGC	18688	AGAG	18865
298	CAATAGAAACTGG GCATGTG	18335	GAG	18512	GAGCCATCTATTGC TTACAT	18689	TTG	18866
299	ACCAATAGAAACT GGGCATG	18336	TGG	18513	AGGGCTGGGCATA AAAGTCA	18690	GGG	18867
302	ATAGAAACTGGGC ATGTGGA	18337	GAC	18514	GGCAGAGCCATCTA TTGCTT	18691	ACA	18868
303	AATAGAAACTGGG CATGTGG	18338	AG	18515	GTCAGGGCAGAGC CATCTAT	18692	TG	18869
306	GTAACCTTGATACC AACCTG	18339	CCC	18516	GGCTCCTGCCCTCC CTGCTC	18693	CTG	18870
307	gaccAATAGAAACT GGGCATGTG	18340	GAGA CAGA	18517	agtcAGGGCAGAGCC ATCTATTG	18694	CTTAC ATT	18871
308	gtctTGTAACCTTGA TACCAACC	18341	TGCCC AGG	18518	cagcCCTGGCTCCTG CCCTCCCT	18695	GCTCC TGG	18872
309	gaccAATAGAAACT GGGCATGTG	18342	GAGA CAGA	18519	agtcAGGGCAGAGCC ATCTATTG	18696	CTTAC ATT	18873
310	gtctTGTAACCTTGA TACCAACC	18343	TGCCC AGG	18520	cagcCCTGGCTCCTG CCCTCCCT	18697	GCTCC TGG	18874
312	tgTAACCTTGATAC CAACCTGCCC	18344	AGGG CC	18521	ccCAGCCCTGGCTCC TGCCCTCCC	18698	TGCTC C	18875

313	aaTAGAAACTGGGC ATGTGGAGA	18345	CAGAG	18522	agGGCTGGGCATAA AAGTCAGGG	18699	CAGAG	18876
314	ATAGAAACTGGGC ATGTGGAG	18346	ACAGA	18523	CATCTATTGCTTAC ATTTGCT	18700	TCTGA	18877
315	AGACCAATAGAAA CTGGGCAT	18347	GTGG	18524	CCAGGGCTGGGCAT AAAAGTC	18701	AGGG	18878
316	ATAGAAACTGGGC ATGTGGAG	18348	ACAG	18525	GCTGGGCATAAAA GTCAGGGC	18702	AGAG	18879
319	AGAAACTGGGCAT GTGGAGA	18349	CAG	18526	GAGCCATCTATTGC TTACAT	18703	TTG	18880
320	TAGAAACTGGGCA TGTGGAG	18350	ACA	18527	GCAGAGCCATCTAT TGCTTA	18704	CAT	18881
321	TAACCTTGATACCA ACCTGC	18351	CCA	18528	GCTCCTGCCCTCCC TGCTCC	18705	TGG	18882
322	gtaaCCTTGATACCA ACCTGCCC	18352	AGGGC	18529	cagcCCTGGCTCCTG CCCTCCCT	18706	GCTCC TGG	18883
323	gtaaCCTTGATACCA ACCTGCCC	18353	AGGGC	18530	cagcCCTGGCTCCTG CCCTCCCT	18707	GCTCC TGG	18884
327	TAGAAACTGGGCA TGTGGAGA	18354	CAGAG	18531	CATCTATTGCTTAC ATTTGCT	18708	TCTGA	18885
328	ATAGAAACTGGGC ATGTGGAG	18355	ACAG	18532	GCTGGGCATAAAA GTCAGGGC	18709	AGAG	18886
329	ACCTTGATACCAA CCTGCCC	18356	AG	18533	CTCCTGCCCTCCCT GCTCCT	18710	GG	18887
333	AACCTTGATACCA ACCTGCC	18357	CAG	18534	CTCCTGCCCTCCCT GCTCCT	18711	GGG	18888
334	AGAAACTGGGCAT GTGGAGA	18358	CAG	18535	CAGAGCCATCTATT GCTTAC	18712	ATT	18889
340	AGAAACTGGGCAT GTGGAGAC	18359	AGAGA	18536	CATCTATTGCTTAC ATTTGCT	18713	TCTGA	18890
343	ACCTTGATACCAA CCTGCCC	18360	AGG	18537	CCTGCCCTCCCTGC TCCTGG	18714	GAG	18891
344	ACCTTGATACCAA CCTGCCC	18361	AGG	18538	TCCTGCCCTCCCTG CTCCTG	18715	GGA	18892
345	GAAACTGGGCATG TGGAGAC	18362	AGA	18539	AGAGCCATCTATTG CTTACA	18716	TTT	18893
346	gtaaCCTTGATACCA ACCTGCCC	18363	AGGGC	18540	cagcCCTGGCTCCTG CCCTCCCT	18717	GCTCC TGG	18894

Capital letters indicate "core nucleotides" while lower case letters indicate "flanking nucleotides." Herein, when an RNA sequence (e.g., a gRNA to produce a second nick) is said to comprise a particular sequence (e.g., a sequence of Table 2 or a portion thereof) that comprises thymine (T), it is of course understood that the RNA sequence may (and frequently does) comprise uracil (U) in place of T. For instance, the RNA sequence may comprise U at every position shown as T in the sequence in Table 2. More specifically, the present disclosure provides an RNA sequence according to every gRNA spacer sequence shown in Table 2, wherein the RNA sequence has a U in place of each T in the sequence in Table 2.

In some embodiments, the systems and methods provided herein may comprise a template sequence listed in **Table 4**. Table 4 provides exemplary template RNA sequences (column 4) and optional second-nick gRNA sequences (column 5) designed to be paired with a gene modifying polypeptide to correct a mutation in the HBB gene. The templates in Table 4 are meant to exemplify the total sequence of: (1) gRNA spacer (e.g., for targeting for first strand nick), (2) gRNA scaffold, (3) heterologous object sequence, and (4) PBS sequence (e.g., for initiating TPRT at first strand nick).

Table 4. Exemplary template RNA sequences and second nick gRNA sequences

Table 4 provides design of RNA components of gene modifying systems for correcting the pathogenic E6V mutation in HBB. The gRNA spacers from Table 1 were filtered, e.g., filtered by occurrence within 15 nt of the desired editing location and use of a Tier 1 Cas enzyme. For each gRNA ID, this table details the sequence of a complete template RNA, optional second-nick gRNA, and Cas variant for use in a Cas-RT fusion gene modifying polypeptide. For exemplification, PBS sequences and post-edit homology regions (after the location of the edit) are set to 12 nt and 30 nt, respectively. Additionally, a second-nick gRNA is selected with preference for a distance near 100 nt from the first nick and a first preference for a design resulting in a PAM-in system, as described elsewhere in this application.

ID	Cas species	strand	Template RNA	SEQ ID NO	second-nick gRNA	SEQ ID NO
1	SauCas9KKH	-	TGGTGCATCTGACTCCTGTGGGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAcccacagggcagtaacggcagacttctcCTCAGGAGTCagat	18895	GCCCAGTTTCTATTGGTCTCCGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	19072
2	SauCas9KKH	-	TGGTGCATCTGACTCCTGTGGGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAcccacagggcagtaacggcagacttctcCTCAGGAGTCagat	18896	GCCCAGTTTCTATTGGTCTCCGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	19073
5	SpyCas9-NG	-	GGTGCATCTGACTCCTGTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCcccacagggcagtaacggcagacttctcCTCAGGAGTCagat	18897	TCTATTGGTCTCCTTAAACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	19074
9	SpyCas9-SpRY	-	GGTGCATCTGACTCCTGTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCcccacagggcagtaacggcagacttctcCTCAGGAGTCagat	18898	TTCTATTGGTCTCCTTAAACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	19075
13	SauCas9	-	ccATGGTGCATCTGACTCCTGTGGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAccacagggcagtaacggcagacttctcCTCAGGAGTCAgatg	18899	tgTAACCTTGATACCAACCTGCCGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	19076
14	SauCas9KKH	-	ATGGTGCATCTGACTCCTGTGGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAccacagggcagtaacggcagacttctcCTCAGGAGTCAgatg	18900	TTGGTCTCCTTAAACCTGTCTGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	19077

15	SauCas9	+	gcAGTAACGGCAGACTTCTCCACGTTTTAGTACT CTGGAAACAGAATCTACTAAAACAAGGCAAAA TGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAa cagaccatggtgcatctgactcctGAGGAGAAGTCTgcc	18901	gaGCCAGGGGCTGGGCATAAAAGTGTTTTAGTA CTCTGGAAACAGAATCTACTAAAACAAGGCA AAATGCCGTGTTTATCTCGTCAACTTGTTGGC GAGA	19078
16	SauCas9KKH	+	AGTAACGGCAGACTTCTCCACGTTTTAGTACTC TGGAAACAGAATCTACTAAAACAAGGCAAAAT GCCGTGTTTATCTCGTCAACTTGTTGGCGAGAac agacaccatggtgcatctgactcctGAGGAGAAGTCTgcc	18902	GAGCCAGGGGCTGGGCATAAAAGTTTTAGTAC TCTGGAAACAGAATCTACTAAAACAAGGCAA AATGCCGTGTTTATCTCGTCAACTTGTTGGCG AGA	19079
17	SauCas9	+	gcAGTAACGGCAGACTTCTCCACGTTTTAGTACT CTGGAAACAGAATCTACTAAAACAAGGCAAAA TGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAa cagaccatggtgcatctgactcctGAGGAGAAGTCTgcc	18903	gaGCCAGGGGCTGGGCATAAAAGTGTTTTAGTA CTCTGGAAACAGAATCTACTAAAACAAGGCA AAATGCCGTGTTTATCTCGTCAACTTGTTGGC GAGA	19080
18	SauCas9KKH	+	AGTAACGGCAGACTTCTCCACGTTTTAGTACTC TGGAAACAGAATCTACTAAAACAAGGCAAAAT GCCGTGTTTATCTCGTCAACTTGTTGGCGAGAac agacaccatggtgcatctgactcctGAGGAGAAGTCTgcc	18904	GAGCCAGGGGCTGGGCATAAAAGTTTTAGTAC TCTGGAAACAGAATCTACTAAAACAAGGCAA AATGCCGTGTTTATCTCGTCAACTTGTTGGCG AGA	19081
23	ScaCas9-Sc++	-	TGGTGCATCTGACTCCTGTGGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCcac agggcagtaacggcagacttctcCTCAGGAGTCAgatg	18905	TTCTATTGGTCTCCTTAAACGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	19082
24	SpyCas9-SpRY	-	TGGTGCATCTGACTCCTGTGGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCcac agggcagtaacggcagacttctcCTCAGGAGTCAgatg	18906	TCTATTGGTCTCCTTAAACCGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	19083
27	ScaCas9-Sc++	+	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCacag acaccatggtgcatctgactcctGAGGAGAAGTCTgcc	18907	GGAGCCAGGGGCTGGGCATAAGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCCG TTATCAACTTGAAAAAGTGGCACCGAGTCGG TGC	19084
28	SpyCas9	+	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCacag acaccatggtgcatctgactcctGAGGAGAAGTCTgcc	18908	CAGGGCTGGGCATAAAAGTCGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCCG TTATCAACTTGAAAAAGTGGCACCGAGTCGG TGC	19085
31	SpyCas9-SpRY	+	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCacag acaccatggtgcatctgactcctGAGGAGAAGTCTgcc	18909	GAGCCAGGGGCTGGGCATAAAGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCCG TTATCAACTTGAAAAAGTGGCACCGAGTCGG TGC	19086
32	SpyCas9-NG	+	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT	18910	GAGCCAGGGGCTGGGCATAAAGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCCG	19087

			CAACTTGAAAAAGTGGCACCGAGTCGGTGCacag acaccatggtgcatctgactcctGAGGAGAAGTCTgcc	18911	TTATCAACTTGAAAAAGTGGCACCGAGTCGG TGC	19088
39	SauCas9	+	ggCAGTAACGGCAGACTTCTCCAGTTTTAGTACT CTGGAAACAGAATCTACTAAAACAAGGCAAAA TGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAc agacaccatggtgcatctgactcctGAGGAGAAGTCTgccg		gaGCCAGGGGCTGGGCATAAAAGTGTTTTAGTA CTCTGGAAACAGAATCTACTAAAACAAGGCA AAATGCCGTGTTTATCTCGTCAACTTGTTGGC GAGA	
40	SauCas9KKH	+	CAGTAACGGCAGACTTCTCCAGTTTTAGTACTC TGGAAACAGAATCTACTAAAACAAGGCAAAAT GCCGTGTTTATCTCGTCAACTTGTTGGCGAGAca gacaccatggtgcatctgactcctGAGGAGAAGTCTgccg	18912	GAGCCAGGGGCTGGGCATAAAAGTTTTAGTAC TCTGGAAACAGAATCTACTAAAACAAGGCAA AATGCCGTGTTTATCTCGTCAACTTGTTGGCG AGA	19089
41	SauCas9KKH	-	CATGGTGCATCTGACTCCTGTGTTTTAGTACTCT GGAAACAGAATCTACTAAAACAAGGCAAAATG CCGTGTTTATCTCGTCAACTTGTTGGCGAGAcaca gggcagtaacggcagacttctcCTCAGGAGTCAGatgc	18913	TTGGTCTCCTTAAACCTGTCTGTTTTAGTACT CTGGAAACAGAATCTACTAAAACAAGGCAA AATGCCGTGTTTATCTCGTCAACTTGTTGGCG AGA	19090
42	SauriCas9	+	CAGTAACGGCAGACTTCTCCAGTTTTAGTACTC TGGAAACAGAATCTACTAAAACAAGGCAAAAT GCCGTGTTTATCTCGTCAACTTGTTGGCGAGAca gacaccatggtgcatctgactcctGAGGAGAAGTCTgccg	18914	GCCAGGGGCTGGGCATAAAAGTGTTTTAGTAC TCTGGAAACAGAATCTACTAAAACAAGGCAA AATGCCGTGTTTATCTCGTCAACTTGTTGGCG AGA	19091
43	SauriCas9-KKH	+	CAGTAACGGCAGACTTCTCCAGTTTTAGTACTC TGGAAACAGAATCTACTAAAACAAGGCAAAAT GCCGTGTTTATCTCGTCAACTTGTTGGCGAGAca gacaccatggtgcatctgactcctGAGGAGAAGTCTgccg	18915	AGCCAGGGGCTGGGCATAAAAGGTTTTAGTAC TCTGGAAACAGAATCTACTAAAACAAGGCAA AATGCCGTGTTTATCTCGTCAACTTGTTGGCG AGA	19092
44	SauriCas9-KKH	-	CATGGTGCATCTGACTCCTGTGTTTTAGTACTCT GGAAACAGAATCTACTAAAACAAGGCAAAATG CCGTGTTTATCTCGTCAACTTGTTGGCGAGAcaca gggcagtaacggcagacttctcCTCAGGAGTCAGatgc	18916	TCTCCACATGCCCAGTTTCTAGTTTTAGTACT CTGGAAACAGAATCTACTAAAACAAGGCAA AATGCCGTGTTTATCTCGTCAACTTGTTGGCG AGA	19093
48	ScaCas9-Sc++	+	AGTAACGGCAGACTTCTCCAGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCcaga caccatggtgcatctgactcctGAGGAGAAGTCTgccg	18917	CCAGGGCTGGGCATAAAAGTGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCCG TTATCAACTTGAAAAAGTGGCACCGAGTCGG TGC	19094
49	SpyCas9-SpRY	+	AGTAACGGCAGACTTCTCCAGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCcaga caccatggtgcatctgactcctGAGGAGAAGTCTgccg	18918	AGCCAGGGGCTGGGCATAAAAGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCCG TTATCAACTTGAAAAAGTGGCACCGAGTCGG TGC	19095
50	SpyCas9-NG	-	ATGGTGCATCTGACTCCTGTGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCcaca gggcagtaacggcagacttctcCTCAGGAGTCAGatgc	18919	TCTATTGGTCTCCTTAAACCGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	19096

54	SpyCas9-SpRY	-	ATGGTGCATCTGACTCCTGTGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCcaca gggcagtaacggcagacttctcCTCAGGAGTCAGatgc	18920	CTATTGGTCTCCTTAAACCTGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	19097
59	SauCas9	-	caCCATGGTGCATCTGACTCCTGGTTTTAGTACT CTGGAAACAGAATCTACTAAAACAAGGCAAAA TGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAa cagggcagtaacggcagacttctcCTCAGGAGTCAGAtgca	18921	tgTAACCTTGATACCAACCTGCCGTTTTAGTAC TCTGGAAACAGAATCTACTAAAACAAGGCAA AATGCCGTGTTTATCTCGTCAACTTGTTGGCG AGA	19098
60	SauCas9KKH	-	CCATGGTGCATCTGACTCCTGGTTTTAGTACTCT GGAAACAGAATCTACTAAAACAAGGCAAAATG CCGTGTTTATCTCGTCAACTTGTTGGCGAGAacag ggcagtaacggcagacttctcCTCAGGAGTCAGAtgca	18922	TTGGTCTCCTTAAACCTGTCTGTTTTAGTACT CTGGAAACAGAATCTACTAAAACAAGGCAA AATGCCGTGTTTATCTCGTCAACTTGTTGGCG AGA	19099
61	SauCas9KKH	+	GCAGTAACGGCAGACTTCTCCGTTTTAGTACTC TGGAAACAGAATCTACTAAAACAAGGCAAAAT GCCGTGTTTATCTCGTCAACTTGTTGGCGAGAag acaccatggtgcatctgactcctGAGGAGAAGTCTGccgt	18923	AGCCAGGGCTGGGCATAAAAGGTTTTAGTAC TCTGGAAACAGAATCTACTAAAACAAGGCAA AATGCCGTGTTTATCTCGTCAACTTGTTGGCG AGA	19100
62	SauriCas9-KKH	+	GCAGTAACGGCAGACTTCTCCGTTTTAGTACTC TGGAAACAGAATCTACTAAAACAAGGCAAAAT GCCGTGTTTATCTCGTCAACTTGTTGGCGAGAag acaccatggtgcatctgactcctGAGGAGAAGTCTGccgt	18924	AGCCAGGGCTGGGCATAAAAGGTTTTAGTAC TCTGGAAACAGAATCTACTAAAACAAGGCAA AATGCCGTGTTTATCTCGTCAACTTGTTGGCG AGA	19101
65	ScaCas9-Sc++	-	CATGGTGCATCTGACTCCTGGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCacag ggcagtaacggcagacttctcCTCAGGAGTCAGAtgca	18925	TTGGTCTCCTTAAACCTGTCGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	19102
66	SpyCas9	-	CATGGTGCATCTGACTCCTGGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCacag ggcagtaacggcagacttctcCTCAGGAGTCAGAtgca	18926	TCCACATGCCCAGTTTCTATGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	19103
69	SpyCas9-SpRY	-	CATGGTGCATCTGACTCCTGGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCacag ggcagtaacggcagacttctcCTCAGGAGTCAGAtgca	18927	TATTGGTCTCCTTAAACCTGGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	19104
70	SpyCas9-NG	-	CATGGTGCATCTGACTCCTGGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCacag ggcagtaacggcagacttctcCTCAGGAGTCAGAtgca	18928	TCTATTGGTCTCCTTAAACCGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	19105
73	SpyCas9-SpRY	+	CAGTAACGGCAGACTTCTCCGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT	18929	GCCAGGGCTGGGCATAAAAGGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCCG	19106

			CAACTTGAAAAAGTGGCACCGAGTCGGTGCagac accatggtgcatctgactcctGAGGAGAAGTCTGccgt		TTATCAACTTGAAAAAGTGGCACCGAGTCGG TGC	
79	SauCas9	-	acACCATGGTGCATCTGACTCCTGTTTTAGTACT CTGGAAACAGAATCTACTAAAACAAGGCAAAA TGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAc agggcagtaacggcagacttctcCTCAGGAGTCAGATgcac	18930	tgTAACCTTGATACCAACCTGCCGTTTTAGTAC TCTGGAAACAGAATCTACTAAAACAAGGCAA AATGCCGTGTTTATCTCGTCAACTTGTTGGCG AGA	19107
80	SauCas9KKH	-	ACCATGGTGCATCTGACTCCTGTTTTAGTACTCT GGAAACAGAATCTACTAAAACAAGGCAAAATG CCGTGTTTATCTCGTCAACTTGTTGGCGAGAcagg gcagtaacggcagacttctcCTCAGGAGTCAGATgcac	18931	TTGGTCTCCTTAAACCTGTCTGTTTTAGTACT CTGGAAACAGAATCTACTAAAACAAGGCAA AATGCCGTGTTTATCTCGTCAACTTGTTGGCG AGA	19108
81	SauCas9KKH	+	GGCAGTAACGGCAGACTTCTCGTTTTAGTACTC TGGAAACAGAATCTACTAAAACAAGGCAAAAT GCCGTGTTTATCTCGTCAACTTGTTGGCGAGAga caccatggtgcatctgactcctGAGGAGAAGTCTGCcgtt	18932	GCCAGGGCTGGGCATAAAAGTGTTTTAGTAC TCTGGAAACAGAATCTACTAAAACAAGGCAA AATGCCGTGTTTATCTCGTCAACTTGTTGGCG AGA	19109
82	SauriCas9	-	ACCATGGTGCATCTGACTCCTGTTTTAGTACTCT GGAAACAGAATCTACTAAAACAAGGCAAAATG CCGTGTTTATCTCGTCAACTTGTTGGCGAGAcagg gcagtaacggcagacttctcCTCAGGAGTCAGATgcac	18933	TCTCCACATGCCCAGTTTCTAGTTTTAGTACT CTGGAAACAGAATCTACTAAAACAAGGCAA AATGCCGTGTTTATCTCGTCAACTTGTTGGCG AGA	19110
83	SauriCas9-KKH	-	ACCATGGTGCATCTGACTCCTGTTTTAGTACTCT GGAAACAGAATCTACTAAAACAAGGCAAAATG CCGTGTTTATCTCGTCAACTTGTTGGCGAGAcagg gcagtaacggcagacttctcCTCAGGAGTCAGATgcac	18934	TCTCCACATGCCCAGTTTCTAGTTTTAGTACT CTGGAAACAGAATCTACTAAAACAAGGCAA AATGCCGTGTTTATCTCGTCAACTTGTTGGCG AGA	19111
86	ScaCas9-Sc++	-	CCATGGTGCATCTGACTCCTGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCcagg gcagtaacggcagacttctcCTCAGGAGTCAGATgcac	18935	TTGGTCTCCTTAAACCTGTCGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	19112
87	SpyCas9-SpRY	-	CCATGGTGCATCTGACTCCTGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCcagg gcagtaacggcagacttctcCTCAGGAGTCAGATgcac	18936	ATTGGTCTCCTTAAACCTGTGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	19113
88	SpyCas9-SpRY	+	GCAGTAACGGCAGACTTCTCGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCgaca ccatggtgcatctgactcctGAGGAGAAGTCTGCcgtt	18937	CCAGGGCTGGGCATAAAAGTGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCCG TTATCAACTTGAAAAAGTGGCACCGAGTCGG TGC	19114
94	SauCas9KKH	-	CACCATGGTGCATCTGACTCCGTTTTAGTACTCT GGAAACAGAATCTACTAAAACAAGGCAAAATG CCGTGTTTATCTCGTCAACTTGTTGGCGAGAaggg cagtaacggcagacttctcCTCAGGAGTCAGATGcacc	18938	TTGGTCTCCTTAAACCTGTCTGTTTTAGTACT CTGGAAACAGAATCTACTAAAACAAGGCAA AATGCCGTGTTTATCTCGTCAACTTGTTGGCG AGA	19115

95	SpyCas9-NG	-	ACCATGGTGCATCTGACTCCGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCaggg cagtaacggcagacttctcCTCAGGAGTCAGATGcacc	18939	TGGTCTCCTTAAACCTGTCTGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	19116
99	SpyCas9-SpRY	-	ACCATGGTGCATCTGACTCCGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCaggg cagtaacggcagacttctcCTCAGGAGTCAGATGcacc	18940	TTGGTCTCCTTAAACCTGTCGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	19117
100	SpyCas9-SpRY	+	GGCAGTAACGGCAGACTTCTGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCacac catggtgcatctgactcctGAGGAGAAGTCTGCCgtta	18941	CAGGGCTGGGCATAAAAGTCGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCCG TTATCAACTTGAAAAAGTGGCACCGAGTCGG TGC	19118
103	ScaCas9-Sc++	-	CACCATGGTGCATCTGACTCGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCgggc agtaacggcagacttctcCTCAGGAGTCAGATGCacca	18942	TTGGTCTCCTTAAACCTGTCGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	19119
104	SpyCas9-SpRY	-	CACCATGGTGCATCTGACTCGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCgggc agtaacggcagacttctcCTCAGGAGTCAGATGCacca	18943	TGGTCTCCTTAAACCTGTCTGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	19120
105	SpyCas9-SpRY	+	GGGCAGTAACGGCAGACTTCGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCcacc atggtgcatctgactcctGAGGAGAAGTCTGCCGttac	18944	AGGGCTGGGCATAAAAGTCAGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCCG TTATCAACTTGAAAAAGTGGCACCGAGTCGG TGC	19121
106	BlatCas9	+	acagGGCAGTAACGGCAGACTTCGTCTATAGTTCC TTACTGAAAGGTAAGTTGCTATAGTAAGGGCAA CAGACCCGAGGCGTTGGGGATCGCCTAGCCCGT GTTTACGGGCTCTCCCCATATTCAAAATAATGA CAGACGAGCACCTTGGAGCATTTATCTCCGAGG TGCTcaccatggtgcatctgactcctGAGGAGAAGTCTGCC Gttac	18945	agccAGGGCTGGGCATAAAAGTCGCTATAGTT CCTTACTGAAAGGTAAGTTGCTATAGTAAGG GCAACAGACCCGAGGCGTTGGGGATCGCCTA GCCCGTGTTTACGGGCTCTCCCCATATTCAAA ATAATGACAGACGAGCACCTTGGAGCATTTA TCTCCGAGGTGCT	19122
107	BlatCas9	+	acagGGCAGTAACGGCAGACTTCGCTATAGTTCC TTACTGAAAGGTAAGTTGCTATAGTAAGGGCAA CAGACCCGAGGCGTTGGGGATCGCCTAGCCCGT GTTTACGGGCTCTCCCCATATTCAAAATAATGA CAGACGAGCACCTTGGAGCATTTATCTCCGAGG TGCTcaccatggtgcatctgactcctGAGGAGAAGTCTGCC Gttac	18946	agccAGGGCTGGGCATAAAAGTCGCTATAGTT CCTTACTGAAAGGTAAGTTGCTATAGTAAGG GCAACAGACCCGAGGCGTTGGGGATCGCCTA GCCCGTGTTTACGGGCTCTCCCCATATTCAAA ATAATGACAGACGAGCACCTTGGAGCATTTA TCTCCGAGGTGCT	19123

10 8	SpyCas9-SpRY	+	AGGGCAGTAACGGCAGACTTGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCacca tggtgcatctgactcctGAGGAGAAGTCTGCCGTTact	18947	GGGCTGGGCATAAAAGTCAGGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCCG TTATCAACTTGAAAAAGTGGCACCGAGTCGG TGC	19124
10 9	SpyCas9-SpRY	-	ACACCATGGTGCATCTGACTGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCggca gtaacggcagacttctcCTCAGGAGTCAGATGCACcat	18948	GGTCTCCTTAAACCTGTCTTGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	19125
11 0	SpyCas9-SpRY	+	CAGGGCAGTAACGGCAGACTGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCcat ggtgcatctgactcctGAGGAGAAGTCTGCCGTTactg	18949	GGCTGGGCATAAAAGTCAGGGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCCG TTATCAACTTGAAAAAGTGGCACCGAGTCGG TGC	19126
11 1	SpyCas9-SpRY	-	GACACCATGGTGCATCTGACGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCgcag taacggcagacttctcCTCAGGAGTCAGATGCACCatg	18950	GTCTCCTTAAACCTGTCTTGGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	19127
11 2	BlatCas9	+	ccacAGGGCAGTAACGGCAGACTGCTATAGTTCC TTACTGAAAGGTAAGTTGCTATAGTAAGGGCAA CAGACCCGAGGCGTTGGGGATCGCCTAGCCCGT GTTTACGGGCTCTCCCCATATTCAAAATAATGA CAGACGAGCACCTTGGAGCATTTATCTCCGAGG TGCTccatggtgcatctgactcctGAGGAGAAGTCTGCCGT Tactg	18951	gggcTGGGCATAAAAGTCAGGGCGCTATAGTT CCTTACTGAAAGGTAAGTTGCTATAGTAAGG GCAACAGACCCGAGGCGTTGGGGATCGCCTA GCCCGTGTTTACGGGCTCTCCCCATATTCAAA ATAATGACAGACGAGCACCTTGGAGCATTTA TCTCCGAGGTGCT	19128
11 3	Nme2Cas9	+	ccCCACAGGGCAGTAACGGCAGACGTTGTAGCT CCCTTTCTCATTTCGGAAACGAAATGAGAACCG TTGCTACAATAAGGCCGTCTGAAAAGATGTGCC GCAACGCTCTGCCCCTTAAAGCTTCTGCTTTAA GGGGCATCGTTTAcatggtgcatctgactcctGAGGAGAA GTCTGCCGTTActgc	18952	agGGCTGGGCATAAAAGTCAGGGCGTTGTAG CTCCCTTTCTCATTTCGGAAACGAAATGAGA ACCGTTGCTACAATAAGGCCGTCTGAAAAGA TGTGCCGCAACGCTCTGCCCCTTAAAGCTTCT GCTTTAAGGGGCATCGTTTA	19129
11 4	SpyCas9-SpRY	+	ACAGGGCAGTAACGGCAGACGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGTTA TCAACTTGAAAAAGTGGCACCGAGTCGGTGCcat ggtgcatctgactcctGAGGAGAAGTCTGCCGTTActgc	18953	GCTGGGCATAAAAGTCAGGGGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCCG TTATCAACTTGAAAAAGTGGCACCGAGTCGG TGC	19130
11 5	SpyCas9-SpRY	-	AGACACCATGGTGCATCTGAGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCcagt aacggcagacttctcCTCAGGAGTCAGATGCACCatgg	18954	TCTCCTTAAACCTGTCTTGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	19131
11 6	BlatCas9	+	cccaCAGGGCAGTAACGGCAGACGCTATAGTTCC TTACTGAAAGGTAAGTTGCTATAGTAAGGGCAA	18955	gggcTGGGCATAAAAGTCAGGGCGCTATAGTT CCTTACTGAAAGGTAAGTTGCTATAGTAAGG	19132

			CAGACCCGAGGCGTTGGGGATCGCCTAGCCCGT GTTTACGGGCTCTCCCCATATTCAAAATAATGA CAGACGAGCACCTTGGAGCATTTATCTCCGAGG TGCTCatggtgcatctgactcctGAGGAGAAGTCTGCCGTT Actgc		GCAACAGACCCGAGGCGTTGGGGATCGCCTA GCCCGTGTTTACGGGCTCTCCCCATATTCAAA ATAATGACAGACGAGCACCTTGGAGCATTTA TCTCCGAGGTGCT	
11 7	SpyCas9-SpRY	+	CACAGGGCAGTAACGGCAGAGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGTTA TCAACTTGAAAAAGTGGCACCGAGTCGGTGCatg gtgcatctgactcctGAGGAGAAGTCTGCCGTTACtgcc	18956	CTGGGCATAAAAGTCAGGGCGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCCG TTATCAACTTGAAAAAGTGGCACCGAGTCGG TGC	19133
11 8	SpyCas9-SpRY	-	CAGACACCATGGTGCATCTGGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCagta acggcagacttctcCTCAGGAGTCAGATGCACCAtggt	18957	CTCCTTAAACCTGTCTTGTAGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	19134
11 9	BlatCas9	-	aaacAGACACCATGGTGCATCTGGCTATAGTTCCT TACTGAAAGGTAAGTTGCTATAGTAAGGGCAAC AGACCCGAGGCGTTGGGGATCGCCTAGCCCGTG TTTACGGGCTCTCCCCATATTCAAAATAATGAC AGACGAGCACCTTGGAGCATTTATCTCCGAGGT GCTagtaacggcagacttctcCTCAGGAGTCAGATGCACC Atggt	18958	ttggTCTCCTTAAACCTGTCTTGGCTATAGTTCC TTACTGAAAGGTAAGTTGCTATAGTAAGGGC AACAGACCCGAGGCGTTGGGGATCGCCTAGC CCGTGTTTACGGGCTCTCCCCATATTCAAAAT AATGACAGACGAGCACCTTGGAGCATTTATC TCCGAGGTGCT	19135
12 0	BlatCas9	-	aaacAGACACCATGGTGCATCTGGCTATAGTTCCT TACTGAAAGGTAAGTTGCTATAGTAAGGGCAAC AGACCCGAGGCGTTGGGGATCGCCTAGCCCGTG TTTACGGGCTCTCCCCATATTCAAAATAATGAC AGACGAGCACCTTGGAGCATTTATCTCCGAGGT GCTagtaacggcagacttctcCTCAGGAGTCAGATGCACC Atggt	18959	ttggTCTCCTTAAACCTGTCTTGGCTATAGTTCC TTACTGAAAGGTAAGTTGCTATAGTAAGGGC AACAGACCCGAGGCGTTGGGGATCGCCTAGC CCGTGTTTACGGGCTCTCCCCATATTCAAAAT AATGACAGACGAGCACCTTGGAGCATTTATC TCCGAGGTGCT	19136
12 1	Nme2Cas9	-	tcAAACAGACACCATGGTGCATCTGTTGTAGCTC CCTTTCTCATTTCGGAAACGAAATGAGAACCGT TGCTACAATAAGGCCGTCTGAAAAGATGTGCCG CAACGCTCTGCCCCTTAAAGCTTCTGCTTTAAG GGGCATCGTTTAgtaacggcagacttctcCTCAGGAGTC AGATGCACCATggtg	18960	taTTGGTCTCCTTAAACCTGTCTTGTTGTAGCT CCCTTTCTCATTTCGGAAACGAAATGAGAAC CGTTGCTACAATAAGGCCGTCTGAAAAGATG TGCCGCAACGCTCTGCCCCTTAAAGCTTCTGC TTTAAGGGGCATCGTTTA	19137
12 2	SpyCas9-SpRY	-	ACAGACACCATGGTGCATCTGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCgtaa cggcagacttctcCTCAGGAGTCAGATGCACCATggtg	18961	TCCTTAAACCTGTCTTGTAAGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	19138
12 3	SpyCas9-SpRY	+	CCACAGGGCAGTAACGGCAGGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGTTA	18962	TGGGCATAAAAGTCAGGGCAGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCCG	19139

			TCAACTTGAAAAAGTGGCACCGAGTCGGTGCtgg tgcatctgactcctGAGGAGAAGTCTGCCGTTACTgccc		TTATCAACTTGAAAAAGTGGCACCGAGTCGG TGC	
12 4	BlatCas9	-	caaaCAGACACCATGGTGCATCTGCTATAGTTCCT TACTGAAAGGTAAGTTGCTATAGTAAGGGCAAC AGACCCGAGGCGTTGGGGATCGCCTAGCCCGTG TTTACGGGCTCTCCCCATATTCAAAATAATGAC AGACGAGCACCTTGGAGCATTTATCTCTCCGAGGT GCTgtaacggcagacttctcCTCAGGAGTCAGATGCACC ATggtg	18963	ttggTCTCCTTAAACCTGTCTTGGCTATAGTTCC TTACTGAAAGGTAAGTTGCTATAGTAAGGGC AACAGACCCGAGGCGTTGGGGATCGCCTAGC CCGTGTTTACGGGCTCTCCCCATATTCAAAAT AATGACAGACGAGCACCTTGGAGCATTTATC TCCGAGGTGCT	19140
12 5	BlatCas9	+	gcccCACAGGGCAGTAACGGCAGGCTATAGTTCC TTACTGAAAGGTAAGTTGCTATAGTAAGGGCAA CAGACCCGAGGCGTTGGGGATCGCCTAGCCCGT GTTTACGGGCTCTCCCCATATTCAAAATAATGA CAGACGAGCACCTTGGAGCATTTATCTCCGAGG TGCTtggtgcatctgactcctGAGGAGAAGTCTGCCGTTA CTgccc	18964	ggctGGCATAAAAGTCAGGGCAGCTATAGTT CCTTACTGAAAGGTAAGTTGCTATAGTAAGG GCAACAGACCCGAGGCGTTGGGGATCGCCTA GCCCGTGTTTACGGGCTCTCCCCATATTCAAA ATAATGACAGACGAGCACCTTGGAGCATTTA TCTCCGAGGTGCT	19141
12 6	BlatCas9	-	caaaCAGACACCATGGTGCATCTGCTATAGTTCCT TACTGAAAGGTAAGTTGCTATAGTAAGGGCAAC AGACCCGAGGCGTTGGGGATCGCCTAGCCCGTG TTTACGGGCTCTCCCCATATTCAAAATAATGAC AGACGAGCACCTTGGAGCATTTATCTCCGAGGT GCTgtaacggcagacttctcCTCAGGAGTCAGATGCACC ATggtg	18965	ttggTCTCCTTAAACCTGTCTTGGCTATAGTTCC TTACTGAAAGGTAAGTTGCTATAGTAAGGGC AACAGACCCGAGGCGTTGGGGATCGCCTAGC CCGTGTTTACGGGCTCTCCCCATATTCAAAAT AATGACAGACGAGCACCTTGGAGCATTTATC TCCGAGGTGCT	19142
12 8	SpyCas9-NG	-	AACAGACACCATGGTGCATCGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCtaac ggcagacttctcCTCAGGAGTCAGATGCACCATGgtgt	18966	TTAAACCTGTCTTTGTAACCTGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	19143
13 1	SpyCas9-SpRY	+	CCCACAGGGCAGTAACGGCAGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCggtg catctgactcctGAGGAGAAGTCTGCCGTTACTGccct	18967	GGGCATAAAAGTCAGGGCAGGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCCG TTATCAACTTGAAAAAGTGGCACCGAGTCGG TGC	19144
13 3	SpyCas9-SpRY	-	AACAGACACCATGGTGCATCGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCtaac ggcagacttctcCTCAGGAGTCAGATGCACCATGgtgt	18968	CCTTAAACCTGTCTTGTAACGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	19145
14 0	ScaCas9-Sc++	-	AAACAGACACCATGGTGCATGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCaacg gcagacttctcCTCAGGAGTCAGATGCACCATGGtgtc	18969	CTTAAACCTGTCTTGTAACCGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	19146

141	SpyCas9-SpRY	-	AAACAGACACCATGGTGCATGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCaacg gcagacttctcCTCAGGAGTCAGATGCACCATGGtgtc	18970	CTTAAACCTGTCTTGTAACCGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	19147
142	SpyCas9-NG	+	CCCCACAGGGCAGTAACGGCGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCgtgc atctgactcctGAGGAGAAGTCTGCCGTTACTGCcctg	18971	GGGCATAAAAGTCAGGGCAGGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCCG TTATCAACTTGAAAAAGTGGCACCGAGTCGG TGC	19148
146	SpyCas9-SpRY	+	CCCCACAGGGCAGTAACGGCGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCgtgc atctgactcctGAGGAGAAGTCTGCCGTTACTGCcctg	18972	GGCATAAAAGTCAGGGCAGAGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCCG TTATCAACTTGAAAAAGTGGCACCGAGTCGG TGC	19149
147	BlatCas9	-	ctcaAACAGACACCATGGTGCATGCTATAGTTCCT TACTGAAAGGTAAGTTTGCTATAGTAAGGGCAAC AGACCCGAGGCGTTGGGGATCGCCTAGCCCGTG TTTACGGGCTCTCCCCATATTCAAAATAATGAC AGACGAGCACCTTGGAGCATTTATCTCCGAGGT GCTaacggcagacttctcCTCAGGAGTCAGATGCACCAT GGtgtc	18973	cttAAACCTGTCTTGTAACCTTGCTATAGTTCC TTACTGAAAGGTAAGTTTGCTATAGTAAGGGC AACAGACCCGAGGCGTTGGGGATCGCCTAGC CCGTGTTTACGGGCTCTCCCCATATTCAAAAT AATGACAGACGAGCACCTTGGAGCATTTATC TCCGAGGTGCT	19150
154	SauCas9KKH	-	TCAAACAGACACCATGGTGCAGTTTTAGTACTC TGGAAACAGAATCTACTAAAACAAGGCAAAAT GCCGTGTTTATCTCGTCAACTTGTTGGCGAGAac ggcagacttctcCTCAGGAGTCAGATGCACCATGGTgtc t	18974	TCCTTAAACCTGTCTTGTAACGTTTTAGTACT CTGGAAACAGAATCTACTAAAACAAGGCAA AATGCCGTGTTTATCTCGTCAACTTGTTGGCG AGA	19151
157	ScaCas9-Sc++	+	GCCCCACAGGGCAGTAACGGGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCtgcat ctgactcctGAGGAGAAGTCTGCCGTTACTGCCctgt	18975	TGGGCATAAAAGTCAGGGCAGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCCG TTATCAACTTGAAAAAGTGGCACCGAGTCGG TGC	19152
158	SpyCas9-SpRY	+	GCCCCACAGGGCAGTAACGGGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCtgcat ctgactcctGAGGAGAAGTCTGCCGTTACTGCCctgt	18976	GCATAAAAGTCAGGGCAGAGGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCCG TTATCAACTTGAAAAAGTGGCACCGAGTCGG TGC	19153
159	SpyCas9-SpRY	-	CAAACAGACACCATGGTGCAGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCacgg cagacttctcCTCAGGAGTCAGATGCACCATGGTgtct	18977	TTAAACCTGTCTTGTAACCTGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	19154
160	BlatCas9	+	cttgCCCCACAGGGCAGTAACGGGCTATAGTTCCT TACTGAAAGGTAAGTTTGCTATAGTAAGGGCAAC AGACCCGAGGCGTTGGGGATCGCCTAGCCCGTG	18978	tgggCATAAAAGTCAGGGCAGAGGCTATAGTT CCTTACTGAAAGGTAAGTTTGCTATAGTAAGG GCAACAGACCCGAGGCGTTGGGGATCGCCTA	19155

			TTTACGGGCTCTCCCCATATTCAAAATAATGAC AGACGAGCACCTTGGAGCATTTATCTCCGAGGT GCTtgcatctgactcctGAGGAGAAGTCTGCCGTTACTG CCctgt		GCCCGTGTTTACGGGCTCTCCCCATATTCAAA ATAATGACAGACGAGCACCTTGGAGCATTTA TCTCCGAGGTGCT	
165	SauCas9KKH	+	TTGCCCCACAGGGCAGTAACGGTTTTAGTACTC TGGAAACAGAATCTACTAAAACAAGGCAAAAT GCCGTGTTTATCTCGTCAACTTGTTGGCGAGAgc atctgactcctGAGGAGAAGTCTGCCGTTACTGCCCtgt g	18979	GGCTGGGCATAAAAGTCAGGGGTTTTAGTAC TCTGGAAACAGAATCTACTAAAACAAGGCAA AATGCCGTGTTTATCTCGTCAACTTGTTGGCG AGA	19156
166	SauriCas9-KKH	+	TTGCCCCACAGGGCAGTAACGGTTTTAGTACTC TGGAAACAGAATCTACTAAAACAAGGCAAAAT GCCGTGTTTATCTCGTCAACTTGTTGGCGAGAgc atctgactcctGAGGAGAAGTCTGCCGTTACTGCCCtgt g	18980	GCTGGGCATAAAAGTCAGGGCGTTTTAGTAC TCTGGAAACAGAATCTACTAAAACAAGGCAA AATGCCGTGTTTATCTCGTCAACTTGTTGGCG AGA	19157
167	SpyCas9-SpRY	+	TGCCCCACAGGGCAGTAACGGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCgcat ctgactcctGAGGAGAAGTCTGCCGTTACTGCCCtgtg	18981	CATAAAAGTCAGGGCAGAGCGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCCG TTATCAACTTGAAAAAGTGGCACCGAGTCGG TGC	19158
168	SpyCas9-SpRY	-	TCAAACAGACACCATGGTGCGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCcggc agacttctcCTCAGGAGTCAGATGCACCATGGTGtctg	18982	TAAACCTGTCTTGTAACCTTGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	19159
172	SauCas9KKH	+	CTTGCCCCACAGGGCAGTAACGTTTTAGTACTC TGGAAACAGAATCTACTAAAACAAGGCAAAAT GCCGTGTTTATCTCGTCAACTTGTTGGCGAGAcat ctgactcctGAGGAGAAGTCTGCCGTTACTGCCCTgtg g	18983	GGCTGGGCATAAAAGTCAGGGGTTTTAGTAC TCTGGAAACAGAATCTACTAAAACAAGGCAA AATGCCGTGTTTATCTCGTCAACTTGTTGGCG AGA	19160
173	SpyCas9-NG	+	TTGCCCCACAGGGCAGTAACGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCcatct gactcctGAGGAGAAGTCTGCCGTTACTGCCCTgtgg	18984	GGGCATAAAAGTCAGGGCAGAGGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCCG TTATCAACTTGAAAAAGTGGCACCGAGTCGG TGC	19161
177	SpyCas9-SpRY	+	TTGCCCCACAGGGCAGTAACGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCcatct gactcctGAGGAGAAGTCTGCCGTTACTGCCCTgtgg	18985	ATAAAAGTCAGGGCAGAGCCGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCCG TTATCAACTTGAAAAAGTGGCACCGAGTCGG TGC	19162
178	SpyCas9-SpRY	-	CTCAAACAGACACCATGGTGGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGgcca gacttctcCTCAGGAGTCAGATGCACCATGGTGTctgt	18986	AAACCTGTCTTGTAACCTTGGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	19163

186	ScaCas9-Sc++	+	CTTGCCCCACAGGGCAGTAAGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCatctg actcctGAGGAGAAGTCTGCCGTTACTGCCCCTGtggg	18987	AGTCAGGGCAGAGCCATCTAGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCCG TTATCAACTTGAAAAAGTGGCACCGAGTCGG TGC	19164
187	SpyCas9	+	CTTGCCCCACAGGGCAGTAAGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCatctg actcctGAGGAGAAGTCTGCCGTTACTGCCCCTGtggg	18988	AGGGCTGGGCATAAAAGTCAGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCCG TTATCAACTTGAAAAAGTGGCACCGAGTCGG TGC	19165
190	SpyCas9-SpRY	+	CTTGCCCCACAGGGCAGTAAGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCatctg actcctGAGGAGAAGTCTGCCGTTACTGCCCCTGtggg	18989	TAAAAGTCAGGGCAGAGCCAGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCCG TTATCAACTTGAAAAAGTGGCACCGAGTCGG TGC	19166
191	SpyCas9-NG	+	CTTGCCCCACAGGGCAGTAAGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCatctg actcctGAGGAGAAGTCTGCCGTTACTGCCCCTGtggg	18990	GTCAGGGCAGAGCCATCTATGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCCG TTATCAACTTGAAAAAGTGGCACCGAGTCGG TGC	19167
194	SpyCas9-SpRY	-	CCTCAAACAGACACCATGGTGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCgcag acttctcCTCAGGAGTCAGATGCACCATGGTGTCTgtt	18991	AACCTGTCTTGTAACCTTGAGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	19168
195	BlatCas9	-	caacCTCAAACAGACACCATGGTGCTATAGTTCC TTACTGAAAGGTAAGTTGCTATAGTAAGGGCAA CAGACCCGAGGCGTTGGGGATCGCCTAGCCCGT GTTTACGGGCTCTCCCCATATTCAAAATAATGA CAGACGAGCACCTTGGAGCATTTATCTCCGAGG TGCTgcagacttctcCTCAGGAGTCAGATGCACCATG GTGTCTgtt	18992	cttaAACCTGTCTTGTAACCTTGGCTATAGTTCC TTACTGAAAGGTAAGTTGCTATAGTAAGGGC AACAGACCCGAGGCGTTGGGGATCGCCTAGC CCGTGTTTACGGGCTCTCCCCATATTCAAAAT AATGACAGACGAGCACCTTGGAGCATTTATC TCCGAGGTGCT	19169
196	BlatCas9	-	caacCTCAAACAGACACCATGGTGCTATAGTTCC TTACTGAAAGGTAAGTTGCTATAGTAAGGGCAA CAGACCCGAGGCGTTGGGGATCGCCTAGCCCGT GTTTACGGGCTCTCCCCATATTCAAAATAATGA CAGACGAGCACCTTGGAGCATTTATCTCCGAGG TGCTgcagacttctcCTCAGGAGTCAGATGCACCATG GTGTCTgtt	18993	cttaAACCTGTCTTGTAACCTTGGCTATAGTTCC TTACTGAAAGGTAAGTTGCTATAGTAAGGGC AACAGACCCGAGGCGTTGGGGATCGCCTAGC CCGTGTTTACGGGCTCTCCCCATATTCAAAAT AATGACAGACGAGCACCTTGGAGCATTTATC TCCGAGGTGCT	19170
198	SauriCas9	+	ACCTTGCCCCACAGGGCAGTAGTTTTAGTACTC TGGAAACAGAATCTACTAAAACAAGGCAAAAT GCCGTGTTTATCTCGTCAACTTGTTGGCGAGAtct gactcctGAGGAGAAGTCTGCCGTTACTGCCCTGTg ggg	18994	CCAGGGCTGGGCATAAAAGTCGTTTTAGTAC TCTGGAAACAGAATCTACTAAAACAAGGCAA AATGCCGTGTTTATCTCGTCAACTTGTTGGCG AGA	19171

199	SauriCas9-KKH	+	ACCTTGCCCCACAGGGCAGTAGTTTTAGTACTC TGGAAACAGAATCTACTAAAACAAGGCAAAAT GCCGTGTTTATCTCGTCAACTTGTTGGCGAGAtct gactcctGAGGAGAAGTCTGCCGTTACTGCCCTGTg ggg	18995	GCTGGGCATAAAAGTCAGGGCGTTTTAGTAC TCTGGAAACAGAATCTACTAAAACAAGGCAA AATGCCGTGTTTATCTCGTCAACTTGTTGGCG AGA	19172
202	ScaCas9-Sc++	+	CCTTGCCCCACAGGGCAGTAGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCtctga ctcctGAGGAGAAGTCTGCCGTTACTGCCCTGTggg g	18996	AGTCAGGGCAGAGCCATCTAGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCCG TTATCAACTTGAAAAAGTGGCACCGAGTCGG TGC	19173
203	SpyCas9-SpRY	+	CCTTGCCCCACAGGGCAGTAGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCtctga ctcctGAGGAGAAGTCTGCCGTTACTGCCCTGTggg g	18997	AAAAGTCAGGGCAGAGCCATGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCCG TTATCAACTTGAAAAAGTGGCACCGAGTCGG TGC	19174
204	SpyCas9-NG	-	ACCTCAAACAGACACCATGGGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCcaga cttctcCTCAGGAGTCAGATGCACCATGGTGTCTgttt	18998	TTAAACCTGTCTTGTAACCTGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	19175
208	SpyCas9-SpRY	-	ACCTCAAACAGACACCATGGGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCcaga cttctcCTCAGGAGTCAGATGCACCATGGTGTCTgttt	18999	ACCTGTCTTGTAACCTTGATGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	19176
209	BlatCas9	+	tcacCTTGCCCCACAGGGCAGTAGCTATAGTTCCT TACTGAAAGGTAAGTTGCTATAGTAAGGGCAAC AGACCCGAGGCGTTGGGGATCGCCTAGCCCGTG TTTACGGGCTCTCCCCATATTCAAAATAATGAC AGACGAGCACCTTGGAGCATTTATCTCCGAGGT GCTtctgactcctGAGGAGAAGTCTGCCGTTACTGCC CTGTgggg	19000	taaaAGTCAGGGCAGAGCCATCTGCTATAGTTC CTTACTGAAAGGTAAGTTGCTATAGTAAGGG CAACAGACCCGAGGCGTTGGGGATCGCCTAG CCCGTGTTTACGGGCTCTCCCCATATTCAAAA TAATGACAGACGAGGCACCTTGGAGCATTTAT CTCCGAGGTGCT	19177
210	BlatCas9	+	tcacCTTGCCCCACAGGGCAGTAGCTATAGTTCCT TACTGAAAGGTAAGTTGCTATAGTAAGGGCAAC AGACCCGAGGCGTTGGGGATCGCCTAGCCCGTG TTTACGGGCTCTCCCCATATTCAAAATAATGAC AGACGAGCACCTTGGAGCATTTATCTCCGAGGT GCTtctgactcctGAGGAGAAGTCTGCCGTTACTGCC CTGTgggg	19001	taaaAGTCAGGGCAGAGCCATCTGCTATAGTTC CTTACTGAAAGGTAAGTTGCTATAGTAAGGG CAACAGACCCGAGGCGTTGGGGATCGCCTAG CCCGTGTTTACGGGCTCTCCCCATATTCAAAA TAATGACAGACGAGCACCTTGGAGCATTTAT CTCCGAGGTGCT	19178
212	SauCas9KKH	+	CACCTTGCCCCACAGGGCAGTGTTTTAGTACTC TGGAAACAGAATCTACTAAAACAAGGCAAAAT GCCGTGTTTATCTCGTCAACTTGTTGGCGAGActg	19002	GGCTGGGCATAAAAGTCAGGGGTTTTAGTAC TCTGGAAACAGAATCTACTAAAACAAGGCAA	19179

			actcctGAGGAGAAGTCTGCCGTTACTGCCCTGTGg ggc	19003	AATGCCGTGTTTATCTCGTCAACTTGTTGGCG AGA	19180
215	ScaCas9-Sc++	-	AACCTCAAACAGACACCATGGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCagac ttctcCTCAGGAGTCAGATGCACCATGGTGTCTGttt g		CTTGTAACCTTGATACCAACGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	
216	SpyCas9-SpRY	-	AACCTCAAACAGACACCATGGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCagac ttctcCTCAGGAGTCAGATGCACCATGGTGTCTGttt g	19004	CCTGTCTTGTAACCTTGATAGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	19181
217	SpyCas9-SpRY	+	ACCTTGCCCCACAGGGCAGTGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCctga ctcctGAGGAGAAGTCTGCCGTTACTGCCCTGTGgg gc	19005	AAAGTCAGGGCAGAGCCATCGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCCG TTATCAACTTGAAAAAGTGGCACCGAGTCGG TGC	19182
221	SpyCas9-NG	-	CAACCTCAAACAGACACCATGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCgactt ctcCTCAGGAGTCAGATGCACCATGGTGTCTGTttg a	19006	TTGTAACCTTGATACCAACCGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	19183
224	SpyCas9-SpRY	+	CACCTTGCCCCACAGGGCAGGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCtgact cctGAGGAGAAGTCTGCCGTTACTGCCCTGTGGgg ca	19007	AAGTCAGGGCAGAGCCATCTGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCCG TTATCAACTTGAAAAAGTGGCACCGAGTCGG TGC	19184
226	SpyCas9-SpRY	-	CAACCTCAAACAGACACCATGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCgactt ctcCTCAGGAGTCAGATGCACCATGGTGTCTGTttg a	19008	CTGTCTTGTAACCTTGATACGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	19185
227	BlatCas9	-	tagcAACCTCAAACAGACACCATGCTATAGTTCCT TACTGAAAGGTAAGTTGCTATAGTAAGGGCAAC AGACCCGAGGCGTTGGGGATCGCCTAGCCCGTG TTTACGGGCTCTCCCCATATTCAAAATAATGAC AGACGAGCACCTTGGAGCATTTATCTCCGAGGT GCTgacttctcCTCAGGAGTCAGATGCACCATGGTG TCTGTttga	19009	aaccTGTCTTGTAACCTTGATACGCTATAGTTC CTTACTGAAAGGTAAGTTGCTATAGTAAGGG CAACAGACCCGAGGCGTTGGGGATCGCCTAG CCCGTGTTTACGGGCTCTCCCCATATTCAAAA TAATGACAGACGAGCACCTTGGAGCATTTAT CTCCGAGGTGCT	19186

232	ScaCas9-Sc++	-	GCAACCTCAAACAGACACCAGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT tcCTCAGGAGTCAGATGCACCATGGTGTCTGTTtg ag	19010	CTTGTAACCTTGATACCAACGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	19187
233	SpyCas9	-	GCAACCTCAAACAGACACCAGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCacttc tcCTCAGGAGTCAGATGCACCATGGTGTCTGTTtg ag	19011	ACCTTGATACCAACCTGCCCGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	19188
236	SpyCas9-SpRY	-	GCAACCTCAAACAGACACCAGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCacttc tcCTCAGGAGTCAGATGCACCATGGTGTCTGTTtg ag	19012	TGTCTTGTAACCTTGATACCGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	19189
237	SpyCas9-NG	-	GCAACCTCAAACAGACACCAGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCacttc tcCTCAGGAGTCAGATGCACCATGGTGTCTGTTtg ag	19013	TTGTAACCTTGATACCAACCGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	19190
240	SpyCas9-SpRY	+	TCACCTTGCCCCACAGGGCAGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCgact cctGAGGAGAAGTCTGCCGTTACTGCCCTGTGGG gcaa	19014	AGTCAGGGCAGAGCCATCTAGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCCG TTATCAACTTGAAAAAGTGGCACCGAGTCGG TGC	19191
241	BlatCas9	+	cgttCACCTTGCCCCACAGGGCAGCTATAGTTCCT TACTGAAAGGTAAGTTGCTATAGTAAGGGCAAC AGACCCGAGGCGTTGGGGATCGCCTAGCCCGTG TTTACGGGCTCTCCCCATATTCAAAATAATGAC AGACGAGCACCTTGGAGCATTTATCTCCGAGGT GCTgactcctGAGGAGAAGTCTGCCGTTACTGCCCT GTGGGgcaa	19015	taaaAGTCAGGGCAGAGCCATCTGCTATAGTTC CTTACTGAAAGGTAAGTTGCTATAGTAAGGG CAACAGACCCGAGGCGTTGGGGATCGCCTAG CCCGTGTTTACGGGCTCTCCCCATATTCAAAA TAATGACAGACGAGCACCTTGGAGCATTTAT CTCCGAGGTGCT	19192
243	SauCas9KKH	+	GTTCACCTTGCCCCACAGGGCGTTTTAGTACTCT GGAAACAGAATCTACTAAAACAAGGCAAAATG CCGTGTTTATCTCGTCAACTTGTTGGCGAGAactc ctGAGGAGAAGTCTGCCGTTACTGCCCTGTGGGG caag	19016	GGCTGGGCATAAAAGTCAGGGGTTTTAGTAC TCTGGAAACAGAATCTACTAAAACAAGGCAA AATGCCGTGTTTATCTCGTCAACTTGTTGGCG AGA	19193
244	SauriCas9	-	TAGCAACCTCAAACAGACACCGTTTTAGTACTC TGGAAACAGAATCTACTAAAACAAGGCAAAAT GCCGTGTTTATCTCGTCAACTTGTTGGCGAGActt	19017	TAACCTTGATACCAACCTGCCGTTTTAGTACT CTGGAAACAGAATCTACTAAAACAAGGCAA	19194

			ctcCTCAGGAGTCAGATGCACCATGGTGTCTGTT Tgagg	19018	AATGCCGTGTTTATCTCGTCAACTTGTTGGCG AGA	19195
245	SauriCas9-KKH	-	TAGCAACCTCAAACAGACACCGTTTTAGTACTC TGGAAACAGAATCTACTAAAACAAGGCAAAAT GCCGTGTTTATCTCGTCAACTTGTTGGCGAGActt ctcCTCAGGAGTCAGATGCACCATGGTGTCTGTT Tgagg		GTAACCTTGATACCAACCTGCGTTTTAGTACT CTGGAAACAGAATCTACTAAAACAAGGCAA AATGCCGTGTTTATCTCGTCAACTTGTTGGCG AGA	
248	ScaCas9-Sc++	-	AGCAACCTCAAACAGACACCGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCttct cCTCAGGAGTCAGATGCACCATGGTGTCTGTTTg agg	19019	CTTGTAACCTTGATACCAACGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	19196
249	SpyCas9-SpRY	-	AGCAACCTCAAACAGACACCGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCttct cCTCAGGAGTCAGATGCACCATGGTGTCTGTTTg agg	19020	GTCTTGTAACCTTGATACCAGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	19197
250	SpyCas9-NG	+	TTCACCTTGCCCCACAGGGCGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCactc ctGAGGAGAAGTCTGCCGTTACTGCCCTGTGGGG caag	19021	GTCAGGGCAGAGCCATCTATGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCCG TTATCAACTTGAAAAAGTGGCACCGAGTCGG TGC	19198
254	SpyCas9-SpRY	+	TTCACCTTGCCCCACAGGGCGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCactc ctGAGGAGAAGTCTGCCGTTACTGCCCTGTGGGG caag	19022	GTCAGGGCAGAGCCATCTATGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCCG TTATCAACTTGAAAAAGTGGCACCGAGTCGG TGC	19199
258	SauCas9KKH	-	CTAGCAACCTCAAACAGACACGTTTTAGTACTC TGGAAACAGAATCTACTAAAACAAGGCAAAAT GCCGTGTTTATCTCGTCAACTTGTTGGCGAGAttc tcCTCAGGAGTCAGATGCACCATGGTGTCTGTTT Gaggt	19023	TGTAACCTTGATACCAACCTGGTTTTAGTACT CTGGAAACAGAATCTACTAAAACAAGGCAA AATGCCGTGTTTATCTCGTCAACTTGTTGGCG AGA	19200
259	SauCas9KKH	-	CTAGCAACCTCAAACAGACACGTTTTAGTACTC TGGAAACAGAATCTACTAAAACAAGGCAAAAT GCCGTGTTTATCTCGTCAACTTGTTGGCGAGAttc tcCTCAGGAGTCAGATGCACCATGGTGTCTGTTT Gaggt	19024	TGTAACCTTGATACCAACCTGGTTTTAGTACT CTGGAAACAGAATCTACTAAAACAAGGCAA AATGCCGTGTTTATCTCGTCAACTTGTTGGCG AGA	19201
262	ScaCas9-Sc++	+	GTTCACCTTGCCCCACAGGGGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT	19025	AGTCAGGGCAGAGCCATCTAGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCCG	19202

			CAACTTGAAAAAGTGGCACCGAGTCGGTGCctct GAGGAGAAGTCTGCCGTTACTGCCCTGTGGGGC aagg	19026	TTATCAACTTGAAAAAGTGGCACCGAGTCGG TGC	19203
263	SpyCas9-SpRY	+	GTTCACCTTGCCCCACAGGGGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCctct GAGGAGAAGTCTGCCGTTACTGCCCTGTGGGGC aagg		TCAGGGCAGAGCCATCTATTGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCCG TTATCAACTTGAAAAAGTGGCACCGAGTCGG TGC	
264	SpyCas9-SpRY	-	TAGCAACCTCAAACAGACACGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCttctc CTCAGGAGTCAGATGCACCATGGTGTCTGTTTTG aggt	19027	TCTTGTAACCTTGATACCAAGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	19204
267	SauriCas9-KKH	+	ACGTTCACCTTGCCCCACAGGGTTTTAGTACTCT GGAAACAGAATCTACTAAAACAAGGCAAAATG CCGTGTTTATCTCGTCAACTTGTTGGCGAGAtcct GAGGAGAAGTCTGCCGTTACTGCCCTGTGGGGC Aaggt	19028	GCTGGGCATAAAAGTCAGGGCGTTTTAGTAC TCTGGAAACAGAATCTACTAAAACAAGGCAA AATGCCGTGTTTATCTCGTCAACTTGTTGGCG AGA	19205
268	SpyCas9-SpRY	+	CGTTCACCTTGCCCCACAGGGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCtcct GAGGAGAAGTCTGCCGTTACTGCCCTGTGGGGC Aaggt	19029	CAGGGCAGAGCCATCTATTGGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCCG TTATCAACTTGAAAAAGTGGCACCGAGTCGG TGC	19206
269	SpyCas9-SpRY	-	CTAGCAACCTCAAACAGACAGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCtctc CTCAGGAGTCAGATGCACCATGGTGTCTGTTTG Aggtt	19030	CTTGTAACCTTGATACCAACGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	19207
270	SauCas9KKH	+	CACGTTCACCTTGCCCCACAGGTTTTAGTACTCT GGAAACAGAATCTACTAAAACAAGGCAAAATG CCGTGTTTATCTCGTCAACTTGTTGGCGAGAcctG AGGAGAAGTCTGCCGTTACTGCCCTGTGGGGCA Aggtg	19031	CATCTATTGCTTACATTTGCTGTTTTAGTACT CTGGAAACAGAATCTACTAAAACAAGGCAA AATGCCGTGTTTATCTCGTCAACTTGTTGGCG AGA	19208
271	SauCas9KKH	+	CACGTTCACCTTGCCCCACAGGTTTTAGTACTCT GGAAACAGAATCTACTAAAACAAGGCAAAATG CCGTGTTTATCTCGTCAACTTGTTGGCGAGAcctG AGGAGAAGTCTGCCGTTACTGCCCTGTGGGGCA Aggtg	19032	CATCTATTGCTTACATTTGCTGTTTTAGTACT CTGGAAACAGAATCTACTAAAACAAGGCAA AATGCCGTGTTTATCTCGTCAACTTGTTGGCG AGA	19209

274	SpyCas9-NG	+	ACGTTCACCTTGCCCCACAGGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCCctG AGGAGAAGTCTGCCGTTACTGCCCTGTGGGGCA Aggtg	19033	GTCAGGGCAGAGCCATCTATGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCCG TTATCAACTTGAAAAAGTGGCACCGAGTCGG TGC	19210
278	SpyCas9-SpRY	+	ACGTTCACCTTGCCCCACAGGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCCctG AGGAGAAGTCTGCCGTTACTGCCCTGTGGGGCA Aggtg	19034	AGGGCAGAGCCATCTATTGCGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCCG TTATCAACTTGAAAAAGTGGCACCGAGTCGG TGC	19211
279	SpyCas9-SpRY	-	ACTAGCAACCTCAAACAGACGGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCctcC TCAGGAGTCAGATGCACCATGGTGTCTGTTTGA Ggttg	19035	TTGTAACCTTGATACCAACCGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	19212
283	ScaCas9-Sc++	+	CACGTTCACCTTGCCCCACAGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCctG AGGAGAAGTCTGCCGTTACTGCCCTGTGGGGCA AGgtga	19036	GAGCCATCTATTGCTTACATGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	19213
284	SpyCas9	+	CACGTTCACCTTGCCCCACAGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCctG AGGAGAAGTCTGCCGTTACTGCCCTGTGGGGCA AGgtga	19037	AGGGCTGGGCATAAAAGTCAGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCCG TTATCAACTTGAAAAAGTGGCACCGAGTCGG TGC	19214
287	SpyCas9-SpRY	+	CACGTTCACCTTGCCCCACAGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCctG AGGAGAAGTCTGCCGTTACTGCCCTGTGGGGCA AGgtga	19038	GGGCAGAGCCATCTATTGCTGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCCG TTATCAACTTGAAAAAGTGGCACCGAGTCGG TGC	19215
288	SpyCas9-NG	+	CACGTTCACCTTGCCCCACAGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCctG AGGAGAAGTCTGCCGTTACTGCCCTGTGGGGCA AGgtga	19039	GTCAGGGCAGAGCCATCTATGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCCG TTATCAACTTGAAAAAGTGGCACCGAGTCGG TGC	19216
291	SpyCas9-SpRY	-	CACTAGCAACCTCAAACAGAGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCATGGTGTCTGTTTGAG CAGGAGTCAGATGCACCATGGTGTCTGTTTTGAG Gttgc	19040	TGTAACCTTGATACCAACCTGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	19217

294	SauriCas9	+	TCCACGTTCACCTTGCCCCACGTTTTAGTACTCT GGAAACAGAATCTACTAAAACAAGGCAAAATG CCGTGTTTATCTCGTCAACTTGTTGGCGAGATGA GGAGAAGTCTGCCGTTACTGCCCTGTGGGGCAA GGtgaa	19041	CCAGGGCTGGGCATAAAAGTCGTTTTAGTAC TCTGGAAACAGAATCTACTAAAACAAGGCAA AATGCCGTGTTTATCTCGTCAACTTGTTGGCG AGA	19218
295	SauriCas9-KKH	+	TCCACGTTCACCTTGCCCCACGTTTTAGTACTCT GGAAACAGAATCTACTAAAACAAGGCAAAATG CCGTGTTTATCTCGTCAACTTGTTGGCGAGATGA GGAGAAGTCTGCCGTTACTGCCCTGTGGGGCAA GGtgaa	19042	GCTGGGCATAAAAGTCAGGGCGTTTTAGTAC TCTGGAAACAGAATCTACTAAAACAAGGCAA AATGCCGTGTTTATCTCGTCAACTTGTTGGCG AGA	19219
298	ScaCas9-Sc++	+	CCACGTTCACCTTGCCCCACGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCtGA GGAGAAGTCTGCCGTTACTGCCCTGTGGGGCAA GGtgaa	19043	GAGCCATCTATTGCTTACATGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	19220
299	SpyCas9	+	CCACGTTCACCTTGCCCCACGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCtGA GGAGAAGTCTGCCGTTACTGCCCTGTGGGGCAA GGtgaa	19044	AGGGCTGGGCATAAAAGTCAGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCCG TTATCAACTTGAAAAAGTGGCACCGAGTCGG TGC	19221
302	SpyCas9-SpRY	+	CCACGTTCACCTTGCCCCACGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCtGA GGAGAAGTCTGCCGTTACTGCCCTGTGGGGCAA GGtgaa	19045	GGCAGAGCCATCTATTGCTTGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	19222
303	SpyCas9-NG	+	CCACGTTCACCTTGCCCCACGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCtGA GGAGAAGTCTGCCGTTACTGCCCTGTGGGGCAA GGtgaa	19046	GTCAGGGCAGAGCCATCTATGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCCG TTATCAACTTGAAAAAGTGGCACCGAGTCGG TGC	19223
306	SpyCas9-SpRY	-	TCACTAGCAACCTCAAACAGGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCcCT CAGGAGTCAGATGCACCATGGTGTCTGTTTGAG GTtgct	19047	GTAACCTTGATACCAACCTGGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCCG TTATCAACTTGAAAAAGTGGCACCGAGTCGG TGC	19224
307	BlatCas9	+	catcCACGTTCACCTTGCCCCACGCTATAGTTCCT TACTGAAAGGTAAGTTGCTATAGTAAGGGCAAC AGACCCGAGGCGTTGGGGATCGCCTAGCCCGTG TTTACGGGCTCTCCCCCATATTCAAAATAATGAC AGACGAGCACCTTGGAGCATTTATCTCCGAGGT	19048	agtcAGGGCAGAGCCATCTATTGGCTATAGTTC CTTACTGAAAGGTAAGTTGCTATAGTAAGGG CAACAGACCCGAGGCGTTGGGGATCGCCTAG CCCGTGTTTACGGGCTCTCCCCATATTCAAAA	19225

			GCTtGAGGAGAAGTCTGCCGTTACTGCCCTGTG GGGCAAGGtgaa		TAATGACAGACGAGGCACCTTGGAGCATTTAT CTCCGAGGTGCT	
30 8	BlatCa s9	-	tgttCACTAGCAACCTCAAACAGGCTATAGTTCCT TACTGAAAGGTAAGTTGCTATAGTAAGGGCAAC AGACCCGAGGCGTTGGGGATCGCCTAGCCCGTG TTTACGGGCTCTCCCCATATTCAAAATAATGAC AGACGAGCACCTTGGAGCATTTATCTCCGAGGT GCTcCTCAGGAGTCAGATGCACCATGGTGTCTG TTTGAGGTtgct	19049	gtctTGTAACCTTGATACCAACCGCTATAGTTC CTTACTGAAAGGTAAGTTGCTATAGTAAGGG CAACAGACCCGAGGCGTTGGGGATCGCCTAG CCCGTGTTTACGGGCTCTCCCCATATTCAAAA TAATGACAGACGAGCACCTTGGAGCATTTAT CTCCGAGGTGCT	19226
30 9	BlatCa s9	+	catcCACGTTCACCTTGCCCCACGCTATAGTTCCT TACTGAAAGGTAAGTTGCTATAGTAAGGGCAAC AGACCCGAGGCGTTGGGGATCGCCTAGCCCGTG TTTACGGGCTCTCCCCATATTCAAAATAATGAC AGACGAGCACCTTGGAGCATTTATCTCCGAGGT GCTtGAGGAGAAGTCTGCCGTTACTGCCCTGTG GGGCAAGGtgaa	19050	agtcAGGGCAGAGCCATCTATTGGCTATAGTTC CTTACTGAAAGGTAAGTTGCTATAGTAAGGG CAACAGACCCGAGGCGTTGGGGATCGCCTAG CCCGTGTTTACGGGCTCTCCCCATATTCAAAA TAATGACAGACGAGCACCTTGGAGCATTTAT CTCCGAGGTGCT	19227
31 0	BlatCa s9	-	tgttCACTAGCAACCTCAAACAGGCTATAGTTCCT TACTGAAAGGTAAGTTGCTATAGTAAGGGCAAC AGACCCGAGGCGTTGGGGATCGCCTAGCCCGTG TTTACGGGCTCTCCCCATATTCAAAATAATGAC AGACGAGCACCTTGGAGCATTTATCTCCGAGGT GCTcCTCAGGAGTCAGATGCACCATGGTGTCTG TTTGAGGTtgct	19051	gtctTGTAACCTTGATACCAACCGCTATAGTTC CTTACTGAAAGGTAAGTTGCTATAGTAAGGG CAACAGACCCGAGGCGTTGGGGATCGCCTAG CCCGTGTTTACGGGCTCTCCCCATATTCAAAA TAATGACAGACGAGCACCTTGGAGCATTTAT CTCCGAGGTGCT	19228
31 2	Nme2 Cas9	-	tgTGTTCACTAGCAACCTCAAACAGTTGTAGCTC CCTTTCTCATTTCGGAAACGAAATGAGAACCGT TGCTACAATAAGGCCGTCTGAAAAGATGTGCCG CAACGCTCTGCCCCTTAAAGCTTCTGCTTTAAG GGGCATCGTTTACTCAGGAGTCAGATGCACCAT GGTGTCTGTTTTGAGGTTgcta	19052	tgTAACCTTGATACCAACCTGCCCGTTGTAGC TCCCTTTCTCATTTCGGAAACGAAATGAGAA CCGTTGCTACAATAAGGCCGTCTGAAAAGAT GTGCCGCAACGCTCTGCCCCTTAAAGCTTCTG CTTTAAGGGGCATCGTTTA	19229
31 3	SauCa s9	+	tcATCCACGTTCACCTTGCCCCAGTTTTTAGTACTC TGGAAACAGAATCTACTAAAACAAGGCAAAAT GCCGTGTTTATCTCGTCAACTTGTTGGCGAGAG AGGAGAAGTCTGCCGTTACTGCCCTGTGGGGCA AGGTgaac	19053	agGGCTGGGCATAAAAGTCAGGGGTTTTAGTA CTCTGGAAACAGAATCTACTAAAACAAGGCA AAATGCCGTGTTTATCTCGTCAACTTGTTGGC GAGA	19230
31 4	SauCa s9KK H	+	ATCCACGTTCACCTTGCCCCAGTTTTTAGTACTCT GGAAACAGAATCTACTAAAACAAGGCAAAATG CCGTGTTTATCTCGTCAACTTGTTGGCGAGAGA GGAGAAGTCTGCCGTTACTGCCCTGTGGGGCAA GGTgaac	19054	CATCTATTGCTTACATTTGCTGTTTTAGTACT CTGGAAACAGAATCTACTAAAACAAGGCAA AATGCCGTGTTTATCTCGTCAACTTGTTGGCG AGA	19231

3155	SauriCas9	+	ATCCACGTTCACCTTGCCCCCAGTTTTAGTACTCT GGAAACAGAATCTACTAAAACAAGGCAAAATG CCGTGTTTATCTCGTCAACTTGTTGGCGAGAGA GGAGAAGTCTGCCGTTACTGCCCTGTGGGGCAA GGTgaac	19055	CCAGGGCTGGGCATAAAAGTCGTTTTAGTAC TCTGGAAACAGAATCTACTAAAACAAGGCAA AATGCCGTGTTTATCTCGTCAACTTGTTGGCG AGA	19232
3156	SauriCas9-KKH	+	ATCCACGTTCACCTTGCCCCAGTTTTAGTACTCT GGAAACAGAATCTACTAAAACAAGGCAAAATG CCGTGTTTATCTCGTCAACTTGTTGGCGAGAGA GGAGAAGTCTGCCGTTACTGCCCTGTGGGGCAA GGTgaac	19056	GCTGGGCATAAAAGTCAGGGCGTTTTAGTAC TCTGGAAACAGAATCTACTAAAACAAGGCAA AATGCCGTGTTTATCTCGTCAACTTGTTGGCG AGA	19233
3159	ScaCas9-Sc++	+	TCCACGTTCACCTTGCCCCAGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCGA GGAGAAGTCTGCCGTTACTGCCCTGTGGGGCAA GGTgaac	19057	GAGCCATCTATTGCTTACATGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	19234
3200	SpyCas9-SpRY	+	TCCACGTTCACCTTGCCCCAGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCGA GGAGAAGTCTGCCGTTACTGCCCTGTGGGGCAA GGTgaac	19058	GCAGAGCCATCTATTGCTTAGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	19235
3201	SpyCas9-SpRY	-	TTCACTAGCAACCTCAAACAGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCCTC AGGAGTCAGATGCACCATGGTGTCTGTTTGAGG TTgcta	19059	TAACCTTGATACCAACCTGCGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	19236
3222	BlatCas9	-	gtgtTCACTAGCAACCTCAAACAGCTATAGTTCCT TACTGAAAGGTAAGTTGCTATAGTAAGGGCAAC AGACCCGAGGCGTTGGGGATCGCCTAGCCCGTG TTTACGGGCTCTCCCCATATTCAAAATAATGAC AGACGAGCACCTTGGAGCATTTATCTCCGAGGT GCTCTCAGGAGTCAGATGCACCATGGTGTCTGT TTGAGGTTgcta	19060	gtaaCCTTGATACCAACCTGCCCCGCTATAGTTC CTTACTGAAAGGTAAGTTGCTATAGTAAGGG CAACAGACCCGAGGCGTTGGGGATCGCCTAG CCCGTGTTTACGGGCTCTCCCCATATTCAAAA TAATGACAGACGAGCACCTTGGAGCATTTAT CTCCGAGGTGCT	19237
3223	BlatCas9	-	gtgtTCACTAGCAACCTCAAACAGCTATAGTTCCT TACTGAAAGGTAAGTTGCTATAGTAAGGGCAAC AGACCCGAGGCGTTGGGGATCGCCTAGCCCGTG TTTACGGGCTCTCCCCATATTCAAAATAATGAC AGACGAGCACCTTGGAGCATTTATCTCCGAGGT GCTCTCAGGAGTCAGATGCACCATGGTGTCTGT TTGAGGTTgcta	19061	gtaaCCTTGATACCAACCTGCCCGCTATAGTTC CTTACTGAAAGGTAAGTTGCTATAGTAAGGG CAACAGACCCGAGGCGTTGGGGATCGCCTAG CCCGTGTTTACGGGCTCTCCCCATATTCAAAA TAATGACAGACGAGCACCTTGGAGCATTTAT CTCCGAGGTGCT	19238

327	SauCas9KKH	+	CATCCACGTTCACCTTGCCCCGTTTTAGTACTCT GGAAACAGAATCTACTAAAACAAGGCAAAATG CCGTGTTTATCTCGTCAACTTGTTGGCGAGAAG GAGAAGTCTGCCGTTACTGCCCTGTGGGGCAAG GTGaacg	19062	CATCTATTGCTTACATTTGCTGTTTTAGTACT CTGGAAACAGAATCTACTAAAACAAGGCAA AATGCCGTGTTTATCTCGTCAACTTGTTGGCG AGA	19239
328	SauriCas9-KKH	+	CATCCACGTTCACCTTGCCCCGTTTTAGTACTCT GGAAACAGAATCTACTAAAACAAGGCAAAATG CCGTGTTTATCTCGTCAACTTGTTGGCGAGAAG GAGAAGTCTGCCGTTACTGCCCTGTGGGGCAAG GTGaacg	19063	GCTGGGCATAAAAGTCAGGGCGTTTTAGTAC TCTGGAAACAGAATCTACTAAAACAAGGCAA AATGCCGTGTTTATCTCGTCAACTTGTTGGCG AGA	19240
329	SpyCas9-NG	-	GTTCACTAGCAACCTCAAACGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCTCA GGAGTCAGATGCACCATGGTGTCTGTTTGAGGT TGctag	19064	ACCTTGATACCAACCTGCCCGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	19241
330	SpyCas9-SpRY	-	GTTCACTAGCAACCTCAAACGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCTCA GGAGTCAGATGCACCATGGTGTCTGTTTGAGGT TGctag	19065	AACCTTGATACCAACCTGCCGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCCG TTATCAACTTGAAAAAGTGGCACCGAGTCGG TGC	19242
331	SpyCas9-SpRY	+	ATCCACGTTCACCTTGCCCCGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCAG GAGAAGTCTGCCGTTACTGCCCTGTGGGGCAAG GTGaacg	19066	CAGAGCCATCTATTGCTTACGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	19243
340	SauCas9KKH	+	TCATCCACGTTCACCTTGCCCGTTTTAGTACTCT GGAAACAGAATCTACTAAAACAAGGCAAAATG CCGTGTTTATCTCGTCAACTTGTTGGCGAGAGG AGAAGTCTGCCGTTACTGCCCTGTGGGGCAAGG TGAacgt	19067	CATCTATTGCTTACATTTGCTGTTTTAGTACT CTGGAAACAGAATCTACTAAAACAAGGCAA AATGCCGTGTTTATCTCGTCAACTTGTTGGCG AGA	19244
343	ScaCas9-Sc++	-	TGTTCACTAGCAACCTCAAAGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCCA GGAGTCAGATGCACCATGGTGTCTGTTTGAGGT TGCtagt	19068	ACCTTGATACCAACCTGCCCGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	19245
344	SpyCas9-SpRY	-	TGTTCACTAGCAACCTCAAAGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT CAACTTGAAAAAGTGGCACCGAGTCGGTGCCA GGAGTCAGATGCACCATGGTGTCTGTTTGAGGT TGCtagt	19069	ACCTTGATACCAACCTGCCCGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	19246

345	SpyCas9-SpRY	+	CATCCACGTTCACCTTGCCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGAGAAGTCTGCCGTTACTGCCCTGTGGGGCAAGGTGAacgt	19070	AGAGCCATCTATTGCTTACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	19247
346	BlatCas9	-	ctgtGTTCACTAGCAACCTCAAAGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCTCAGGAGTCAGATGCACCATGGTGTCTGTTTGAGGTTGCtagt	19071	gtaaCCTTGATACCAACCTGCCCGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCT	19248

Capital letters indicate "core nucleotides" while lower case letters indicate "flanking nucleotides." Herein, when an RNA sequence (e.g., a template RNA sequence) is said to comprise a particular sequence (e.g., a sequence of Table 4 or a portion thereof) that comprises thymine (T), it is of course understood that the RNA sequence may (and frequently does) comprise uracil (U) in place of T. For instance, the RNA sequence may comprise U at every position shown as T in the sequence in Table 4. More specifically, the present disclosure provides an RNA sequence according to every template sequence shown in Table 4, wherein the RNA sequence has a U in place of each T in the sequence of Table 4.

In some embodiments, the systems and methods provided herein may comprise a template sequence listed in any of **Tables 5A-5D**. Tables 5A-5D provide exemplary template RNA sequences (column 2) designed to be paired with a gene modifying polypeptide to correct a mutation in the HBB gene. The templates in Tables 5A-5D are meant to exemplify the total sequence of: (1) gRNA spacer (e.g., for targeting for first strand nick), (2) gRNA scaffold, (3) RT (heterologous object sequence) sequence, and (4) PBS sequence (e.g., for initiating TPRT at first strand nick).

Table 5A. Exemplary template RNA sequences

Table 5A provides design of exemplary DNA components of gene modifying systems for correcting the pathogenic E6V mutation in HBB to the wild-type form. This table details the sequence of a complete template RNA for use in exemplary gene modifying systems comprising a gene

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modifying polypeptide. Templates in this table employ the HBB5 spacer (CATGGTGCACCTGACTCCTG SEQ ID NO: 19249) and a gRNA scaffold sequence of GTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC (SEQ ID NO: 20923). For exemplification, the lengths of the RT (heterologous object) sequences and PBS sequences were varied at the 3' end. The length of these respective sequences is reflected in columns 3 and 4, respectively. The longest form of the RT sequence is AGTAACGGCAGACTTCTCTTCAG (SEQ ID NO: 20954). The longest form of the PBS is GAGTCAGGTGCACCATG (SEQ ID NO: 19431).

Sequence Name	Full DNA sequence	SEQ ID NO	RT length	PBS length	Total length
HBB5_corr_WT_RT23_PBS17	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGTAACGGCAGACTTCTCTTCAGGAGTCAGGTGCACCATG	20958	23	17	136
HBB5_corr_WT_RT23_PBS16	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGTAACGGCAGACTTCTCTTCAGGAGTCAGGTGCACCAT	20959	23	16	135
HBB5_corr_WT_RT23_PBS15	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGTAACGGCAGACTTCTCTTCAGGAGTCAGGTGCACCA	20960	23	15	134
HBB5_corr_WT_RT23_PBS14	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGTAACGGCAGACTTCTCTTCAGGAGTCAGGTGCACC	20961	23	14	133
HBB5_corr_WT_RT23_PBS13	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGTAACGGCAGACTTCTCTTCAGGAGTCAGGTGCAC	20962	23	13	132
HBB5_corr_WT_RT23_PBS12	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGTAACGGCAGACTTCTCTTCAGGAGTCAGGTGCA	20963	23	12	131
HBB5_corr_WT_RT23_PBS11	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGTAACGGCAGACTTCTCTTCAGGAGTCAGGTGC	20964	23	11	130

HBB5_corr_WT_RT23_PBS10	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGTAACGG CAGACTTCTCTTCAGGAGTCAGGTG	20965	23	10	129
HBB5_corr_WT_RT23_PBS9	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGTAACGG CAGACTTCTCTTCAGGAGTCAGGT	20966	23	9	128
HBB5_corr_WT_RT23_PBS8	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGTAACGG CAGACTTCTCTTCAGGAGTCAGG	20967	23	8	127
HBB5_corr_WT_RT22_PBS17	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTAACGGC AGACTTCTCTTCAGGAGTCAGGTGCACCATG	20968	22	17	135
HBB5_corr_WT_RT22_PBS16	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTAACGGC AGACTTCTCTTCAGGAGTCAGGTGCACCAT	20969	22	16	134
HBB5_corr_WT_RT22_PBS15	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTAACGGC AGACTTCTCTTCAGGAGTCAGGTGCACCA	20970	22	15	133
HBB5_corr_WT_RT22_PBS14	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTAACGGC AGACTTCTCTTCAGGAGTCAGGTGCACC	20971	22	14	132
HBB5_corr_WT_RT22_PBS13	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTAACGGC AGACTTCTCTTCAGGAGTCAGGTGCAC	20972	22	13	131
HBB5_corr_WT_RT22_PBS12	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTAACGGC AGACTTCTCTTCAGGAGTCAGGTGCA	20973	22	12	130
HBB5_corr_WT_RT22_PBS11	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTAACGGC AGACTTCTCTTCAGGAGTCAGGTGC	20974	22	11	129
HBB5_corr_WT_RT22_PBS10	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTAACGGC AGACTTCTCTTCAGGAGTCAGGTG	20975	22	10	128
HBB5_corr_WT_RT22_PBS9	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTAACGGC AGACTTCTCTTCAGGAGTCAGGT	20976	22	9	127

HBB5_corr_WT_RT22_PBS8	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTAACGGCAGACTTCTCTTCAGGAGTCAGG	20977	22	8	126
HBB5_corr_WT_RT21_PBS17	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTAACGGCAGACTTCTCTTCAGGAGTCAGGTGCACCATG	20978	21	17	134
HBB5_corr_WT_RT21_PBS16	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTAACGGCAGACTTCTCTTCAGGAGTCAGGTGCACCAT	20979	21	16	133
HBB5_corr_WT_RT21_PBS15	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTAACGGCAGACTTCTCTTCAGGAGTCAGGTGCACCA	20980	21	15	132
HBB5_corr_WT_RT21_PBS14	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTAACGGCAGACTTCTCTTCAGGAGTCAGGTGCACC	20981	21	14	131
HBB5_corr_WT_RT21_PBS13	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTAACGGCAGACTTCTCTTCAGGAGTCAGGTGCAC	20982	21	13	130
HBB5_corr_WT_RT21_PBS12	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTAACGGCAGACTTCTCTTCAGGAGTCAGGTGCA	20983	21	12	129
HBB5_corr_WT_RT21_PBS11	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTAACGGCAGACTTCTCTTCAGGAGTCAGGTGC	20984	21	11	128
HBB5_corr_WT_RT21_PBS10	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTAACGGCAGACTTCTCTTCAGGAGTCAGGTG	20985	21	10	127
HBB5_corr_WT_RT21_PBS9	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTAACGGCAGACTTCTCTTCAGGAGTCAGGT	20986	21	9	126
HBB5_corr_WT_RT21_PBS8	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTAACGGCAGACTTCTCTTCAGGAGTCAGG	20987	21	8	125
HBB5_corr_WT_RT20_PBS17	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACGGCAGACTTCTCTTCAGGAGTCAGGTGCACCATG	20988	20	17	133

HBB5_corr_WT_RT20_PBS16	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACGGCAG ACTTCTCTTCAGGAGTCAGGTGCACCAT	20989	20	16	132
HBB5_corr_WT_RT20_PBS15	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACGGCAG ACTTCTCTTCAGGAGTCAGGTGCACCA	20990	20	15	131
HBB5_corr_WT_RT20_PBS14	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACGGCAG ACTTCTCTTCAGGAGTCAGGTGCACC	20991	20	14	130
HBB5_corr_WT_RT20_PBS13	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACGGCAG ACTTCTCTTCAGGAGTCAGGTGCAC	20992	20	13	129
HBB5_corr_WT_RT20_PBS12	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACGGCAG ACTTCTCTTCAGGAGTCAGGTGCA	20993	20	12	128
HBB5_corr_WT_RT20_PBS11	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACGGCAG ACTTCTCTTCAGGAGTCAGGTGC	20994	20	11	127
HBB5_corr_WT_RT20_PBS10	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACGGCAG ACTTCTCTTCAGGAGTCAGGTG	20995	20	10	126
HBB5_corr_WT_RT20_PBS9	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACGGCAG ACTTCTCTTCAGGAGTCAGGT	20996	20	9	125
HBB5_corr_WT_RT20_PBS8	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACGGCAG ACTTCTCTTCAGGAGTCAGG	20997	20	8	124
HBB5_corr_WT_RT19_PBS17	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACGGCAGA CTTCTCTTCAGGAGTCAGGTGCACCATG	20998	19	17	132
HBB5_corr_WT_RT19_PBS16	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACGGCAGA CTTCTCTTCAGGAGTCAGGTGCACCAT	20999	19	16	131
HBB5_corr_WT_RT19_PBS15	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACGGCAGA CTTCTCTTCAGGAGTCAGGTGCACCA	21000	19	15	130

HBB5_corr_WT_RT19_PBS14	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACGGCAGA CTTCTCTTCAGGAGTCAGGTGCACC	21001	19	14	129
HBB5_corr_WT_RT19_PBS13	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACGGCAGA CTTCTCTTCAGGAGTCAGGTGCAC	21002	19	13	128
HBB5_corr_WT_RT19_PBS12	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACGGCAGA CTTCTCTTCAGGAGTCAGGTGCA	21003	19	12	127
HBB5_corr_WT_RT19_PBS11	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACGGCAGA CTTCTCTTCAGGAGTCAGGTGC	21004	19	11	126
HBB5_corr_WT_RT19_PBS10	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACGGCAGA CTTCTCTTCAGGAGTCAGGTG	21005	19	10	125
HBB5_corr_WT_RT19_PBS9	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACGGCAGA CTTCTCTTCAGGAGTCAGGT	21006	19	9	124
HBB5_corr_WT_RT19_PBS8	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACGGCAGA CTTCTCTTCAGGAGTCAGG	21007	19	8	123
HBB5_corr_WT_RT18_PBS17	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGGCAGAC TTCTCTTCAGGAGTCAGGTGCACCATG	21008	18	17	131
HBB5_corr_WT_RT18_PBS16	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGGCAGAC TTCTCTTCAGGAGTCAGGTGCACCAT	21009	18	16	130
HBB5_corr_WT_RT18_PBS15	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGGCAGAC TTCTCTTCAGGAGTCAGGTGCACCA	21010	18	15	129
HBB5_corr_WT_RT18_PBS14	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGGCAGAC TTCTCTTCAGGAGTCAGGTGCACC	21011	18	14	128
HBB5_corr_WT_RT18_PBS13	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGGCAGAC TTCTCTTCAGGAGTCAGGTGCAC	21012	18	13	127

HBB5_corr_WT_RT18_PBS12	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGGCAGAC TTCTCTTCAGGAGTCAGGTGCA	21013	18	12	126
HBB5_corr_WT_RT18_PBS11	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGGCAGAC TTCTCTTCAGGAGTCAGGTGC	21014	18	11	125
HBB5_corr_WT_RT18_PBS10	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGGCAGAC TTCTCTTCAGGAGTCAGGTG	21015	18	10	124
HBB5_corr_WT_RT18_PBS9	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGGCAGAC TTCTCTTCAGGAGTCAGGT	21016	18	9	123
HBB5_corr_WT_RT18_PBS8	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGGCAGAC TTCTCTTCAGGAGTCAGG	21017	18	8	122
HBB5_corr_WT_RT17_PBS17	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGCAGACT TCTCTTCAGGAGTCAGGTGCACCATG	21018	17	17	130
HBB5_corr_WT_RT17_PBS16	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGCAGACT TCTCTTCAGGAGTCAGGTGCACCAT	21019	17	16	129
HBB5_corr_WT_RT17_PBS15	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGCAGACT TCTCTTCAGGAGTCAGGTGCACCA	21020	17	15	128
HBB5_corr_WT_RT17_PBS14	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGCAGACT TCTCTTCAGGAGTCAGGTGCACC	21021	17	14	127
HBB5_corr_WT_RT17_PBS13	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGCAGACT TCTCTTCAGGAGTCAGGTGCAC	21022	17	13	126
HBB5_corr_WT_RT17_PBS12	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGCAGACT TCTCTTCAGGAGTCAGGTGCA	21023	17	12	125
HBB5_corr_WT_RT17_PBS11	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGCAGACT TCTCTTCAGGAGTCAGGTGC	21024	17	11	124

HBB5_corr_WT_RT17_PBS10	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGCAGACTTCTCTTCAGGAGTCAGGTG	21025	17	10	123
HBB5_corr_WT_RT17_PBS9	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGCAGACTTCTCTTCAGGAGTCAGGT	21026	17	9	122
HBB5_corr_WT_RT17_PBS8	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGCAGACTTCTCTTCAGGAGTCAGG	21027	17	8	121
HBB5_corr_WT_RT16_PBS17	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCAGACTTCTCTTCAGGAGTCAGGTGCACCATG	21028	16	17	129
HBB5_corr_WT_RT16_PBS16	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCAGACTTCTCTTCAGGAGTCAGGTGCACCAT	21029	16	16	128
HBB5_corr_WT_RT16_PBS15	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCAGACTTCTCTTCAGGAGTCAGGTGCACCA	21030	16	15	127
HBB5_corr_WT_RT16_PBS14	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCAGACTTCTCTTCAGGAGTCAGGTGCACC	21031	16	14	126
HBB5_corr_WT_RT16_PBS13	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCAGACTTCTCTTCAGGAGTCAGGTGCAC	21032	16	13	125
HBB5_corr_WT_RT16_PBS12	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCAGACTTCTCTTCAGGAGTCAGGTGCA	21033	16	12	124
HBB5_corr_WT_RT16_PBS11	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCAGACTTCTCTTCAGGAGTCAGGTGC	21034	16	11	123
HBB5_corr_WT_RT16_PBS10	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCAGACTTCTCTTCAGGAGTCAGGTG	21035	16	10	122
HBB5_corr_WT_RT16_PBS9	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCAGACTTCTCTTCAGGAGTCAGGT	21036	16	9	121

HBB5_corr_WT_RT16_PBS8	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCAGACTTCTCTTCAGGAGTCAGG	21037	16	8	120
HBB5_corr_WT_RT15_PBS17	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAGACTTCTCTTCAGGAGTCAGGTGCACCATG	21038	15	17	128
HBB5_corr_WT_RT15_PBS16	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAGACTTCTCTTCAGGAGTCAGGTGCACCAT	21039	15	16	127
HBB5_corr_WT_RT15_PBS15	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAGACTTCTCTTCAGGAGTCAGGTGCACCA	21040	15	15	126
HBB5_corr_WT_RT15_PBS14	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAGACTTCTCTTCAGGAGTCAGGTGCACC	21041	15	14	125
HBB5_corr_WT_RT15_PBS13	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAGACTTCTCTTCAGGAGTCAGGTGCAC	21042	15	13	124
HBB5_corr_WT_RT15_PBS12	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAGACTTCTCTTCAGGAGTCAGGTGCA	21043	15	12	123
HBB5_corr_WT_RT15_PBS11	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAGACTTCTCTTCAGGAGTCAGGTGC	21044	15	11	122
HBB5_corr_WT_RT15_PBS10	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAGACTTCTCTTCAGGAGTCAGGTG	21045	15	10	121
HBB5_corr_WT_RT15_PBS9	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAGACTTCTCTTCAGGAGTCAGGT	21046	15	9	120
HBB5_corr_WT_RT15_PBS8	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAGACTTCTCTTCAGGAGTCAGG	21047	15	8	119
HBB5_corr_WT_RT14_PBS17	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGACTTCTCTTCAGGAGTCAGGTGCACCATG	21048	14	17	127

HBB5_corr_WT_RT14_PBS16	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGACTTCT CTTCAGGAGTCAGGTGCACCAT	21049	14	16	126
HBB5_corr_WT_RT14_PBS15	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGACTTCT CTTCAGGAGTCAGGTGCACCA	21050	14	15	125
HBB5_corr_WT_RT14_PBS14	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGACTTCT CTTCAGGAGTCAGGTGCACC	21051	14	14	124
HBB5_corr_WT_RT14_PBS13	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGACTTCT CTTCAGGAGTCAGGTGCAC	21052	14	13	123
HBB5_corr_WT_RT14_PBS12	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGACTTCT CTTCAGGAGTCAGGTGCA	21053	14	12	122
HBB5_corr_WT_RT14_PBS11	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGACTTCT CTTCAGGAGTCAGGTGC	21054	14	11	121
HBB5_corr_WT_RT14_PBS10	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGACTTCT CTTCAGGAGTCAGGTG	21055	14	10	120
HBB5_corr_WT_RT14_PBS9	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGACTTCT CTTCAGGAGTCAGGT	21056	14	9	119
HBB5_corr_WT_RT14_PBS8	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGACTTCT CTTCAGGAGTCAGG	21057	14	8	118
HBB5_corr_WT_RT13_PBS17	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGACTTCTC TTCAGGAGTCAGGTGCACCATG	21058	13	17	126
HBB5_corr_WT_RT13_PBS16	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGACTTCTC TTCAGGAGTCAGGTGCACCAT	21059	13	16	125
HBB5_corr_WT_RT13_PBS15	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGACTTCTC TTCAGGAGTCAGGTGCACCA	21060	13	15	124

HBB5_corr_WT_RT13_PBS14	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGACTTCTC TTCAGGAGTCAGGTGCACC	21061	13	14	123
HBB5_corr_WT_RT13_PBS13	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGACTTCTC TTCAGGAGTCAGGTGCAC	21062	13	13	122
HBB5_corr_WT_RT13_PBS12	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGACTTCTC TTCAGGAGTCAGGTGCA	21063	13	12	121
HBB5_corr_WT_RT13_PBS11	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGACTTCTC TTCAGGAGTCAGGTGC	21064	13	11	120
HBB5_corr_WT_RT13_PBS10	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGACTTCTC TTCAGGAGTCAGGTG	21065	13	10	119
HBB5_corr_WT_RT13_PBS9	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGACTTCTC TTCAGGAGTCAGGT	21066	13	9	118
HBB5_corr_WT_RT13_PBS8	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGACTTCTC TTCAGGAGTCAGG	21067	13	8	117
HBB5_corr_WT_RT12_PBS17	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTTCTCT TCAGGAGTCAGGTGCACCATG	21068	12	17	125
HBB5_corr_WT_RT12_PBS16	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTTCTCT TCAGGAGTCAGGTGCACCAT	21069	12	16	124
HBB5_corr_WT_RT12_PBS15	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTTCTCT TCAGGAGTCAGGTGCACCA	21070	12	15	123
HBB5_corr_WT_RT12_PBS14	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTTCTCT TCAGGAGTCAGGTGCACC	21071	12	14	122
HBB5_corr_WT_RT12_PBS13	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTTCTCT TCAGGAGTCAGGTGCAC	21072	12	13	121

HBB5_corr_WT_RT12_PBS12	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTTCTCTTCAGGAGTCAGGTGCA	21073	12	12	120
HBB5_corr_WT_RT12_PBS11	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTTCTCTTCAGGAGTCAGGTGC	21074	12	11	119
HBB5_corr_WT_RT12_PBS10	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTTCTCTTCAGGAGTCAGGTG	21075	12	10	118
HBB5_corr_WT_RT12_PBS9	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTTCTCTTCAGGAGTCAGGT	21076	12	9	117
HBB5_corr_WT_RT12_PBS8	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTTCTCTTCAGGAGTCAGG	21077	12	8	116
HBB5_corr_WT_RT11_PBS17	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTCTCTTCTTCAGGAGTCAGGTGCACCATG	21078	11	17	124
HBB5_corr_WT_RT11_PBS16	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTCTCTTCAGGAGTCAGGTGCACCAT	21079	11	16	123
HBB5_corr_WT_RT11_PBS15	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTCTCTTCAGGAGTCAGGTGCACCA	21080	11	15	122
HBB5_corr_WT_RT11_PBS14	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTCTCTTCAGGAGTCAGGTGCACC	21081	11	14	121
HBB5_corr_WT_RT11_PBS13	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTCTCTTCAGGAGTCAGGTGCAC	21082	11	13	120
HBB5_corr_WT_RT11_PBS12	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTCTCTTCAGGAGTCAGGTGCA	21083	11	12	119
HBB5_corr_WT_RT11_PBS11	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTCTCTTCAGGAGTCAGGTGC	21084	11	11	118

HBB5_corr_WT_RT11_PBS10	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTCTCTTCAGGAGTCAGGTG	21085	11	10	117
HBB5_corr_WT_RT11_PBS9	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTCTCTTCAGGAGTCAGGT	21086	11	9	116
HBB5_corr_WT_RT11_PBS8	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTCTCTTCAGGAGTCAGG	21087	11	8	115
HBB5_corr_WT_RT10_PBS17	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTCTCTTCAGGAGTCAGGTGCACCATG	21088	10	17	123
HBB5_corr_WT_RT10_PBS16	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTCTCTTCAGGAGTCAGGTGCACCAT	21089	10	16	122
HBB5_corr_WT_RT10_PBS15	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTCTCTTCAGGAGTCAGGTGCACCA	21090	10	15	121
HBB5_corr_WT_RT10_PBS14	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTCTCTTCAGGAGTCAGGTGCACC	21091	10	14	120
HBB5_corr_WT_RT10_PBS13	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTCTCTTCAGGAGTCAGGTGCAC	21092	10	13	119
HBB5_corr_WT_RT10_PBS12	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTCTCTTCAGGAGTCAGGTGCA	21093	10	12	118
HBB5_corr_WT_RT10_PBS11	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTCTCTTCAGGAGTCAGGTGC	21094	10	11	117
HBB5_corr_WT_RT10_PBS10	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTCTCTTCAGGAGTCAGGTG	21095	10	10	116
HBB5_corr_WT_RT10_PBS9	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTCTCTTCAGGAGTCAGGT	21096	10	9	115

HBB5_corr_WT_RT10_PBS8	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTCTCTTCAGGAGTCAGG	21097	10	8	114
HBB5_corr_WT_RT9_PBS17	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCTCTTCAGGAGTCAGGTGCACCATG	21098	9	17	122
HBB5_corr_WT_RT9_PBS16	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCTCTTCAGGAGTCAGGTGCACCAT	21099	9	16	121
HBB5_corr_WT_RT9_PBS15	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCTCTTCAGGAGTCAGGTGCACCA	21100	9	15	120
HBB5_corr_WT_RT9_PBS14	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCTCTTCAGGAGTCAGGTGCACC	21101	9	14	119
HBB5_corr_WT_RT9_PBS13	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCTCTTCAGGAGTCAGGTGCAC	21102	9	13	118
HBB5_corr_WT_RT9_PBS12	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCTCTTCAGGAGTCAGGTGCA	21103	9	12	117
HBB5_corr_WT_RT9_PBS11	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCTCTTCAGGAGTCAGGTGC	21104	9	11	116
HBB5_corr_WT_RT9_PBS10	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCTCTTCAGGAGTCAGGTG	21105	9	10	115
HBB5_corr_WT_RT9_PBS9	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCTCTTCAGGAGTCAGGT	21106	9	9	114
HBB5_corr_WT_RT9_PBS8	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCTCTTCAGGAGTCAGG	21107	9	8	113
HBB5_corr_WT_RT8_PBS17	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCTTCAGGAGTCAGGTGCACCATG	21108	8	17	121

HBB5_corr_WT_RT8_PBS16	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCTTCAGGAGTCAGGTGCACCAT	21109	8	16	120
HBB5_corr_WT_RT8_PBS15	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCTTCAGGAGTCAGGTGCACCA	21110	8	15	119
HBB5_corr_WT_RT8_PBS14	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCTTCAGGAGTCAGGTGCACC	21111	8	14	118
HBB5_corr_WT_RT8_PBS13	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCTTCAGGAGTCAGGTGCAC	21112	8	13	117
HBB5_corr_WT_RT8_PBS12	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCTTCAGGAGTCAGGTGCA	21113	8	12	116
HBB5_corr_WT_RT8_PBS11	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCTTCAGGAGTCAGGTGC	21114	8	11	115
HBB5_corr_WT_RT8_PBS10	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCTTCAGGAGTCAGGTG	21115	8	10	114
HBB5_corr_WT_RT8_PBS9	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCTTCAGGAGTCAGGT	21116	8	9	113
HBB5_corr_WT_RT8_PBS8	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCTTCAGGAGTCAGG	21117	8	8	112

Table 5B. Exemplary template RNA sequences

Table 5B provides design of exemplary DNA components of gene modifying systems for correcting the pathogenic E6V mutation in HBB to the Makassar form. This table details the sequence of a complete template RNA for use in an exemplary gene modifying system comprising a gene modifying polypeptide. Templates in this table employ the HBB5 spacer (CATGGTGCACCTGACTCCTG SEQ ID NO: 19249) and a gRNA

scaffold sequence of GTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC (SEQ ID NO: 20923). For exemplification, the lengths of the RT (heterologous object) sequences and PBS sequences were varied at the 3' end. The length of these respective sequences is reflected in columns 3 and 4, respectively. The longest form of the RT sequence is AGTAACGGCAGACTTCTCTGCAG (SEQ ID NO: 20955). The longest form of the PBS is GAGTCAGGTGCACCATG (SEQ ID NO: 19431).

Sequence Name	Full DNA sequence	SEQ ID NO	RT length	PBS length	Total length
HBB5_corr_Mak_RT23_PBS17	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGTAACGGCAGACTTCTCTGCAGGAGTCAGGTGCACCATG	21118	23	17	136
HBB5_corr_Mak_RT23_PBS16	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGTAACGGCAGACTTCTCTGCAGGAGTCAGGTGCACCAT	21119	23	16	135
HBB5_corr_Mak_RT23_PBS15	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGTAACGGCAGACTTCTCTGCAGGAGTCAGGTGCACCA	21120	23	15	134
HBB5_corr_Mak_RT23_PBS14	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGTAACGGCAGACTTCTCTGCAGGAGTCAGGTGCACC	21121	23	14	133
HBB5_corr_Mak_RT23_PBS13	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGTAACGGCAGACTTCTCTGCAGGAGTCAGGTGCAC	21122	23	13	132
HBB5_corr_Mak_RT23_PBS12	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGTAACGGCAGACTTCTCTGCAGGAGTCAGGTGCA	21123	23	12	131
HBB5_corr_Mak_RT23_PBS11	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGTAACGGCAGACTTCTCTGCAGGAGTCAGGTGC	21124	23	11	130
HBB5_corr_Mak_RT23_PBS10	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGTAACGGCAGACTTCTCTGCAGGAGTCAGGTG	21125	23	10	129

HBB5_corr_Mak_RT23_PBS9	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGTAACGGCAG ACTTCTCTGCAGGAGTCAGGT	21126	23	9	128
HBB5_corr_Mak_RT23_PBS8	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGTAACGGCAG ACTTCTCTGCAGGAGTCAGG	21127	23	8	127
HBB5_corr_Mak_RT22_PBS17	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTAACGGCAGAC TTCTCTGCAGGAGTCAGGTGCACCATG	21128	22	17	135
HBB5_corr_Mak_RT22_PBS16	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTAACGGCAGAC TTCTCTGCAGGAGTCAGGTGCACCAT	21129	22	16	134
HBB5_corr_Mak_RT22_PBS15	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTAACGGCAGAC TTCTCTGCAGGAGTCAGGTGCACCA	21130	22	15	133
HBB5_corr_Mak_RT22_PBS14	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTAACGGCAGAC TTCTCTGCAGGAGTCAGGTGCACC	21131	22	14	132
HBB5_corr_Mak_RT22_PBS13	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTAACGGCAGAC TTCTCTGCAGGAGTCAGGTGCAC	21132	22	13	131
HBB5_corr_Mak_RT22_PBS12	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTAACGGCAGAC TTCTCTGCAGGAGTCAGGTGCA	21133	22	12	130
HBB5_corr_Mak_RT22_PBS11	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTAACGGCAGAC TTCTCTGCAGGAGTCAGGTGC	21134	22	11	129
HBB5_corr_Mak_RT22_PBS10	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTAACGGCAGAC TTCTCTGCAGGAGTCAGGTG	21135	22	10	128
HBB5_corr_Mak_RT22_PBS9	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTAACGGCAGAC TTCTCTGCAGGAGTCAGGT	21136	22	9	127
HBB5_corr_Mak_RT22_PBS8	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTAACGGCAGAC TTCTCTGCAGGAGTCAGG	21137	22	8	126

HBB5_corr_Mak_RT21_PBS17	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTAACGGCAGACT TCTCTGCAGGAGTCAGGTGCACCATG	21138	21	17	134
HBB5_corr_Mak_RT21_PBS16	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTAACGGCAGACT TCTCTGCAGGAGTCAGGTGCACCAT	21139	21	16	133
HBB5_corr_Mak_RT21_PBS15	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTAACGGCAGACT TCTCTGCAGGAGTCAGGTGCACCA	21140	21	15	132
HBB5_corr_Mak_RT21_PBS14	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTAACGGCAGACT TCTCTGCAGGAGTCAGGTGCACC	21141	21	14	131
HBB5_corr_Mak_RT21_PBS13	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTAACGGCAGACT TCTCTGCAGGAGTCAGGTGCAC	21142	21	13	130
HBB5_corr_Mak_RT21_PBS12	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTAACGGCAGACT TCTCTGCAGGAGTCAGGTGCA	21143	21	12	129
HBB5_corr_Mak_RT21_PBS11	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTAACGGCAGACT TCTCTGCAGGAGTCAGGTGC	21144	21	11	128
HBB5_corr_Mak_RT21_PBS10	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTAACGGCAGACT TCTCTGCAGGAGTCAGGTG	21145	21	10	127
HBB5_corr_Mak_RT21_PBS9	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTAACGGCAGACT TCTCTGCAGGAGTCAGGT	21146	21	9	126
HBB5_corr_Mak_RT21_PBS8	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTAACGGCAGACT TCTCTGCAGGAGTCAGG	21147	21	8	125
HBB5_corr_Mak_RT20_PBS17	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACGGCAGACTTT CTCTGCAGGAGTCAGGTGCACCATG	21148	20	17	133
HBB5_corr_Mak_RT20_PBS16	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACGGCAGACTTT CTCTGCAGGAGTCAGGTGCACCAT	21149	20	16	132

HBB5_corr_Mak_RT20_PBS15	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACGGCAGACTT CTCTGCAGGAGTCAGGTGCACCA	21150	20	15	131
HBB5_corr_Mak_RT20_PBS14	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACGGCAGACTT CTCTGCAGGAGTCAGGTGCACC	21151	20	14	130
HBB5_corr_Mak_RT20_PBS13	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACGGCAGACTT CTCTGCAGGAGTCAGGTGCAC	21152	20	13	129
HBB5_corr_Mak_RT20_PBS12	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACGGCAGACTT CTCTGCAGGAGTCAGGTGCA	21153	20	12	128
HBB5_corr_Mak_RT20_PBS11	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACGGCAGACTT CTCTGCAGGAGTCAGGTGC	21154	20	11	127
HBB5_corr_Mak_RT20_PBS10	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACGGCAGACTT CTCTGCAGGAGTCAGGTG	21155	20	10	126
HBB5_corr_Mak_RT20_PBS9	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACGGCAGACTT CTCTGCAGGAGTCAGGT	21156	20	9	125
HBB5_corr_Mak_RT20_PBS8	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACGGCAGACTT CTCTGCAGGAGTCAGG	21157	20	8	124
HBB5_corr_Mak_RT19_PBS17	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACGGCAGACTTC TCTGCAGGAGTCAGGTGCACCATG	21158	19	17	132
HBB5_corr_Mak_RT19_PBS16	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACGGCAGACTTC TCTGCAGGAGTCAGGTGCACCAT	21159	19	16	131
HBB5_corr_Mak_RT19_PBS15	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACGGCAGACTTC TCTGCAGGAGTCAGGTGCACCA	21160	19	15	130
HBB5_corr_Mak_RT19_PBS14	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACGGCAGACTTC TCTGCAGGAGTCAGGTGCACC	21161	19	14	129

HBB5_corr_Mak_RT19_PBS13	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACGGCAGACTTC TCTGCAGGAGTCAGGTGCAC	21162	19	13	128
HBB5_corr_Mak_RT19_PBS12	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACGGCAGACTTC TCTGCAGGAGTCAGGTGCA	21163	19	12	127
HBB5_corr_Mak_RT19_PBS11	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACGGCAGACTTC TCTGCAGGAGTCAGGTGC	21164	19	11	126
HBB5_corr_Mak_RT19_PBS10	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACGGCAGACTTC TCTGCAGGAGTCAGGTG	21165	19	10	125
HBB5_corr_Mak_RT19_PBS9	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACGGCAGACTTC TCTGCAGGAGTCAGGT	21166	19	9	124
HBB5_corr_Mak_RT19_PBS8	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACGGCAGACTTC TCTGCAGGAGTCAGG	21167	19	8	123
HBB5_corr_Mak_RT18_PBS17	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGGCAGACTTCT CTGCAGGAGTCAGGTGCACCATG	21168	18	17	131
HBB5_corr_Mak_RT18_PBS16	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGGCAGACTTCT CTGCAGGAGTCAGGTGCACCAT	21169	18	16	130
HBB5_corr_Mak_RT18_PBS15	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGGCAGACTTCT CTGCAGGAGTCAGGTGCACCA	21170	18	15	129
HBB5_corr_Mak_RT18_PBS14	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGGCAGACTTCT CTGCAGGAGTCAGGTGCACC	21171	18	14	128
HBB5_corr_Mak_RT18_PBS13	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGGCAGACTTCT CTGCAGGAGTCAGGTGCAC	21172	18	13	127
HBB5_corr_Mak_RT18_PBS12	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGGCAGACTTCT CTGCAGGAGTCAGGTGCA	21173	18	12	126

HBB5_corr_Mak_RT18_PBS11	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGGCAGACTTCT CTGCAGGAGTCAGGTGC	21174	18	11	125
HBB5_corr_Mak_RT18_PBS10	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGGCAGACTTCT CTGCAGGAGTCAGGTG	21175	18	10	124
HBB5_corr_Mak_RT18_PBS9	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGGCAGACTTCT CTGCAGGAGTCAGGT	21176	18	9	123
HBB5_corr_Mak_RT18_PBS8	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGGCAGACTTCT CTGCAGGAGTCAGG	21177	18	8	122
HBB5_corr_Mak_RT17_PBS17	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGCAGACTTCTC TGCAGGAGTCAGGTGCACCATG	21178	17	17	130
HBB5_corr_Mak_RT17_PBS16	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGCAGACTTCTC TGCAGGAGTCAGGTGCACCAT	21179	17	16	129
HBB5_corr_Mak_RT17_PBS15	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGCAGACTTCTC TGCAGGAGTCAGGTGCACCA	21180	17	15	128
HBB5_corr_Mak_RT17_PBS14	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGCAGACTTCTC TGCAGGAGTCAGGTGCACC	21181	17	14	127
HBB5_corr_Mak_RT17_PBS13	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGCAGACTTCTC TGCAGGAGTCAGGTGCAC	21182	17	13	126
HBB5_corr_Mak_RT17_PBS12	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGCAGACTTCTC TGCAGGAGTCAGGTGCA	21183	17	12	125
HBB5_corr_Mak_RT17_PBS11	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGCAGACTTCTC TGCAGGAGTCAGGTGC	21184	17	11	124
HBB5_corr_Mak_RT17_PBS10	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGCAGACTTCTC TGCAGGAGTCAGGTG	21185	17	10	123

HBB5_corr_Mak_RT17_PBS9	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGCAGACTTCTC TGCAGGAGTCAGGT	21186	17	9	122
HBB5_corr_Mak_RT17_PBS8	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGCAGACTTCTC TGCAGGAGTCAGG	21187	17	8	121
HBB5_corr_Mak_RT16_PBS17	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCAGACTTCTCT GCAGGAGTCAGGTGCACCATG	21188	16	17	129
HBB5_corr_Mak_RT16_PBS16	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCAGACTTCTCT GCAGGAGTCAGGTGCACCAT	21189	16	16	128
HBB5_corr_Mak_RT16_PBS15	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCAGACTTCTCT GCAGGAGTCAGGTGCACCA	21190	16	15	127
HBB5_corr_Mak_RT16_PBS14	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCAGACTTCTCT GCAGGAGTCAGGTGCACC	21191	16	14	126
HBB5_corr_Mak_RT16_PBS13	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCAGACTTCTCT GCAGGAGTCAGGTGCAC	21192	16	13	125
HBB5_corr_Mak_RT16_PBS12	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCAGACTTCTCT GCAGGAGTCAGGTGCA	21193	16	12	124
HBB5_corr_Mak_RT16_PBS11	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCAGACTTCTCT GCAGGAGTCAGGTGC	21194	16	11	123
HBB5_corr_Mak_RT16_PBS10	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCAGACTTCTCT GCAGGAGTCAGGTG	21195	16	10	122
HBB5_corr_Mak_RT16_PBS9	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCAGACTTCTCT GCAGGAGTCAGGT	21196	16	9	121
HBB5_corr_Mak_RT16_PBS8	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCAGACTTCTCT GCAGGAGTCAGG	21197	16	8	120

HBB5_corr_Mak_RT15_PBS17	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAGACTTCTCTG CAGGAGTCAGGTGCACCATG	21198	15	17	128
HBB5_corr_Mak_RT15_PBS16	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAGACTTCTCTG CAGGAGTCAGGTGCACCAT	21199	15	16	127
HBB5_corr_Mak_RT15_PBS15	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAGACTTCTCTG CAGGAGTCAGGTGCACCA	21200	15	15	126
HBB5_corr_Mak_RT15_PBS14	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAGACTTCTCTG CAGGAGTCAGGTGCACC	21201	15	14	125
HBB5_corr_Mak_RT15_PBS13	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAGACTTCTCTG CAGGAGTCAGGTGCAC	21202	15	13	124
HBB5_corr_Mak_RT15_PBS12	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAGACTTCTCTG CAGGAGTCAGGTGCA	21203	15	12	123
HBB5_corr_Mak_RT15_PBS11	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAGACTTCTCTG CAGGAGTCAGGTGC	21204	15	11	122
HBB5_corr_Mak_RT15_PBS10	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAGACTTCTCTG CAGGAGTCAGGTG	21205	15	10	121
HBB5_corr_Mak_RT15_PBS9	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAGACTTCTCTG CAGGAGTCAGGT	21206	15	9	120
HBB5_corr_Mak_RT15_PBS8	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAGACTTCTCTG CAGGAGTCAGG	21207	15	8	119
HBB5_corr_Mak_RT14_PBS17	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGACTTCTCTGC AGGAGTCAGGTGCACCATG	21208	14	17	127
HBB5_corr_Mak_RT14_PBS16	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGACTTCTCTGC AGGAGTCAGGTGCACCAT	21209	14	16	126

HBB5_corr_ Mak_RT14_ PBS15	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGACTTCTCTGC AGGAGTCAGGTGCACCA	21210	14	15	125
HBB5_corr_ Mak_RT14_ PBS14	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGACTTCTCTGC AGGAGTCAGGTGCACC	21211	14	14	124
HBB5_corr_ Mak_RT14_ PBS13	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGACTTCTCTGC AGGAGTCAGGTGCAC	21212	14	13	123
HBB5_corr_ Mak_RT14_ PBS12	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGACTTCTCTGC AGGAGTCAGGTGCA	21213	14	12	122
HBB5_corr_ Mak_RT14_ PBS11	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGACTTCTCTGC AGGAGTCAGGTGC	21214	14	11	121
HBB5_corr_ Mak_RT14_ PBS10	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGACTTCTCTGC AGGAGTCAGGTG	21215	14	10	120
HBB5_corr_ Mak_RT14_ PBS9	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGACTTCTCTGC AGGAGTCAGGT	21216	14	9	119
HBB5_corr_ Mak_RT14_ PBS8	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGACTTCTCTGC AGGAGTCAGG	21217	14	8	118
HBB5_corr_ Mak_RT13_ PBS17	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGACTTCTCTGCA GGAGTCAGGTGCACCATG	21218	13	17	126
HBB5_corr_ Mak_RT13_ PBS16	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGACTTCTCTGCA GGAGTCAGGTGCACCAT	21219	13	16	125
HBB5_corr_ Mak_RT13_ PBS15	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGACTTCTCTGCA GGAGTCAGGTGCACCA	21220	13	15	124
HBB5_corr_ Mak_RT13_ PBS14	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGACTTCTCTGCA GGAGTCAGGTGCACC	21221	13	14	123

HBB5_corr_Mak_RT13_PBS13	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGACTTCTCTGCA GGAGTCAGGTGCAC	21222	13	13	122
HBB5_corr_Mak_RT13_PBS12	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGACTTCTCTGCA GGAGTCAGGTGCA	21223	13	12	121
HBB5_corr_Mak_RT13_PBS11	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGACTTCTCTGCA GGAGTCAGGTGC	21224	13	11	120
HBB5_corr_Mak_RT13_PBS10	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGACTTCTCTGCA GGAGTCAGGTG	21225	13	10	119
HBB5_corr_Mak_RT13_PBS9	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGACTTCTCTGCA GGAGTCAGGT	21226	13	9	118
HBB5_corr_Mak_RT13_PBS8	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGACTTCTCTGCA GGAGTCAGG	21227	13	8	117
HBB5_corr_Mak_RT12_PBS17	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTTCTCTGCAG GAGTCAGGTGCACCATG	21228	12	17	125
HBB5_corr_Mak_RT12_PBS16	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTTCTCTGCAG GAGTCAGGTGCACCAT	21229	12	16	124
HBB5_corr_Mak_RT12_PBS15	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTTCTCTGCAG GAGTCAGGTGCACCA	21230	12	15	123
HBB5_corr_Mak_RT12_PBS14	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTTCTCTGCAG GAGTCAGGTGCACC	21231	12	14	122
HBB5_corr_Mak_RT12_PBS13	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTTCTCTGCAG GAGTCAGGTGCAC	21232	12	13	121
HBB5_corr_Mak_RT12_PBS12	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTTCTCTGCAG GAGTCAGGTGCA	21233	12	12	120

HBB5_corr_Mak_RT12_PBS11	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTTCTCTGCAGGAGTCAGGTGC	21234	12	11	119
HBB5_corr_Mak_RT12_PBS10	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTTCTCTGCAGGAGTCAGGTG	21235	12	10	118
HBB5_corr_Mak_RT12_PBS9	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTTCTCTGCAGGAGTCAGGT	21236	12	9	117
HBB5_corr_Mak_RT12_PBS8	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTTCTCTGCAGGAGTCAGG	21237	12	8	116
HBB5_corr_Mak_RT11_PBS17	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTCTCTGCAGGAGTCAGGTGCACCATG	21238	11	17	124
HBB5_corr_Mak_RT11_PBS16	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTCTCTGCAGGAGTCAGGTGCACCAT	21239	11	16	123
HBB5_corr_Mak_RT11_PBS15	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTCTCTGCAGGAGTCAGGTGCACCA	21240	11	15	122
HBB5_corr_Mak_RT11_PBS14	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTCTCTGCAGGAGTCAGGTGCACC	21241	11	14	121
HBB5_corr_Mak_RT11_PBS13	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTCTCTGCAGGAGTCAGGTGCAC	21242	11	13	120
HBB5_corr_Mak_RT11_PBS12	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTCTCTGCAGGAGTCAGGTGCA	21243	11	12	119
HBB5_corr_Mak_RT11_PBS11	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTCTCTGCAGGAGTCAGGTGC	21244	11	11	118
HBB5_corr_Mak_RT11_PBS10	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTCTCTGCAGGAGTCAGGTG	21245	11	10	117

HBB5_corr_Mak_RT11_PBS9	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTCTCTGCAGG AGTCAGGT	21246	11	9	116
HBB5_corr_Mak_RT11_PBS8	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTCTCTGCAGG AGTCAGG	21247	11	8	115
HBB5_corr_Mak_RT10_PBS17	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTCTCTGCAGGA GTCAGGTGCACCATG	21248	10	17	123
HBB5_corr_Mak_RT10_PBS16	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTCTCTGCAGGA GTCAGGTGCACCAT	21249	10	16	122
HBB5_corr_Mak_RT10_PBS15	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTCTCTGCAGGA GTCAGGTGCACCA	21250	10	15	121
HBB5_corr_Mak_RT10_PBS14	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTCTCTGCAGGA GTCAGGTGCACC	21251	10	14	120
HBB5_corr_Mak_RT10_PBS13	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTCTCTGCAGGA GTCAGGTGCAC	21252	10	13	119
HBB5_corr_Mak_RT10_PBS12	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTCTCTGCAGGA GTCAGGTGCA	21253	10	12	118
HBB5_corr_Mak_RT10_PBS11	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTCTCTGCAGGA GTCAGGTGC	21254	10	11	117
HBB5_corr_Mak_RT10_PBS10	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTCTCTGCAGGA GTCAGGTG	21255	10	10	116
HBB5_corr_Mak_RT10_PBS9	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTCTCTGCAGGA GTCAGGT	21256	10	9	115
HBB5_corr_Mak_RT10_PBS8	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTCTCTGCAGGA GTCAGG	21257	10	8	114

HBB5_corr_Mak_RT9_P BS17	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCTCTGCAGGAG TCAGGTGCACCATG	21258	9	17	122
HBB5_corr_Mak_RT9_P BS16	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCTCTGCAGGAG TCAGGTGCACCAT	21259	9	16	121
HBB5_corr_Mak_RT9_P BS15	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCTCTGCAGGAG TCAGGTGCACCA	21260	9	15	120
HBB5_corr_Mak_RT9_P BS14	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCTCTGCAGGAG TCAGGTGCACC	21261	9	14	119
HBB5_corr_Mak_RT9_P BS13	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCTCTGCAGGAG TCAGGTGCAC	21262	9	13	118
HBB5_corr_Mak_RT9_P BS12	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCTCTGCAGGAG TCAGGTGCA	21263	9	12	117
HBB5_corr_Mak_RT9_P BS11	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCTCTGCAGGAG TCAGGTGC	21264	9	11	116
HBB5_corr_Mak_RT9_P BS10	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCTCTGCAGGAG TCAGGTG	21265	9	10	115
HBB5_corr_Mak_RT9_P BS9	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCTCTGCAGGAG TCAGGT	21266	9	9	114
HBB5_corr_Mak_RT9_P BS8	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCTCTGCAGGAG TCAGG	21267	9	8	113
HBB5_corr_Mak_RT8_P BS17	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCTGCAGGAGT CAGGTGCACCATG	21268	8	17	121
HBB5_corr_Mak_RT8_P BS16	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCTGCAGGAGT CAGGTGCACCAT	21269	8	16	120

HBB5_corr_Mak_RT8_PBS15	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCTGCAGGAGTCAGGTGCACCA	21270	8	15	119
HBB5_corr_Mak_RT8_PBS14	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCTGCAGGAGTCAGGTGCACC	21271	8	14	118
HBB5_corr_Mak_RT8_PBS13	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCTGCAGGAGTCAGGTGCAC	21272	8	13	117
HBB5_corr_Mak_RT8_PBS12	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCTGCAGGAGTCAGGTGCA	21273	8	12	116
HBB5_corr_Mak_RT8_PBS11	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCTGCAGGAGTCAGGTGC	21274	8	11	115
HBB5_corr_Mak_RT8_PBS10	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCTGCAGGAGTCAGGTG	21275	8	10	114
HBB5_corr_Mak_RT8_PBS9	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCTGCAGGAGTCAGGT	21276	8	9	113
HBB5_corr_Mak_RT8_PBS8	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCTGCAGGAGTCAGG	21277	8	8	112

Table 5C. Exemplary template RNA sequences

Table 5C provides design of exemplary DNA components of gene modifying systems for correcting the pathogenic E6V mutation in HBB to the wild-type form. This table details the sequence of a complete template RNA for use in exemplary gene modifying systems comprising a gene modifying polypeptide. Templates in this table employ the HBB8 spacer (GTAACGGCAGACTTCTCCAC SEQ ID NO: 19971) and a gRNA scaffold sequence of

GTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC (SEQ ID NO: 20923). For exemplification, the lengths of the RT (heterologous object) sequences and PBS sequences were varied at the 3' end. The length of these respective sequences is reflected in columns 3 and 4, respectively. The longest form of the RT sequence is CCATGGTGCACCTGACTCCTGAG (SEQ ID NO: 20956). The longest form of the PBS is GAGAAGTCTGCCGTTAC (SEQ ID NO: 20957).

Sequence Name	Full DNA sequence	SEQ ID NO	RT length	PBS length	Total length
HBB8_corr_WT_RT23_PBS17	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCATGGTGCACCTGACTCCTGAGGAGAAGTCTGCCGTTAC	21278	23	17	136
HBB8_corr_WT_RT23_PBS16	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCATGGTGCACCTGACTCCTGAGGAGAAGTCTGCCGTTA	21279	23	16	135
HBB8_corr_WT_RT23_PBS15	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCATGGTGCACCTGACTCCTGAGGAGAAGTCTGCCGTT	21280	23	15	134
HBB8_corr_WT_RT23_PBS14	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCATGGTGCACCTGACTCCTGAGGAGAAGTCTGCCGT	21281	23	14	133
HBB8_corr_WT_RT23_PBS13	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCATGGTGCACCTGACTCCTGAGGAGAAGTCTGCCG	21282	23	13	132
HBB8_corr_WT_RT23_PBS12	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCATGGTGCACCTGACTCCTGAGGAGAAGTCTGCC	21283	23	12	131
HBB8_corr_WT_RT23_PBS11	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCATGGTGCACCTGACTCCTGAGGAGAAGTCTGC	21284	23	11	130
HBB8_corr_WT_RT23_PBS10	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCATGGTGCACCTGACTCCTGAGGAGAAGTCTG	21285	23	10	129

HBB8_corr_WT_RT23_PBS9	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCATGGTGCACCTGACTCCTGAGGAGAAGTCT	21286	23	9	128
HBB8_corr_WT_RT23_PBS8	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCATGGTGCACCTGACTCCTGAGGAGAAGTC	21287	23	8	127
HBB8_corr_WT_RT22_PBS17	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCATGGTGCACCTGACTCCTGAGGAGAAGTCTGCCGTTAC	21288	22	17	135
HBB8_corr_WT_RT22_PBS16	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCATGGTGCACCTGACTCCTGAGGAGAAGTCTGCCGTTA	21289	22	16	134
HBB8_corr_WT_RT22_PBS15	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCATGGTGCACCTGACTCCTGAGGAGAAGTCTGCCGTT	21290	22	15	133
HBB8_corr_WT_RT22_PBS14	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCATGGTGCACCTGACTCCTGAGGAGAAGTCTGCCGT	21291	22	14	132
HBB8_corr_WT_RT22_PBS13	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCATGGTGCACCTGACTCCTGAGGAGAAGTCTGCCG	21292	22	13	131
HBB8_corr_WT_RT22_PBS12	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCATGGTGCACCTGACTCCTGAGGAGAAGTCTGCC	21293	22	12	130
HBB8_corr_WT_RT22_PBS11	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCATGGTGCACCTGACTCCTGAGGAGAAGTCTGC	21294	22	11	129
HBB8_corr_WT_RT22_PBS10	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCATGGTGCACCTGACTCCTGAGGAGAAGTCTG	21295	22	10	128
HBB8_corr_WT_RT22_PBS9	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCATGGTGCACCTGACTCCTGAGGAGAAGTCT	21296	22	9	127
HBB8_corr_WT_RT22_PBS8	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCATGGTGCACCTGACTCCTGAGGAGAAGTC	21297	22	8	126

HBB8_corr_WT_RT21_PBS17	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATGGTGCACCTGACTCCTGAGGAGAAGTCTGCCGTTAC	21298	21	17	134
HBB8_corr_WT_RT21_PBS16	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATGGTGCACCTGACTCCTGAGGAGAAGTCTGCCGTTA	21299	21	16	133
HBB8_corr_WT_RT21_PBS15	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATGGTGCACCTGACTCCTGAGGAGAAGTCTGCCGTT	21300	21	15	132
HBB8_corr_WT_RT21_PBS14	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATGGTGCACCTGACTCCTGAGGAGAAGTCTGCCGT	21301	21	14	131
HBB8_corr_WT_RT21_PBS13	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATGGTGCACCTGACTCCTGAGGAGAAGTCTGCCG	21302	21	13	130
HBB8_corr_WT_RT21_PBS12	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATGGTGCACCTGACTCCTGAGGAGAAGTCTGCC	21303	21	12	129
HBB8_corr_WT_RT21_PBS11	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATGGTGCACCTGACTCCTGAGGAGAAGTCTGC	21304	21	11	128
HBB8_corr_WT_RT21_PBS10	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATGGTGCACCTGACTCCTGAGGAGAAGTCTG	21305	21	10	127
HBB8_corr_WT_RT21_PBS9	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATGGTGCACCTGACTCCTGAGGAGAAGTCT	21306	21	9	126
HBB8_corr_WT_RT21_PBS8	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATGGTGCACCTGACTCCTGAGGAGAAGTC	21307	21	8	125
HBB8_corr_WT_RT20_PBS17	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTGCACCTGACTCCTGAGGAGAAGTCTGCCGTTAC	21308	20	17	133
HBB8_corr_WT_RT20_PBS16	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTGCACCTGACTCCTGAGGAGAAGTCTGCCGTTA	21309	20	16	132

HBB8_corr_WT_RT20_PBS15	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTGCACCTGACTCCTGAGGAGAAGTCTGCCGTT	21310	20	15	131
HBB8_corr_WT_RT20_PBS14	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTGCACCTGACTCCTGAGGAGAAGTCTGCCGT	21311	20	14	130
HBB8_corr_WT_RT20_PBS13	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTGCACCTGACTCCTGAGGAGAAGTCTGCCG	21312	20	13	129
HBB8_corr_WT_RT20_PBS12	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTGCACCTGACTCCTGAGGAGAAGTCTGCC	21313	20	12	128
HBB8_corr_WT_RT20_PBS11	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTGCACCTGACTCCTGAGGAGAAGTCTGC	21314	20	11	127
HBB8_corr_WT_RT20_PBS10	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTGCACCTGACTCCTGAGGAGAAGTCTG	21315	20	10	126
HBB8_corr_WT_RT20_PBS9	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTGCACCTGACTCCTGAGGAGAAGTCT	21316	20	9	125
HBB8_corr_WT_RT20_PBS8	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTGCACCTGACTCCTGAGGAGAAGTC	21317	20	8	124
HBB8_corr_WT_RT19_PBS17	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTGACTCCTGAGGAGAAGTCTGCCGTTAC	21318	19	17	132
HBB8_corr_WT_RT19_PBS16	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTGCACCTGACTCCTGAGGAGAAGTCTGCCGTTA	21319	19	16	131
HBB8_corr_WT_RT19_PBS15	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTGCACCTGACTCCTGAGGAGAAGTCTGCCGTT	21320	19	15	130
HBB8_corr_WT_RT19_PBS14	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTGCACCTGACTCCTGAGGAGAAGTCTGCCGT	21321	19	14	129

HBB8_corr_WT_RT19_PBS13	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC TAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTGCACCTGACTCC TGAGGAGAAGTCTGCCG	21322	19	13	128
HBB8_corr_WT_RT19_PBS12	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC TAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTGCACCTGACTCC TGAGGAGAAGTCTGCC	21323	19	12	127
HBB8_corr_WT_RT19_PBS11	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC TAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTGCACCTGACTCC TGAGGAGAAGTCTGC	21324	19	11	126
HBB8_corr_WT_RT19_PBS10	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC TAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTGCACCTGACTCC TGAGGAGAAGTCTG	21325	19	10	125
HBB8_corr_WT_RT19_PBS9	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC TAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTGCACCTGACTCC TGAGGAGAAGTCT	21326	19	9	124
HBB8_corr_WT_RT19_PBS8	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC TAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTGCACCTGACTCC TGAGGAGAAGTC	21327	19	8	123
HBB8_corr_WT_RT18_PBS17	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC TAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGCACCTGACTCCT GAGGAGAAGTCTGCCGTTAC	21328	18	17	131
HBB8_corr_WT_RT18_PBS16	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC TAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGCACCTGACTCCT GAGGAGAAGTCTGCCGTTA	21329	18	16	130
HBB8_corr_WT_RT18_PBS15	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC TAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGCACCTGACTCCT GAGGAGAAGTCTGCCGTT	21330	18	15	129
HBB8_corr_WT_RT18_PBS14	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC TAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGCACCTGACTCCT GAGGAGAAGTCTGCCGT	21331	18	14	128
HBB8_corr_WT_RT18_PBS13	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC TAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGCACCTGACTCCT GAGGAGAAGTCTGCCG	21332	18	13	127
HBB8_corr_WT_RT18_PBS12	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC TAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGCACCTGACTCCT GAGGAGAAGTCTGCC	21333	18	12	126

HBB8_corr_WT_RT18_PBS11	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGCACCTGACTCCTGAGGAGAAGTCTGC	21334	18	11	125
HBB8_corr_WT_RT18_PBS10	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGCACCTGACTCCTGAGGAGAAGTCTG	21335	18	10	124
HBB8_corr_WT_RT18_PBS9	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGCACCTGACTCCTGAGGAGAAGTCT	21336	18	9	123
HBB8_corr_WT_RT18_PBS8	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGCACCTGACTCCTGAGGAGAAGTC	21337	18	8	122
HBB8_corr_WT_RT17_PBS17	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCACCTGACTCCTGAGGAGAAGTCTGCCGTTAC	21338	17	17	130
HBB8_corr_WT_RT17_PBS16	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCACCTGACTCCTGAGGAGAAGTCTGCCGTTA	21339	17	16	129
HBB8_corr_WT_RT17_PBS15	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCACCTGACTCCTGAGGAGAAGTCTGCCGTT	21340	17	15	128
HBB8_corr_WT_RT17_PBS14	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCACCTGACTCCTGAGGAGAAGTCTGCCGT	21341	17	14	127
HBB8_corr_WT_RT17_PBS13	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCACCTGACTCCTGAGGAGAAGTCTGCCG	21342	17	13	126
HBB8_corr_WT_RT17_PBS12	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCACCTGACTCCTGAGGAGAAGTCTGCC	21343	17	12	125
HBB8_corr_WT_RT17_PBS11	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCACCTGACTCCTGAGGAGAAGTCTGC	21344	17	11	124
HBB8_corr_WT_RT17_PBS10	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCACCTGACTCCTGAGGAGAAGTCTG	21345	17	10	123

HBB8_corr_WT_RT17_PBS9	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCACCTGACTCCTGAGGAGAAGTCT	21346	17	9	122
HBB8_corr_WT_RT17_PBS8	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCACCTGACTCCTGAGGAGAAGTC	21347	17	8	121
HBB8_corr_WT_RT16_PBS17	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCACCTGACTCCTGAGGAGAAGTCTGCCGTTAC	21348	16	17	129
HBB8_corr_WT_RT16_PBS16	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCACCTGACTCCTGAGGAGAAGTCTGCCGTTA	21349	16	16	128
HBB8_corr_WT_RT16_PBS15	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCACCTGACTCCTGAGGAGAAGTCTGCCGTT	21350	16	15	127
HBB8_corr_WT_RT16_PBS14	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCACCTGACTCCTGAGGAGAAGTCTGCCGT	21351	16	14	126
HBB8_corr_WT_RT16_PBS13	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCACCTGACTCCTGAGGAGAAGTCTGCCG	21352	16	13	125
HBB8_corr_WT_RT16_PBS12	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCACCTGACTCCTGAGGAGAAGTCTGCC	21353	16	12	124
HBB8_corr_WT_RT16_PBS11	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCACCTGACTCCTGAGGAGAAGTCTGC	21354	16	11	123
HBB8_corr_WT_RT16_PBS10	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCACCTGACTCCTGAGGAGAAGTCTG	21355	16	10	122
HBB8_corr_WT_RT16_PBS9	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCACCTGACTCCTGAGGAGAAGTCT	21356	16	9	121
HBB8_corr_WT_RT16_PBS8	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCACCTGACTCCTGAGGAGAAGTC	21357	16	8	120

HBB8_corr_WT_RT15_PBS17	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACCTGACTCCTGAGGAGAAGTCTGCCGTTAC	21358	15	17	128
HBB8_corr_WT_RT15_PBS16	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACCTGACTCCTGAGGAGAAGTCTGCCGTTA	21359	15	16	127
HBB8_corr_WT_RT15_PBS15	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACCTGACTCCTGAGGAGAAGTCTGCCGTT	21360	15	15	126
HBB8_corr_WT_RT15_PBS14	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACCTGACTCCTGAGGAGAAGTCTGCCGT	21361	15	14	125
HBB8_corr_WT_RT15_PBS13	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACCTGACTCCTGAGGAGAAGTCTGCCG	21362	15	13	124
HBB8_corr_WT_RT15_PBS12	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACCTGACTCCTGAGGAGAAGTCTGCC	21363	15	12	123
HBB8_corr_WT_RT15_PBS11	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACCTGACTCCTGAGGAGAAGTCTGC	21364	15	11	122
HBB8_corr_WT_RT15_PBS10	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACCTGACTCCTGAGGAGAAGTCTG	21365	15	10	121
HBB8_corr_WT_RT15_PBS9	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACCTGACTCCTGAGGAGAAGTCT	21366	15	9	120
HBB8_corr_WT_RT15_PBS8	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACCTGACTCCTGAGGAGAAGTC	21367	15	8	119
HBB8_corr_WT_RT14_PBS17	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTGACTCCTGAGGAGAAGTCTGCCGTTAC	21368	14	17	127
HBB8_corr_WT_RT14_PBS16	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTGACTCCTGAGGAGAAGTCTGCCGTTA	21369	14	16	126

HBB8_corr_WT_RT14_PBS15	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTGACTCCTGAGGAGAAGTCTGCCGTT	21370	14	15	125
HBB8_corr_WT_RT14_PBS14	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTGACTCCTGAGGAGAAGTCTGCCGT	21371	14	14	124
HBB8_corr_WT_RT14_PBS13	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTGACTCCTGAGGAGAAGTCTGCCG	21372	14	13	123
HBB8_corr_WT_RT14_PBS12	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTGACTCCTGAGGAGAAGTCTGCC	21373	14	12	122
HBB8_corr_WT_RT14_PBS11	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTGACTCCTGAGGAGAAGTCTGC	21374	14	11	121
HBB8_corr_WT_RT14_PBS10	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTGACTCCTGAGGAGAAGTCTG	21375	14	10	120
HBB8_corr_WT_RT14_PBS9	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTGACTCCTGAGGAGAAGTCT	21376	14	9	119
HBB8_corr_WT_RT14_PBS8	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTGACTCCTGAGGAGAAGTC	21377	14	8	118
HBB8_corr_WT_RT13_PBS17	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTGACTCCTGAGGAGAAGTCTGCCGTTAC	21378	13	17	126
HBB8_corr_WT_RT13_PBS16	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTGACTCCTGAGGAGAAGTCTGCCGTTA	21379	13	16	125
HBB8_corr_WT_RT13_PBS15	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTGACTCCTGAGGAGAAGTCTGCCGTT	21380	13	15	124
HBB8_corr_WT_RT13_PBS14	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTGACTCCTGAGGAGAAGTCTGCCGT	21381	13	14	123

HBB8_corr_WT_RT13_PBS13	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTGACTCCTGAGGAGAAGTCTGCCG	21382	13	13	122
HBB8_corr_WT_RT13_PBS12	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTGACTCCTGAGGAGAAGTCTGCC	21383	13	12	121
HBB8_corr_WT_RT13_PBS11	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTGACTCCTGAGGAGAAGTCTGC	21384	13	11	120
HBB8_corr_WT_RT13_PBS10	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTGACTCCTGAGGAGAAGTCTG	21385	13	10	119
HBB8_corr_WT_RT13_PBS9	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTGACTCCTGAGGAGAAGTCT	21386	13	9	118
HBB8_corr_WT_RT13_PBS8	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTGACTCCTGAGGAGAAGTC	21387	13	8	117
HBB8_corr_WT_RT12_PBS17	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGACTCCTGAGGAGAAGTCTGCCGTTAC	21388	12	17	125
HBB8_corr_WT_RT12_PBS16	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGACTCCTGAGGAGAAGTCTGCCGTTA	21389	12	16	124
HBB8_corr_WT_RT12_PBS15	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGACTCCTGAGGAGAAGTCTGCCGTT	21390	12	15	123
HBB8_corr_WT_RT12_PBS14	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGACTCCTGAGGAGAAGTCTGCCGT	21391	12	14	122
HBB8_corr_WT_RT12_PBS13	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGACTCCTGAGGAGAAGTCTGCCG	21392	12	13	121
HBB8_corr_WT_RT12_PBS12	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGACTCCTGAGGAGAAGTCTGCC	21393	12	12	120

HBB8_corr_WT_RT12_PBS11	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGACTCCTGAGGAGAAGTCTGC	21394	12	11	119
HBB8_corr_WT_RT12_PBS10	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGACTCCTGAGGAGAAGTCTG	21395	12	10	118
HBB8_corr_WT_RT12_PBS9	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGACTCCTGAGGAGAAGTCT	21396	12	9	117
HBB8_corr_WT_RT12_PBS8	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGACTCCTGAGGAGAAGTC	21397	12	8	116
HBB8_corr_WT_RT11_PBS17	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGACTCCTGAGGAGAAGTCTGCCGTTAC	21398	11	17	124
HBB8_corr_WT_RT11_PBS16	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGACTCCTGAGGAGAAGTCTGCCGTTA	21399	11	16	123
HBB8_corr_WT_RT11_PBS15	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGACTCCTGAGGAGAAGTCTGCCGTT	21400	11	15	122
HBB8_corr_WT_RT11_PBS14	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGACTCCTGAGGAGAAGTCTGCCGT	21401	11	14	121
HBB8_corr_WT_RT11_PBS13	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGACTCCTGAGGAGAAGTCTGCCG	21402	11	13	120
HBB8_corr_WT_RT11_PBS12	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGACTCCTGAGGAGAAGTCTGCC	21403	11	12	119
HBB8_corr_WT_RT11_PBS11	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGACTCCTGAGGAGAAGTCTGC	21404	11	11	118
HBB8_corr_WT_RT11_PBS10	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGACTCCTGAGGAGAAGTCTG	21405	11	10	117

HBB8_corr_WT_RT11_PBS9	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGACTCCTGAGGAGAAGTCT	21406	11	9	116
HBB8_corr_WT_RT11_PBS8	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGACTCCTGAGGAGAAGTC	21407	11	8	115
HBB8_corr_WT_RT10_PBS17	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGACTCCTGAGGAGAAGTCTGCCGTTAC	21408	10	17	123
HBB8_corr_WT_RT10_PBS16	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGACTCCTGAGGAGAAGTCTGCCGTTA	21409	10	16	122
HBB8_corr_WT_RT10_PBS15	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGACTCCTGAGGAGAAGTCTGCCGTT	21410	10	15	121
HBB8_corr_WT_RT10_PBS14	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGACTCCTGAGGAGAAGTCTGCCGT	21411	10	14	120
HBB8_corr_WT_RT10_PBS13	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGACTCCTGAGGAGAAGTCTGCCG	21412	10	13	119
HBB8_corr_WT_RT10_PBS12	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGACTCCTGAGGAGAAGTCTGCC	21413	10	12	118
HBB8_corr_WT_RT10_PBS11	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGACTCCTGAGGAGAAGTCTGC	21414	10	11	117
HBB8_corr_WT_RT10_PBS10	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGACTCCTGAGGAGAAGTCTG	21415	10	10	116
HBB8_corr_WT_RT10_PBS9	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGACTCCTGAGGAGAAGTCT	21416	10	9	115
HBB8_corr_WT_RT10_PBS8	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGACTCCTGAGGAGAAGTC	21417	10	8	114

HBB8_corr_WT_RT9_PBS17	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTCCTGAGGAGAAGTCTGCCGTTAC	21418	9	17	122
HBB8_corr_WT_RT9_PBS16	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTCCTGAGGAGAAGTCTGCCGTTA	21419	9	16	121
HBB8_corr_WT_RT9_PBS15	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTCCTGAGGAGAAGTCTGCCGTT	21420	9	15	120
HBB8_corr_WT_RT9_PBS14	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTCCTGAGGAGAAGTCTGCCGT	21421	9	14	119
HBB8_corr_WT_RT9_PBS13	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTCCTGAGGAGAAGTCTGCCG	21422	9	13	118
HBB8_corr_WT_RT9_PBS12	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTCCTGAGGAGAAGTCTGCC	21423	9	12	117
HBB8_corr_WT_RT9_PBS11	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTCCTGAGGAGAAGTCTGC	21424	9	11	116
HBB8_corr_WT_RT9_PBS10	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTCCTGAGGAGAAGTCTG	21425	9	10	115
HBB8_corr_WT_RT9_PBS9	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTCCTGAGGAGAAGTCT	21426	9	9	114
HBB8_corr_WT_RT9_PBS8	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTCCTGAGGAGAAGTC	21427	9	8	113
HBB8_corr_WT_RT8_PBS17	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCCTGAGGAGAAGTCTGCCGTTAC	21428	8	17	121
HBB8_corr_WT_RT8_PBS16	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCCTGAGGAGAAGTCTGCCGTTA	21429	8	16	120

HBB8_corr_WT_RT8_PBS15	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCCTGAGGAGAAGTCTGCCGTT	21430	8	15	119
HBB8_corr_WT_RT8_PBS14	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCCTGAGGAGAAGTCTGCCGT	21431	8	14	118
HBB8_corr_WT_RT8_PBS13	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCCTGAGGAGAAGTCTGCCG	21432	8	13	117
HBB8_corr_WT_RT8_PBS12	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCCTGAGGAGAAGTCTGCC	21433	8	12	116
HBB8_corr_WT_RT8_PBS11	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCCTGAGGAGAAGTCTGC	21434	8	11	115
HBB8_corr_WT_RT8_PBS10	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCCTGAGGAGAAGTCTG	21435	8	10	114
HBB8_corr_WT_RT8_PBS9	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCCTGAGGAGAAGTCT	21436	8	9	113
HBB8_corr_WT_RT8_PBS8	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCCTGAGGAGAAGTC	21437	8	8	112

Table 5D. Exemplary template RNA sequences

Table 5D provides design of exemplary DNA components of gene modifying systems for correcting the pathogenic E6V mutation in HBB to the Makassar form. This table details the sequence of a complete template RNA for use in exemplary gene modifying systems comprising a gene modifying polypeptide. Templates in this table employ the HBB8 spacer (GTAACGGCAGACTTCTCCAC SEQ ID NO: 19971) and a gRNA

scaffold sequence of GTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC (SEQ ID NO: 20923). For exemplification, the lengths of the RT (heterologous object) sequences and PBS sequences were varied at the 3' end. The length of these respective sequences is reflected in columns 3 and 4, respectively. The longest form of the RT sequence is CCATGGTGCACCTGACTCCTGCG (SEQ ID NO: 21906). The longest form of the PBS is GAGAAGTCTGCCGTTAC (SEQ ID NO: 20957).

Sequence Name	Full DNA sequence	SEQ ID NO	RT length	PBS length	Total length
HBB8_corr_Mak_RT23_PBS17	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCATGGTGCACCTGACTCCTGCGGAGAAGTCTGCCGTTAC	21438	23	17	136
HBB8_corr_Mak_RT23_PBS16	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCATGGTGCACCTGACTCCTGCGGAGAAGTCTGCCGTTA	21439	23	16	135
HBB8_corr_Mak_RT23_PBS15	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCATGGTGCACCTGACTCCTGCGGAGAAGTCTGCCGTT	21440	23	15	134
HBB8_corr_Mak_RT23_PBS14	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCATGGTGCACCTGACTCCTGCGGAGAAGTCTGCCGT	21441	23	14	133
HBB8_corr_Mak_RT23_PBS13	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCATGGTGCACCTGACTCCTGCGGAGAAGTCTGCCG	21442	23	13	132
HBB8_corr_Mak_RT23_PBS12	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCATGGTGCACCTGACTCCTGCGGAGAAGTCTGCC	21443	23	12	131
HBB8_corr_Mak_RT23_PBS11	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCATGGTGCACCTGACTCCTGCGGAGAAGTCTGC	21444	23	11	130
HBB8_corr_Mak_RT23_PBS10	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCATGGTGCACCTGACTCCTGCGGAGAAGTCTG	21445	23	10	129

HBB8_corr_Mak_RT23_PBS9	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCATGGTGCACCTGACTCCTGCGGAGAAGTCT	21446	23	9	128
HBB8_corr_Mak_RT23_PBS8	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCATGGTGCACCTGACTCCTGCGGAGAAGTC	21447	23	8	127
HBB8_corr_Mak_RT22_PBS17	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCATGGTGCACCTGACTCCTGCGGAGAAGTCTGCCGTTAC	21448	22	17	135
HBB8_corr_Mak_RT22_PBS16	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCATGGTGCACCTGACTCCTGCGGAGAAGTCTGCCGTTA	21449	22	16	134
HBB8_corr_Mak_RT22_PBS15	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCATGGTGCACCTGACTCCTGCGGAGAAGTCTGCCGTT	21450	22	15	133
HBB8_corr_Mak_RT22_PBS14	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCATGGTGCACCTGACTCCTGCGGAGAAGTCTGCCGT	21451	22	14	132
HBB8_corr_Mak_RT22_PBS13	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCATGGTGCACCTGACTCCTGCGGAGAAGTCTGCCG	21452	22	13	131
HBB8_corr_Mak_RT22_PBS12	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCATGGTGCACCTGACTCCTGCGGAGAAGTCTGCC	21453	22	12	130
HBB8_corr_Mak_RT22_PBS11	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCATGGTGCACCTGACTCCTGCGGAGAAGTCTGC	21454	22	11	129
HBB8_corr_Mak_RT22_PBS10	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCATGGTGCACCTGACTCCTGCGGAGAAGTCTG	21455	22	10	128
HBB8_corr_Mak_RT22_PBS9	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCATGGTGCACCTGACTCCTGCGGAGAAGTCT	21456	22	9	127
HBB8_corr_Mak_RT22_PBS8	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCATGGTGCACCTGACTCCTGCGGAGAAGTC	21457	22	8	126

HBB8_corr_M ak_RT21_PBS 17	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATGGTGCA CCTGACTCCTGCGGAGAAGTCTGCCGTTAC	21458	21	17		134
HBB8_corr_M ak_RT21_PBS 16	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATGGTGCA CCTGACTCCTGCGGAGAAGTCTGCCGTTA	21459	21	16		133
HBB8_corr_M ak_RT21_PBS 15	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATGGTGCA CCTGACTCCTGCGGAGAAGTCTGCCGTT	21460	21	15		132
HBB8_corr_M ak_RT21_PBS 14	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATGGTGCA CCTGACTCCTGCGGAGAAGTCTGCCGT	21461	21	14		131
HBB8_corr_M ak_RT21_PBS 13	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATGGTGCA CCTGACTCCTGCGGAGAAGTCTGCCG	21462	21	13		130
HBB8_corr_M ak_RT21_PBS 12	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATGGTGCA CCTGACTCCTGCGGAGAAGTCTGCC	21463	21	12		129
HBB8_corr_M ak_RT21_PBS 11	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATGGTGCA CCTGACTCCTGCGGAGAAGTCTGC	21464	21	11		128
HBB8_corr_M ak_RT21_PBS 10	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATGGTGCA CCTGACTCCTGCGGAGAAGTCTG	21465	21	10		127
HBB8_corr_M ak_RT21_PBS 9	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATGGTGCA CCTGACTCCTGCGGAGAAGTCT	21466	21	9		126
HBB8_corr_M ak_RT21_PBS 8	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATGGTGCA CCTGACTCCTGCGGAGAAGTC	21467	21	8		125
HBB8_corr_M ak_RT20_PBS 17	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTGCACC TGACTCCTGCGGAGAAGTCTGCCGTTAC	21468	20	17		133
HBB8_corr_M ak_RT20_PBS 16	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA GGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTGCACC TGACTCCTGCGGAGAAGTCTGCCGTTA	21469	20	16		132

HBB8_corr_Mak_RT20_PBS15	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTGCACCTGACTCCTGCGGAGAAGTCTGCCGTT	21470	20	15	131
HBB8_corr_Mak_RT20_PBS14	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTGCACCTGACTCCTGCGGAGAAGTCTGCCGT	21471	20	14	130
HBB8_corr_Mak_RT20_PBS13	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTGCACCTGACTCCTGCGGAGAAGTCTGCCG	21472	20	13	129
HBB8_corr_Mak_RT20_PBS12	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTGCACCTGACTCCTGCGGAGAAGTCTGCC	21473	20	12	128
HBB8_corr_Mak_RT20_PBS11	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTGCACCTGACTCCTGCGGAGAAGTCTGC	21474	20	11	127
HBB8_corr_Mak_RT20_PBS10	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTGCACCTGACTCCTGCGGAGAAGTCTG	21475	20	10	126
HBB8_corr_Mak_RT20_PBS9	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTGCACCTGACTCCTGCGGAGAAGTCT	21476	20	9	125
HBB8_corr_Mak_RT20_PBS8	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTGCACCTGACTCCTGCGGAGAAGTC	21477	20	8	124
HBB8_corr_Mak_RT19_PBS17	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTGCACCTGACTCCTGCGGAGAAGTCTGCCGTTAC	21478	19	17	132
HBB8_corr_Mak_RT19_PBS16	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTGCACCTGACTCCTGCGGAGAAGTCTGCCGTTA	21479	19	16	131
HBB8_corr_Mak_RT19_PBS15	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTGCACCTGACTCCTGCGGAGAAGTCTGCCGTT	21480	19	15	130
HBB8_corr_Mak_RT19_PBS14	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTGCACCTGACTCCTGCGGAGAAGTCTGCCGT	21481	19	14	129

HBB8_corr_Mak_RT19_PBS13	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTGCACCTGACTCCTGCGGAGAAGTCTGCCG	21482	19	13	128
HBB8_corr_Mak_RT19_PBS12	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTGCACCTGACTCCTGCGGAGAAGTCTGCC	21483	19	12	127
HBB8_corr_Mak_RT19_PBS11	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTGCACCTGACTCCTGCGGAGAAGTCTGC	21484	19	11	126
HBB8_corr_Mak_RT19_PBS10	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTGCACCTGACTCCTGCGGAGAAGTCTG	21485	19	10	125
HBB8_corr_Mak_RT19_PBS9	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTGCACCTGACTCCTGCGGAGAAGTCT	21486	19	9	124
HBB8_corr_Mak_RT19_PBS8	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTGCACCTGACTCCTGCGGAGAAGTC	21487	19	8	123
HBB8_corr_Mak_RT18_PBS17	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTGCACCTGACCTCCTGCGGAGAAGTCTGCCGTTAC	21488	18	17	131
HBB8_corr_Mak_RT18_PBS16	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTGCACCTGACTCCTGCGGAGAAGTCTGCCGTTA	21489	18	16	130
HBB8_corr_Mak_RT18_PBS15	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTGCACCTGACTCCTGCGGAGAAGTCTGCCGTT	21490	18	15	129
HBB8_corr_Mak_RT18_PBS14	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTGCACCTGACTCCTGCGGAGAAGTCTGCCGT	21491	18	14	128
HBB8_corr_Mak_RT18_PBS13	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTGCACCTGACTCCTGCGGAGAAGTCTGCCG	21492	18	13	127
HBB8_corr_Mak_RT18_PBS12	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTGCACCTGACTCCTGCGGAGAAGTCTGCC	21493	18	12	126

HBB8_corr_Mak_RT18_PBS11	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGCACCTGACTCCTGCGGAGAAGTCTGC	21494	18	11	125
HBB8_corr_Mak_RT18_PBS10	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGCACCTGACTCCTGCGGAGAAGTCTG	21495	18	10	124
HBB8_corr_Mak_RT18_PBS9	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGCACCTGACTCCTGCGGAGAAGTCT	21496	18	9	123
HBB8_corr_Mak_RT18_PBS8	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGCACCTGACTCCTGCGGAGAAGTC	21497	18	8	122
HBB8_corr_Mak_RT17_PBS17	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCACCTGACTCCTGCGGAGAAGTCTGCCGTTAC	21498	17	17	130
HBB8_corr_Mak_RT17_PBS16	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCACCTGACTCCTGCGGAGAAGTCTGCCGTTA	21499	17	16	129
HBB8_corr_Mak_RT17_PBS15	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCACCTGACTCCTGCGGAGAAGTCTGCCGTT	21500	17	15	128
HBB8_corr_Mak_RT17_PBS14	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCACCTGACTCCTGCGGAGAAGTCTGCCGT	21501	17	14	127
HBB8_corr_Mak_RT17_PBS13	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCACCTGACTCCTGCGGAGAAGTCTGCCG	21502	17	13	126
HBB8_corr_Mak_RT17_PBS12	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCACCTGACTCCTGCGGAGAAGTCTGCC	21503	17	12	125
HBB8_corr_Mak_RT17_PBS11	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCACCTGACTCCTGCGGAGAAGTCTGC	21504	17	11	124
HBB8_corr_Mak_RT17_PBS10	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCACCTGACTCCTGCGGAGAAGTCTG	21505	17	10	123

HBB8_corr_Mak_RT17_PBS9	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCTGCACCTGACTCCTGCGGAGAAGTCT	21506	17	9	122
HBB8_corr_Mak_RT17_PBS8	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCTGCACCTGACTCCTGCGGAGAAGTC	21507	17	8	121
HBB8_corr_Mak_RT16_PBS17	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCACCTGACTCCTGCGGAGAAGTCTGCCGTTAC	21508	16	17	129
HBB8_corr_Mak_RT16_PBS16	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCACCTGACTCCTGCGGAGAAGTCTGCCGTTA	21509	16	16	128
HBB8_corr_Mak_RT16_PBS15	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCACCTGACTCCTGCGGAGAAGTCTGCCGTT	21510	16	15	127
HBB8_corr_Mak_RT16_PBS14	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCACCTGACTCCTGCGGAGAAGTCTGCCGT	21511	16	14	126
HBB8_corr_Mak_RT16_PBS13	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCACCTGACTCCTGCGGAGAAGTCTGCCG	21512	16	13	125
HBB8_corr_Mak_RT16_PBS12	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCACCTGACTCCTGCGGAGAAGTCTGCC	21513	16	12	124
HBB8_corr_Mak_RT16_PBS11	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCACCTGACTCCTGCGGAGAAGTCTGC	21514	16	11	123
HBB8_corr_Mak_RT16_PBS10	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCACCTGACTCCTGCGGAGAAGTCTG	21515	16	10	122
HBB8_corr_Mak_RT16_PBS9	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCACCTGACTCCTGCGGAGAAGTCT	21516	16	9	121
HBB8_corr_Mak_RT16_PBS8	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCACCTGACTCCTGCGGAGAAGTC	21517	16	8	120

HBB8_corr_Mak_RT15_PBS17	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACCTGACTCCTGCGGAGAAGTCTGCCGTTAC	21518	15	17	128
HBB8_corr_Mak_RT15_PBS16	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACCTGACTCCTGCGGAGAAGTCTGCCGTTA	21519	15	16	127
HBB8_corr_Mak_RT15_PBS15	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACCTGACTCCTGCGGAGAAGTCTGCCGTT	21520	15	15	126
HBB8_corr_Mak_RT15_PBS14	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACCTGACTCCTGCGGAGAAGTCTGCCGT	21521	15	14	125
HBB8_corr_Mak_RT15_PBS13	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACCTGACTCCTGCGGAGAAGTCTGCCG	21522	15	13	124
HBB8_corr_Mak_RT15_PBS12	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACCTGACTCCTGCGGAGAAGTCTGCC	21523	15	12	123
HBB8_corr_Mak_RT15_PBS11	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACCTGACTCCTGCGGAGAAGTCTGC	21524	15	11	122
HBB8_corr_Mak_RT15_PBS10	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACCTGACTCCTGCGGAGAAGTCTG	21525	15	10	121
HBB8_corr_Mak_RT15_PBS9	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACCTGACTCCTGCGGAGAAGTCT	21526	15	9	120
HBB8_corr_Mak_RT15_PBS8	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACCTGACTCCTGCGGAGAAGTC	21527	15	8	119
HBB8_corr_Mak_RT14_PBS17	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTGACTCCTGCGGAGAAGTCTGCCGTTAC	21528	14	17	127
HBB8_corr_Mak_RT14_PBS16	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTGACTCCTGCGGAGAAGTCTGCCGTTA	21529	14	16	126

HBB8_corr_Mak_RT14_PBS15	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTGACTCCTGCGGAGAAGTCTGCCGTT	21530	14	15	125
HBB8_corr_Mak_RT14_PBS14	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTGACTCCTGCGGAGAAGTCTGCCGT	21531	14	14	124
HBB8_corr_Mak_RT14_PBS13	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTGACTCCTGCGGAGAAGTCTGCCG	21532	14	13	123
HBB8_corr_Mak_RT14_PBS12	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTGACTCCTGCGGAGAAGTCTGCC	21533	14	12	122
HBB8_corr_Mak_RT14_PBS11	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTGACTCCTGCGGAGAAGTCTGC	21534	14	11	121
HBB8_corr_Mak_RT14_PBS10	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTGACTCCTGCGGAGAAGTCTG	21535	14	10	120
HBB8_corr_Mak_RT14_PBS9	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTGACTCCTGCGGAGAAGTCT	21536	14	9	119
HBB8_corr_Mak_RT14_PBS8	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTGACTCCTGCGGAGAAGTC	21537	14	8	118
HBB8_corr_Mak_RT13_PBS17	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTGACTCCTGCGGAGAAGTCTGCCGTTAC	21538	13	17	126
HBB8_corr_Mak_RT13_PBS16	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTGACTCCTGCGGAGAAGTCTGCCGTTA	21539	13	16	125
HBB8_corr_Mak_RT13_PBS15	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTGACTCCTGCGGAGAAGTCTGCCGTT	21540	13	15	124
HBB8_corr_Mak_RT13_PBS14	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTGACTCCTGCGGAGAAGTCTGCCGT	21541	13	14	123

HBB8_corr_Mak_RT13_PBS13	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTGACTCCTGCGGAGAAGTCTGCCG	21542	13	13		122
HBB8_corr_Mak_RT13_PBS12	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTGACTCCTGCGGAGAAGTCTGCC	21543	13	12		121
HBB8_corr_Mak_RT13_PBS11	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTGACTCCTGCGGAGAAGTCTGC	21544	13	11		120
HBB8_corr_Mak_RT13_PBS10	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTGACTCCTGCGGAGAAGTCTG	21545	13	10		119
HBB8_corr_Mak_RT13_PBS9	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTGACTCCTGCGGAGAAGTCT	21546	13	9		118
HBB8_corr_Mak_RT13_PBS8	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTGACTCCTGCGGAGAAGTC	21547	13	8		117
HBB8_corr_Mak_RT12_PBS17	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGACTCCTGCGGAGAAGTCTGCCGTTAC	21548	12	17		125
HBB8_corr_Mak_RT12_PBS16	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGACTCCTGCGGAGAAGTCTGCCGTTA	21549	12	16		124
HBB8_corr_Mak_RT12_PBS15	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGACTCCTGCGGAGAAGTCTGCCGTT	21550	12	15		123
HBB8_corr_Mak_RT12_PBS14	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGACTCCTGCGGAGAAGTCTGCCGT	21551	12	14		122
HBB8_corr_Mak_RT12_PBS13	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGACTCCTGCGGAGAAGTCTGCCG	21552	12	13		121
HBB8_corr_Mak_RT12_PBS12	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGACTCCTGCGGAGAAGTCTGCC	21553	12	12		120

HBB8_corr_Mak_RT12_PBS11	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGACTCCTGCGGAGAAGTCTGC	21554	12	11		119
HBB8_corr_Mak_RT12_PBS10	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGACTCCTGCGGAGAAGTCTG	21555	12	10		118
HBB8_corr_Mak_RT12_PBS9	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGACTCCTGCGGAGAAGTCT	21556	12	9		117
HBB8_corr_Mak_RT12_PBS8	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGACTCCTGCGGAGAAGTC	21557	12	8		116
HBB8_corr_Mak_RT11_PBS17	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGACTCCTGCGGAGAAGTCTGCCGTTAC	21558	11	17		124
HBB8_corr_Mak_RT11_PBS16	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGACTCCTGCGGAGAAGTCTGCCGTTA	21559	11	16		123
HBB8_corr_Mak_RT11_PBS15	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGACTCCTGCGGAGAAGTCTGCCGTT	21560	11	15		122
HBB8_corr_Mak_RT11_PBS14	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGACTCCTGCGGAGAAGTCTGCCGT	21561	11	14		121
HBB8_corr_Mak_RT11_PBS13	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGACTCCTGCGGAGAAGTCTGCCG	21562	11	13		120
HBB8_corr_Mak_RT11_PBS12	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGACTCCTGCGGAGAAGTCTGCC	21563	11	12		119
HBB8_corr_Mak_RT11_PBS11	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGACTCCTGCGGAGAAGTCTGC	21564	11	11		118
HBB8_corr_Mak_RT11_PBS10	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGACTCCTGCGGAGAAGTCTG	21565	11	10		117

HBB8_corr_Mak_RT11_PBS9	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGACTCCTGCGGAGAAGTCT	21566	11	9	116
HBB8_corr_Mak_RT11_PBS8	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGACTCCTGCGGAGAAGTC	21567	11	8	115
HBB8_corr_Mak_RT10_PBS17	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGACTCCTGCGGAGAAGTCTGCCGTTAC	21568	10	17	123
HBB8_corr_Mak_RT10_PBS16	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGACTCCTGCGGAGAAGTCTGCCGTTA	21569	10	16	122
HBB8_corr_Mak_RT10_PBS15	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGACTCCTGCGGAGAAGTCTGCCGTT	21570	10	15	121
HBB8_corr_Mak_RT10_PBS14	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGACTCCTGCGGAGAAGTCTGCCGT	21571	10	14	120
HBB8_corr_Mak_RT10_PBS13	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGACTCCTGCGGAGAAGTCTGCCG	21572	10	13	119
HBB8_corr_Mak_RT10_PBS12	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGACTCCTGCGGAGAAGTCTGCC	21573	10	12	118
HBB8_corr_Mak_RT10_PBS11	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGACTCCTGCGGAGAAGTCTGC	21574	10	11	117
HBB8_corr_Mak_RT10_PBS10	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGACTCCTGCGGAGAAGTCTG	21575	10	10	116
HBB8_corr_Mak_RT10_PBS9	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGACTCCTGCGGAGAAGTCT	21576	10	9	115
HBB8_corr_Mak_RT10_PBS8	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGACTCCTGCGGAGAAGTC	21577	10	8	114

HBB8_corr_Mak_RT9_PBS17	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTCCTGCGGAGAAGTCTGCCGTTAC	21578	9	17	122
HBB8_corr_Mak_RT9_PBS16	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTCCTGCGGAGAAGTCTGCCGTTA	21579	9	16	121
HBB8_corr_Mak_RT9_PBS15	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTCCTGCGGAGAAGTCTGCCGTT	21580	9	15	120
HBB8_corr_Mak_RT9_PBS14	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTCCTGCGGAGAAGTCTGCCGT	21581	9	14	119
HBB8_corr_Mak_RT9_PBS13	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTCCTGCGGAGAAGTCTGCCG	21582	9	13	118
HBB8_corr_Mak_RT9_PBS12	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTCCTGCGGAGAAGTCTGCC	21583	9	12	117
HBB8_corr_Mak_RT9_PBS11	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTCCTGCGGAGAAGTCTGC	21584	9	11	116
HBB8_corr_Mak_RT9_PBS10	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTCCTGCGGAGAAGTCTG	21585	9	10	115
HBB8_corr_Mak_RT9_PBS9	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTCCTGCGGAGAAGTCT	21586	9	9	114
HBB8_corr_Mak_RT9_PBS8	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTCCTGCGGAGAAGTC	21587	9	8	113
HBB8_corr_Mak_RT8_PBS17	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCCTGCGGAGAAGTCTGCCGTTAC	21588	8	17	121
HBB8_corr_Mak_RT8_PBS16	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCCTGCGGAGAAGTCTGCCGTTA	21589	8	16	120

HBB8_corr_Mak_RT8_PBS15	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCCTGCGGAGAAGTCTGCCGTT	21590	8	15	119
HBB8_corr_Mak_RT8_PBS14	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCCTGCGGAGAAGTCTGCCGT	21591	8	14	118
HBB8_corr_Mak_RT8_PBS13	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCCTGCGGAGAAGTCTGCCG	21592	8	13	117
HBB8_corr_Mak_RT8_PBS12	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCCTGCGGAGAAGTCTGCC	21593	8	12	116
HBB8_corr_Mak_RT8_PBS11	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCCTGCGGAGAAGTCTGC	21594	8	11	115
HBB8_corr_Mak_RT8_PBS10	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCCTGCGGAGAAGTCTG	21595	8	10	114
HBB8_corr_Mak_RT8_PBS9	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCCTGCGGAGAAGTCT	21596	8	9	113
HBB8_corr_Mak_RT8_PBS8	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCCTGCGGAGAAGTC	21597	8	8	112

In some embodiments, the systems and methods provided herein may comprise second strand-targeting gRNAs comprising a spacer sequence listed in **Table 6A**. Table 6A provides exemplary second strand-targeting gRNA spacer sequences (Column 2) designed to be paired with a gene modifying polypeptide and a template RNA to correct a mutation in the HBB gene.

In some embodiments, the second strand-targeting gRNA targets a sequence overlapping the target mutation of the template RNA. In some embodiments, such an overlapping second strand-targeting gRNA comprises a sequence (e.g., spacer sequence) complementary to the sickle cell mutation. In some embodiments, such an overlapping second strand-targeting gRNA comprises a

sequence (e.g., spacer sequence) complementary to the wild-type sequence at the sickle cell locus. In some embodiments, such an overlapping second strand-targeting gRNA comprises a sequence (e.g., spacer sequence) complementary to the Makassar sequence at the sickle cell locus. In some embodiments, such an overlapping second strand-targeting gRNA comprises a sequence (e.g., spacer sequence) complementary to a SNP proximal to the sickle cell locus, e.g., a SNP contained in the genomic DNA of a subject (e.g., a patient). In some embodiments, such an overlapping second strand-targeting gRNA comprises a sequence (e.g., spacer sequence) complementary to or comprising one or more silent substitutions proximal to the sickle cell locus. Examples of such second strand-targeting gRNAs can be found in Table 6A.

Table 6A. Exemplary second-strand targeting (second-nick) gRNA sequences

Table 6A provides spacer sequences for second strand-targeting gRNAs and relevant characteristics. Second-nick gRNAs in this table are designed to be used in combination with template RNAs comprising either the HBB5 (SEQ ID NO: 19249) or HBB8 (SEQ ID NO:19971) spacers, as noted in Column 5. PAM orientation is included in Column 4. In some embodiments, second-nick gRNA is selected with preference for a distance of less than or equal to 100 nt from the first nick (i.e., the nick specified by the template RNA). In some embodiments, a second-nick gRNA is selected with a preference for a PAM-in orientation with the template RNA of the gene modifying system, as described elsewhere in this application.

Name	Second-strand-targeting gRNA	SEQ ID NO	PAM orientation	Spacer
HBB5_27_rev	GGGTGTGGCTCCACAGGGTG	21598	PAM out	HBB5
HBB5_32_rev	CCCTAGGGTGTGGCTCCACA	21599	PAM out	HBB5
HBB5_33_rev	ACCCTAGGGTGTGGCTCCAC	21600	PAM out	HBB5
HBB5_42_rev	GATTGGCCAACCCTAGGGTG	21601	PAM out	HBB5
HBB5_47_rev	GAGTAGATTGGCCAACCCTA	21602	PAM out	HBB5
HBB5_48_rev	GGAGTAGATTGGCCAACCCT	21603	PAM out	HBB5
HBB5_59_rev	CCCTGCTCCTGGGAGTAGAT	21604	PAM out	HBB5
HBB5_69_rev	CTCCTGCCCTCCCTGCTCCT	21605	PAM out	HBB5

HBB5_70_rev	GCTCCTGCCCTCCCTGCTCC	21606	PAM out	HBB5
HBB5_92_rev	CTGACTTTTATGCCCAGCCC	21607	PAM out	HBB5
HBB5_122_rev	AAGCAAATGTAAGCAATAGA	21608	PAM out	HBB5
HBB5_170_rev	TGCACCATGGTGTCTGTTTG	21609	PAM out	HBB5
HBB5_g24	CTCAGGAGTCAGATGCACCA	21610	PAM out	HBB5
HBB5_g34	CAGACTTCTCCTCAGGAGTC	21611	PAM out	HBB5
HBB5_g34_mut	CAGACTTCTCtgCAGGAGTC	21612	PAM out	HBB5
HBB5_g34_mut2	CAGACTTCTCtgccGGAGTC	21613	PAM out	HBB5
HBB5_g34_mut3	CAGACTTCTCttccGGAGTC	21614	PAM out	HBB5
HBB5_g34_mut4	CAGACTTCTCgtccGGAGTC	21615	PAM out	HBB5
HBB5_g34_mut5	CAGACTTCTCatccGGAGTC	21616	PAM out	HBB5
HBB5_g41	GTAACGGCAGACTTCTCCTC	21617	PAM in	HBB5
HBB5_g41_mut	GTAACGGCAGACTTCTCtgC	21618	PAM in	HBB5
HBB5_g41_mut2	GTAACGGCAGACTTCTCttc	21619	PAM in	HBB5
HBB5_g41_mut3	GTAACGGCAGACTTCTCgtc	21620	PAM in	HBB5
HBB5_g41_mut4	GTAACGGCAGACTTCTCatc	21621	PAM in	HBB5
HBB5_216_rev	CTTGCCCCACAGGGCAGTAA	21622	PAM in	HBB5
HBB5_g37	CACGTTCACCTTGCCCCACA	21623	PAM in	HBB5
HBB5_g38	CCACGTTCACCTTGCCCCAC	21624	PAM in	HBB5
HBB5_g27	CCTTGATACCAACCTGCCCA	21625	PAM in	HBB5
HBB5_g39	ACCTTGATACCAACCTGCCC	21626	PAM in	HBB5
HBB5_g40	TCCACATGCCCAGTTTCTAT	21627	PAM in	HBB5
HBB8_37_fw	ATCACTTAGACCTCACCCTG	21628	PAM in	HBB8
HBB8_51_fw	ACCCTGTGGAGCCACACCCT	21629	PAM in	HBB8
HBB8_52_fw	CCCTGTGGAGCCACACCCTA	21630	PAM in	HBB8
HBB8_56_fw	GTGGAGCCACACCCTAGGGT	21631	PAM in	HBB8
HBB8_72_fw	GGGTTGGCCAATCTACTCCC	21632	PAM in	HBB8
HBB8_78_fw	GCCAATCTACTCCCAGGAGC	21633	PAM in	HBB8
HBB8_79_fw	CCAATCTACTCCCAGGAGCA	21634	PAM in	HBB8

HBB8_82_fw	ATCTACTCCCAGGAGCAGGG	21635	PAM in	HBB8
HBB8_83_fw	TCTACTCCCAGGAGCAGGGA	21636	PAM in	HBB8
HBB8_87_fw	CTCCCAGGAGCAGGGAGGGC	21637	PAM in	HBB8
HBB8_94_fw	GAGCAGGGAGGGCAGGAGCC	21638	PAM in	HBB8
HBB8_95_fw	AGCAGGGAGGGCAGGAGCCA	21639	PAM in	HBB8
HBB8_99_fw	GGGAGGGCAGGAGCCAGGGC	21640	PAM in	HBB8
HBB8_g4	GGAGGGCAGGAGCCAGGGCT	21641	PAM in	HBB8
HBB8_g1	CAGGGCTGGGCATAAAAGTC	21642	PAM in	HBB8
HBB8_g2	AGGGCTGGGCATAAAAGTCA	21643	PAM in	HBB8
HBB8_g3	GCAACCTCAAACAGACACCA	21644	PAM in	HBB8
HBB8_204_fw	CATGGTGCATCTGACTCCTG	21645	PAM in	HBB8
HBB8_204_fw_mut	CATGGTGCACCTGACTCCTG	21646	PAM in	HBB8
HBB8_230_fw	AGTCTGCCGTTACTGCCCTG	21647	PAM out	HBB8
HBB8_231_fw	GTCTGCCGTTACTGCCCTGT	21648	PAM out	HBB8
HBB8_232_fw	TCTGCCGTTACTGCCCTGTG	21649	PAM out	HBB8
HBB8_237_fw	CGTTACTGCCCTGTGGGGCA	21650	PAM out	HBB8
HBB8_246_fw	CCTGTGGGGCAAGGTGAACG	21651	PAM out	HBB8
HBB8_256_fw	AAGGTGAACGTGGATGAAGT	21652	PAM out	HBB8
HBB8_259_fw	GTGAACGTGGATGAAGTTGG	21653	PAM out	HBB8
HBB8_264_fw	CGTGGATGAAGTTGGTGGTG	21654	PAM out	HBB8
HBB8_270_fw	TGAAGTTGGTGGTGAGGCCC	21655	PAM out	HBB8
HBB8_271_fw	GAAGTTGGTGGTGAGGCCCT	21656	PAM out	HBB8
HBB8_275_fw	TTGGTGGTGAGGCCCTGGGC	21657	PAM out	HBB8
HBB8_279_fw	TGGTGAGGCCCTGGGCAGGT	21658	PAM out	HBB8
HBB8_287_fw	CCCTGGGCAGGTTGGTATCA	21659	PAM out	HBB8
HBB8_299_fw	TGGTATCAAGGTTACAAGAC	21660	PAM out	HBB8
HBB8_306_fw	AAGGTTACAAGACAGGTTTA	21661	PAM out	HBB8
HBB8_323_fw	TTAAGGAGACCAATAGAAAC	21662	PAM out	HBB8
HBB8_324_fw	TAAGGAGACCAATAGAAACT	21663	PAM out	HBB8

HBB8_331_fw	ACCAATAGAAACTGGGCATG	21664	PAM out	HBB8
HBB8_350_fw	GTGGAGACAGAGAAGACTCT	21665	PAM out	HBB8
HBB8_351_fw	TGGAGACAGAGAAGACTCTT	21666	PAM out	HBB8
HBB8_362_fw	AAGACTCTTGGGTTTCTGAT	21667	PAM out	HBB8

The template RNA sequences shown in Tables 1-4, 5A-5D, and 6A may be customized depending on the cell being targeted. For example, in some embodiments it is desired to inactivate a PAM sequence upon editing (e.g., using a "PAM-kill" modification) to decrease the potential for further gene editing (e.g., by Cas retargeting) following the initial edit. Consequently, certain template RNAs described herein are designed to write a mutation (e.g., a substitution) into the PAM of the target site, such that upon editing, the PAM site will be mutated to a sequence no longer recognized by the gene modifying polypeptide. Thus, a mutation region within the heterologous object sequence of the template RNA may comprise a PAM-kill sequence. Without wishing to be bound by theory, in some embodiments, a PAM-kill sequence prevents re-engagement of the gene modifying polypeptide upon completion of a genetic modification, or decreases re-engagement relative to a template RNA lacking a PAM-kill sequence. In some embodiments, a PAM-kill sequence does not alter the amino acid sequence encoded by a gene, e.g., the PAM-kill sequence results in a silent mutation. In other embodiments, it is desired to leave the PAM sequence intact (no PAM-kill).

Similarly, in some embodiments, to decrease the potential for further gene editing (e.g., by Cas retargeting) following the initial edit, it may be desirable to alter the first three nucleotides of the RT template sequence via a "seed-kill" motif. Consequently, certain template RNAs described herein are designed to write a mutation (e.g., a substitution) into the portion of the target site corresponding to the first three nucleotides of the RT template sequence, such that upon editing, the target site will be mutated to a sequence with lower homology to the RT template sequence. Thus, a mutation region within the heterologous object sequence of the template RNA may comprise a seed-kill sequence. Without wishing to be bound by theory, in some embodiments, a seed-kill sequence prevents re-engagement of the gene modifying polypeptide upon completion of genetic modification, or decreases re-engagement relative to an otherwise similar template RNA lacking a seed-kill sequence. In some embodiments, a seed-kill sequence does not alter the amino acid sequence encoded by a gene, e.g., the seed-kill sequence results in a silent mutation. In other embodiments, it is desired to leave the seed region intact, and a seed-kill sequence is not used.

In further embodiments, to optimize or improve gene editing efficiency, it may be desirable to evade the target cell's mismatch repair or nucleotide repair pathways or to bias the target cell's repair pathways toward preservation of the edited strand. In some embodiments,

multiple silent mutations (for example, silent substitutions) may be introduced within the RT template sequence to evade the target cell's mismatch repair or nucleotide repair pathways or to bias the target cell's repair pathways toward preservation of the edited strand.

Table 7A provides exemplary silent mutations for various positions within the HBB gene.

Table 7A. Exemplary Silent Mutation Codons for the HBB Gene

Amino Acid Position (counting initial Met)	WT Amino Acid	WT CODON	ALL CODONS					
2	V	GTG	GTT	GTC	GTA	GTG		
3	H	CAT	CAT	CAC				
4	L	CTG	TTA	TTG	CTT	CTC	CTA	CTG
5	T	ACT	ACT	ACC	ACA	ACG		
6	P	CCT	CCT	CCC	CCA	CCG		
8	E	GAG	GAA	GAG				
9	K	AAG	AAA	AAG				
10	S	TCT	TCT	TCC	TCA	TCG	AGT	AGC
11	A	GCC	GCT	GCC	GCA	GCG		
12	V	GTT	GTT	GTC	GTA	GTG		
13	T	ACT	ACT	ACC	ACA	ACG		
14	A	GCC	GCT	GCC	GCA	GCG		
15	L	CTG	TTA	TTG	CTT	CTC	CTA	CTG
16	W	TGG	TGG					
17	G	GGC	GGT	GGC	GGA	GGG		
18	K	AAG	AAA	AAG				
19	V	GTG	GTT	GTC	GTA	GTG		
20	N	AAC	AAT	AAC				
21	V	GTG	GTT	GTC	GTA	GTG		
22	D	GAT	GAT	GAC				
23	E	GAA	GAA	GAG				
24	V	GTT	GTT	GTC	GTA	GTG		
25	G	GGT	GGT	GGC	GGA	GGG		
26	G	GGT	GGT	GGC	GGA	GGG		
27	E	GAG	GAA	GAG				
28	A	GCC	GCT	GCC	GCA	GCG		
29	L	CTG	TTA	TTG	CTT	CTC	CTA	CTG
30	G	GGC	GGT	GGC	GGA	GGG		

In some embodiments, the template RNA comprises one or more silent mutations.

In some embodiments, the silent mutation comprises a mutation of the codon encoding the 6th amino acid, counting the initial methionine, of the HBB gene (proline), e.g., to CCC or CCG.

In some embodiments, the template RNA comprises one or more silent substitions as illustrated in Tables X1-X4 herein.

It should be understood that the silent mutations illustrated in Table 7A may be used individually or combined in any manner in a template RNA sequence described herein.

gRNAs with inducible activity

In some embodiments, a gRNA described herein (e.g., a gRNA that is part of a template RNA or a gRNA used for second strand nicking) has inducible activity. Inducible activity may be achieved by the template nucleic acid, e.g., template RNA, further comprising (in addition to the gRNA) a blocking domain, wherein the sequence of a portion of or all of the blocking domain is at least partially complementary to a portion or all of the gRNA. The blocking domain is thus capable of hybridizing or substantially hybridizing to a portion of or all of the gRNA. In some embodiments, the blocking domain and inducibly active gRNA are disposed on the template nucleic acid, e.g., template RNA, such that the gRNA can adopt a first conformation where the blocking domain is hybridized or substantially hybridized to the gRNA, and a second conformation where the blocking domain is not hybridized or not substantially hybridized to the gRNA. In some embodiments, in the first conformation the gRNA is unable to bind to the gene modifying polypeptide (e.g., the template nucleic acid binding domain, DNA binding domain, or endonuclease domain (e.g., a CRISPR/Cas protein)) or binds with substantially decreased affinity compared to an otherwise similar template RNA lacking the blocking domain. In some embodiments, in the second conformation the gRNA is able to bind to the gene modifying polypeptide (e.g., the template nucleic acid binding domain, DNA binding domain, or endonuclease domain (e.g., a CRISPR/Cas protein)). In some embodiments, whether the gRNA is in the first or second conformation can influence whether the DNA binding or endonuclease activities of the gene modifying polypeptide (e.g., of the CRISPR/Cas protein the gene modifying polypeptide comprises) are active.

In some embodiments, the gRNA that coordinates the second nick has inducible activity. In some embodiments, the gRNA that coordinates the second nick is induced after the template is reverse transcribed. In some embodiments, hybridization of the gRNA to the blocking domain can be disrupted using an opener molecule. In some embodiments, an opener molecule comprises an agent that binds to a portion or all of the gRNA or blocking domain and inhibits hybridization of the gRNA to the blocking domain. In some embodiments, the opener molecule comprises a nucleic acid, e.g., comprising a sequence that is partially or wholly complementary to the gRNA, blocking domain, or both. By choosing or designing an appropriate opener molecule, providing the opener molecule can promote a change in the conformation of the gRNA such that it can associate with a CRISPR/Cas protein and provide the associated functions of the CRISPR/Cas protein (e.g., DNA binding and/or endonuclease activity). Without wishing to be bound by theory, providing the opener molecule at a selected time and/or location may allow for spatial and temporal control of the activity of the gRNA, CRISPR/Cas protein, or gene modifying system comprising the same. In some embodiments, the opener molecule is exogenous to the cell comprising the gene modifying polypeptide and or template nucleic acid. In some embodiments, the opener molecule comprises an endogenous agent (e.g., endogenous to the cell comprising the gene modifying polypeptide and or template nucleic acid comprising the gRNA and blocking domain). For example, an inducible gRNA, blocking domain, and opener molecule may be chosen such that the opener molecule is an endogenous agent expressed in a target cell or tissue, e.g., thereby ensuring activity of a gene modifying system in the target cell or tissue. As a further example, an inducible gRNA, blocking domain, and opener molecule may be chosen such that the opener molecule is absent or not substantially expressed in one or more non-target cells or tissues, e.g., thereby ensuring that activity of a gene modifying system does not occur or substantially occur in the one or more non-target cells or tissues, or occurs at a reduced level compared to a target cell or tissue. Exemplary blocking domains, opener molecules, and uses thereof are described in PCT App. Publication WO2020044039A1, which is incorporated herein by reference in its entirety. In some embodiments, the template nucleic acid, e.g., template RNA, may comprise one or more sequences or structures for binding by one or more components of a gene modifying polypeptide, e.g., by a reverse transcriptase or RNA binding domain, and a gRNA. In some embodiments, the gRNA facilitates interaction with the template nucleic acid binding domain (e.g., RNA binding domain) of the gene modifying

polypeptide. In some embodiments, the gRNA directs the gene modifying polypeptide to the matching target sequence, e.g., in a target cell genome.

Circular RNAs and Ribozymes in Gene Modifying Systems

It is contemplated that it may be useful to employ circular and/or linear RNA states during the formulation, delivery, or gene modifying reaction within the target cell. Thus, in some embodiments of any of the aspects described herein, a gene modifying system comprises one or more circular RNAs (circRNAs). In some embodiments of any of the aspects described herein, a gene modifying system comprises one or more linear RNAs. In some embodiments, a nucleic acid as described herein (e.g., a template nucleic acid, a nucleic acid molecule encoding a gene modifying polypeptide, or both) is a circRNA. In some embodiments, a circular RNA molecule encodes the gene modifying polypeptide. In some embodiments, the circRNA molecule encoding the gene modifying polypeptide is delivered to a host cell. In some embodiments, a circular RNA molecule encodes a recombinase, e.g., as described herein. In some embodiments, the circRNA molecule encoding the recombinase is delivered to a host cell. In some embodiments, the circRNA molecule encoding the gene modifying polypeptide is linearized (e.g., in the host cell, e.g., in the nucleus of the host cell) prior to translation.

Circular RNAs (circRNAs) have been found to occur naturally in cells and have been found to have diverse functions, including both non-coding and protein coding roles in human cells. It has been shown that a circRNA can be engineered by incorporating a self-splicing intron into an RNA molecule (or DNA encoding the RNA molecule) that results in circularization of the RNA, and that an engineered circRNA can have enhanced protein production and stability (Wesselhoeft et al. *Nature Communications* 2018). In some embodiments, the gene modifying polypeptide is encoded as circRNA. In certain embodiments, the template nucleic acid is a DNA, such as a dsDNA or ssDNA. In certain embodiments, the circDNA comprises a template RNA.

In some embodiments, the circRNA comprises one or more ribozyme sequences. In some embodiments, the ribozyme sequence is activated for autocleavage, e.g., in a host cell, e.g., thereby resulting in linearization of the circRNA. In some embodiments, the ribozyme is activated when the concentration of magnesium reaches a sufficient level for cleavage, e.g., in a host cell. In some embodiments the circRNA is maintained in a low magnesium environment prior to delivery to the host cell. In some embodiments, the ribozyme is a protein-responsive

ribozyme. In some embodiments, the ribozyme is a nucleic acid-responsive ribozyme. In some embodiments, the circRNA comprises a cleavage site. In some embodiments, the circRNA comprises a second cleavage site.

In some embodiments, the circRNA is linearized in the nucleus of a target cell. In some embodiments, linearization of a circRNA in the nucleus of a cell involves components present in the nucleus of the cell, e.g., to activate a cleavage event. In some embodiments, a ribozyme, e.g., a ribozyme from a B2 or ALU element, that is responsive to a nuclear element, e.g., a nuclear protein, e.g., a genome-interacting protein, e.g., an epigenetic modifier, e.g., EZH2, is incorporated into a circRNA, e.g., of a gene modifying system. In some embodiments, nuclear localization of the circRNA results in an increase in autocatalytic activity of the ribozyme and linearization of the circRNA.

In some embodiments, the ribozyme is heterologous to one or more of the other components of the gene modifying system. In some embodiments, an inducible ribozyme (e.g., in a circRNA as described herein) is created synthetically, for example, by utilizing a protein ligand-responsive aptamer design. A system for utilizing the satellite RNA of tobacco ringspot virus hammerhead ribozyme with an MS2 coat protein aptamer has been described (Kennedy et al. Nucleic Acids Res 42(19):12306-12321 (2014), incorporated herein by reference in its entirety) that results in activation of the ribozyme activity in the presence of the MS2 coat protein. In embodiments, such a system responds to protein ligand localized to the cytoplasm or the nucleus. In some embodiments the protein ligand is not MS2. Methods for generating RNA aptamers to target ligands have been described, for example, based on the systematic evolution of ligands by exponential enrichment (SELEX) (Tuerk and Gold, Science 249(4968):505-510 (1990); Ellington and Szostak, Nature 346(6287):818-822 (1990); the methods of each of which are incorporated herein by reference) and have, in some instances, been aided by *in silico* design (Bell et al. PNAS 117(15):8486-8493, the methods of which are incorporated herein by reference). Thus, in some embodiments, an aptamer for a target ligand is generated and incorporated into a synthetic ribozyme system, e.g., to trigger ribozyme-mediated cleavage and circRNA linearization, e.g., in the presence of the protein ligand. In some embodiments, circRNA linearization is triggered in the cytoplasm, e.g., using an aptamer that associates with a ligand in the cytoplasm. In some embodiments, circRNA linearization is triggered in the nucleus,

e.g., using an aptamer that associates with a ligand in the nucleus. In embodiments, the ligand in the nucleus comprises an epigenetic modifier or a transcription factor. In some embodiments the ligand that triggers linearization is present at higher levels in on-target cells than off-target cells.

It is further contemplated that a nucleic acid-responsive ribozyme system can be employed for circRNA linearization. For example, biosensors that sense defined target nucleic acid molecules to trigger ribozyme activation are described, e.g., in Penchovsky (Biotechnology Advances 32(5):1015-1027 (2014), incorporated herein by reference). By these methods, a ribozyme naturally folds into an inactive state and is only activated in the presence of a defined target nucleic acid molecule (e.g., an RNA molecule). In some embodiments, a circRNA of a gene modifying system comprises a nucleic acid-responsive ribozyme that is activated in the presence of a defined target nucleic acid, e.g., an RNA, e.g., an mRNA, miRNA, guide RNA, gRNA, sgRNA, ncRNA, lncRNA, tRNA, snRNA, or mtRNA. In some embodiments the nucleic acid that triggers linearization is present at higher levels in on-target cells than off-target cells.

In some embodiments of any of the aspects herein, a gene modifying system incorporates one or more ribozymes with inducible specificity to a target tissue or target cell of interest, e.g., a ribozyme that is activated by a ligand or nucleic acid present at higher levels in a target tissue or target cell of interest. In some embodiments, the gene modifying system incorporates a ribozyme with inducible specificity to a subcellular compartment, e.g., the nucleus, nucleolus, cytoplasm, or mitochondria. In some embodiments, the ribozyme that is activated by a ligand or nucleic acid present at higher levels in the target subcellular compartment. In some embodiments, an RNA component of a gene modifying system is provided as circRNA, e.g., that is activated by linearization. In some embodiments, linearization of a circRNA encoding a gene modifying polypeptide activates the molecule for translation. In some embodiments, a signal that activates a circRNA component of a gene modifying system is present at higher levels in on-target cells or tissues, e.g., such that the system is specifically activated in these cells.

In some embodiments, an RNA component of a gene modifying system is provided as a circRNA that is inactivated by linearization. In some embodiments, a circRNA encoding the gene modifying polypeptide is inactivated by cleavage and degradation. In some embodiments, a circRNA encoding the gene modifying polypeptide is inactivated by cleavage that separates a translation signal from the coding sequence of the polypeptide. In some embodiments, a signal

that inactivates a circRNA component of a gene modifying system is present at higher levels in off-target cells or tissues, such that the system is specifically inactivated in these cells.

Target Nucleic Acid Site

In some embodiments, after gene modification, the target site surrounding the edited sequence contains a limited number of insertions or deletions, for example, in less than about 50% or 10% of editing events, e.g., as determined by long-read amplicon sequencing of the target site, e.g., as described in Karst et al. (2020) *bioRxiv* doi.org/10.1101/645903 (incorporated by reference herein in its entirety). In some embodiments, the target site does not show multiple consecutive editing events, e.g., head-to-tail or head-to-head duplications, e.g., as determined by long-read amplicon sequencing of the target site, e.g., as described in Karst et al. *bioRxiv* doi.org/10.1101/645903 (2020) (incorporated herein by reference in its entirety). In some embodiments, the target site contains an integrated sequence corresponding to the template RNA. In some embodiments, the target site does not contain insertions resulting from endogenous RNA in more than about 1% or 10% of events, e.g., as determined by long-read amplicon sequencing of the target site, e.g., as described in Karst et al. *bioRxiv* doi.org/10.1101/645903 (2020) (incorporated herein by reference in its entirety). In some embodiments, the target site contains the integrated sequence corresponding to the template RNA.

In certain aspects of the present invention, the host DNA-binding site integrated into by the gene modifying system can be in a gene, in an intron, in an exon, an ORF, outside of a coding region of any gene, in a regulatory region of a gene, or outside of a regulatory region of a gene. In other aspects, the polypeptide may bind to one or more than one host DNA sequence.

In some embodiments, a gene modifying system is used to edit a target locus in multiple alleles. In some embodiments, a gene modifying system is designed to edit a specific allele. For example, a gene modifying polypeptide may be directed to a specific sequence that is only present on one allele, e.g., comprises a template RNA with homology to a target allele, e.g., a gRNA or annealing domain, but not to a second cognate allele. In some embodiments, a gene modifying system can alter a haplotype-specific allele. In some embodiments, a gene modifying system that targets a specific allele preferentially targets that allele, e.g., has at least a 2, 4, 6, 8, or 10-fold preference for a target allele.

Second Strand Nicking

In some embodiments, a gene modifying system described herein comprises a nickase activity (e.g., in the gene modifying polypeptide) that nicks the first strand, and a nickase activity (e.g., in a polypeptide separate from the gene modifying polypeptide) that nicks the second strand of target DNA. As discussed herein, without wishing to be bound by theory, nicking of the first strand of the target site DNA is thought to provide a 3′ OH that can be used by an RT domain to reverse transcribe a sequence of a template RNA, e.g., a heterologous object sequence. Without wishing to be bound by theory, it is thought that introducing an additional nick to the second strand may bias the cellular DNA repair machinery to adopt the heterologous object sequence-based sequence more frequently than the original genomic sequence. In some embodiments, the additional nick to the second strand is made by the same endonuclease domain (e.g., nickase domain) as the nick to the first strand. In some embodiments, the same gene modifying polypeptide performs both the nick to the first strand and the nick to the second strand. In some embodiments, the gene modifying polypeptide comprises a CRISPR/Cas domain and the additional nick to the second strand is directed by an additional nucleic acid, e.g., comprising a second gRNA directing the CRISPR/Cas domain to nick the second strand. In other embodiments, the additional second strand nick is made by a different endonuclease domain (e.g., nickase domain) than the nick to the first strand. In some embodiments, that different endonuclease domain is situated in an additional polypeptide (e.g., a system of the invention further comprises the additional polypeptide), separate from the gene modifying polypeptide. In some embodiments, the additional polypeptide comprises an endonuclease domain (e.g., nickase domain) described herein. In some embodiments, the additional polypeptide comprises a DNA binding domain, e.g., described herein.

It is contemplated herein that the position at which the second strand nick occurs relative to the first strand nick may influence the extent to which one or more of: desired gene modifying DNA modifications are obtained, undesired double-strand breaks (DSBs) occur, undesired insertions occur, or undesired deletions occur. Without wishing to be bound by theory, second strand nicking may occur in two general orientations: inward nicks and outward nicks.

In some embodiments, in the inward nick orientation, the RT domain polymerizes (e.g., using the template RNA (e.g., the heterologous object sequence)) away from the second strand nick. In some embodiments, in the inward nick orientation, the location of the nick to the first

strand and the location of the nick to the second strand are positioned between the first PAM site and second PAM site (e.g., in a scenario wherein both nicks are made by a polypeptide (e.g., a gene modifying polypeptide) comprising a CRISPR/Cas domain). When there are two PAMs on the outside and two nicks on the inside, this inward nick orientation can also be referred to as "PAM-out". In some embodiments, in the inward nick orientation, the location of the nick to the first strand and the location of the nick to the second strand are between the sites where the polypeptide and the additional polypeptide bind to the target DNA. In some embodiments, in the inward nick orientation, the location of the nick to the second strand is positioned between the binding sites of the polypeptide and additional polypeptide, and the nick to the first strand is also located between the binding sites of the polypeptide and additional polypeptide. In some embodiments, in the inward nick orientation, the location of the nick to the first strand and the location of the nick to the second strand are positioned between the PAM site and the binding site of the second polypeptide which is at a distance from the target site.

An example of a gene modifying system that provides an inward nick orientation comprises a gene modifying polypeptide comprising a CRISPR/Cas domain, a template RNA comprising a gRNA that directs nicking of the target site DNA on the first strand, and an additional nucleic acid comprising an additional gRNA that directs nicking at a site a distance from the location of the first nick, wherein the location of the first nick and the location of the second nick are between the PAM sites of the sites to which the two gRNAs direct the gene modifying polypeptide. As a further example, another gene modifying system that provides an inward nick orientation comprises a gene modifying polypeptide comprising a zinc finger molecule and a first nickase domain wherein the zinc finger molecule binds to the target DNA in a manner that directs the first nickase domain to nick the first strand of the target site; an additional polypeptide comprising a CRISPR/Cas domain, and an additional nucleic acid comprising a gRNA that directs the additional polypeptide to nick a site a distance from the target site DNA on the second strand, wherein the location of the first nick and the location of the second nick are between the PAM site and the site to which the zinc finger molecule binds. As a further example, another gene modifying system that provides an inward nick orientation comprises a gene modifying polypeptide comprising a zinc finger molecule and a first nickase domain wherein the zinc finger molecule binds to the target DNA in a manner that directs the first nickase domain to nick the first strand of the target site; an additional polypeptide

comprising a TAL effector molecule and a second nickase domain wherein the TAL effector molecule binds to a site a distance from the target site in a manner that directs the additional polypeptide to nick the second strand, wherein the location of the first nick and the location of the second nick are between the site to which the TAL effector molecule binds and the site to which the zinc finger molecule binds.

In some embodiments, in the outward nick orientation, the RT domain polymerizes (e.g., using the template RNA (e.g., the heterologous object sequence)) toward the second strand nick. In some embodiments, in the outward nick orientation when both the first and second nicks are made by a polypeptide comprising a CRISPR/Cas domain (e.g., a gene modifying polypeptide), the first PAM site and second PAM site are positioned between the location of the nick to the first strand and the location of the nick to the second strand. When there are two PAMs on the inside and two nicks on the outside, this outward nick orientation also can be referred to as "PAM-in". In some embodiments, in the outward nick orientation, the polypeptide (e.g., the gene modifying polypeptide) and the additional polypeptide bind to sites on the target DNA between the location of the nick to the first strand and the location of the nick to the second. In some embodiments, in the outward nick orientation, the location of the nick to the second strand is positioned on the opposite side of the binding sites of the polypeptide and additional polypeptide relative to the location of the nick to the first strand. In some embodiments, in the outward orientation, the PAM site and the binding site of the second polypeptide which is at a distance from the target site are positioned between the location of the nick to the first strand and the location of the nick to the second strand.

An example of a gene modifying system that provides an outward nick orientation comprises a gene modifying polypeptide comprising a CRISPR/Cas domain, a template RNA comprising a gRNA that directs nicking of the target site DNA on the first strand, and an additional nucleic acid comprising an additional gRNA that directs nicking at a site a distance from the location of the first nick, wherein the location of the first nick and the location of the second nick are outside of the PAM sites of the sites to which the two gRNAs direct the gene modifying polypeptide (i.e., the PAM sites are between the location of the first nick and the location of the second nick). As a further example, another gene modifying system that provides an outward nick orientation comprises a gene modifying polypeptide comprising a zinc finger molecule and a first nickase domain wherein the zinc finger molecule binds to the target DNA in

a manner that directs the first nickase domain to nick the first strand of the target site; an additional polypeptide comprising a CRISPR/Cas domain, and an additional nucleic acid comprising a gRNA that directs the additional polypeptide to nick a site a distance from the target site DNA on the second strand, wherein the location of the first nick and the location of the second nick are outside the PAM site and the site to which the zinc finger molecule binds (i.e., the PAM site and the site to which the zinc finger molecule binds are between the location of the first nick and the location of the second nick). As a further example, another gene modifying system that provides an outward nick orientation comprises a gene modifying polypeptide comprising a zinc finger molecule and a first nickase domain wherein the zinc finger molecule binds to the target DNA in a manner that directs the first nickase domain to nick the first strand of the target site; an additional polypeptide comprising a TAL effector molecule and a second nickase domain wherein the TAL effector molecule binds to a site a distance from the target site in a manner that directs the additional polypeptide to nick the second strand, wherein the location of the first nick and the location of the second nick are outside the site to which the TAL effector molecule binds and the site to which the zinc finger molecule binds (i.e., the site to which the TAL effector molecule binds and the site to which the zinc finger molecule binds are between the location of the first nick and the location of the second nick).

Without wishing to be bound by theory, it is thought that, for gene modifying systems where a second strand nick is provided, an outward nick orientation is preferred in some embodiments. As is described herein, an inward nick may produce a higher number of double-strand breaks (DSBs) than an outward nick orientation. DSBs may be recognized by the DSB repair pathways in the nucleus of a cell, which can result in undesired insertions and deletions. An outward nick orientation may provide a decreased risk of DSB formation, and a corresponding lower amount of undesired insertions and deletions. In some embodiments, undesired insertions and deletions are insertions and deletions not encoded by the heterologous object sequence, e.g., an insertion or deletion produced by the double-strand break repair pathway unrelated to the modification encoded by the heterologous object sequence. In some embodiments, a desired gene modification comprises a change to the target DNA (e.g., a substitution, insertion, or deletion) encoded by the heterologous object sequence (e.g., and achieved by the gene modifying writing the heterologous object sequence into the target site). In some embodiments, the first strand nick and the second strand nick are in an outward orientation.

In addition, the distance between the first strand nick and second strand nick may influence the extent to which one or more of: desired gene modifying system DNA modifications are obtained, undesired double-strand breaks (DSBs) occur, undesired insertions occur, or undesired deletions occur. Without wishing to be bound by theory, it is thought the second strand nick benefit, the biasing of DNA repair toward incorporation of the heterologous object sequence into the target DNA, increases as the distance between the first strand nick and second strand nick decreases. However, it is thought that the risk of DSB formation also increases as the distance between the first strand nick and second strand nick decreases. Correspondingly, it is thought that the number of undesired insertions and/or deletions may increase as the distance between the first strand nick and second strand nick decreases. In some embodiments, the distance between the first strand nick and second strand nick is chosen to balance the benefit of biasing DNA repair toward incorporation of the heterologous object sequence into the target DNA and the risk of DSB formation and of undesired deletions and/or insertions. In some embodiments, a system where the first strand nick and the second strand nick are at least a threshold distance apart has an increased level of desired gene modifying system modification outcomes, a decreased level of undesired deletions, and/or a decreased level of undesired insertions relative to an otherwise similar inward nick orientation system where the first nick and the second nick are less than the a threshold distance apart. In some embodiments the threshold distance(s) is given below.

In some embodiments, the first nick and the second nick are at least 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, or 200 nucleotides apart. In some embodiments, the first nick and the second nick are no more than 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, or 250 nucleotides apart. In some embodiments, the first nick and the second nick are 20-200, 30-200, 40-200, 50-200, 60-200, 70-200, 80-200, 90-200, 100-200, 110-200, 120-200, 130-200, 140-200, 150-200, 160-200, 170-200, 180-200, 190-200, 20-190, 30-190, 40-190, 50-190, 60-190, 70-190, 80-190, 90-190, 100-190, 110-190, 120-190, 130-190, 140-190, 150-190, 160-190, 170-190, 180-190, 20-180, 30-180, 40-180, 50-180, 60-180, 70-180, 80-180, 90-180, 100-180, 110-180, 120-180, 130-180, 140-180, 150-180, 160-180, 170-180, 20-170, 30-170, 40-170, 50-170, 60-170, 70-170, 80-170, 90-170, 100-170, 110-170, 120-170, 130-170, 140-170, 150-170, 160-170, 20-160, 30-160, 40-160, 50-160, 60-160, 70-160, 80-160, 90-160,

100-160, 110-160, 120-160, 130-160, 140-160, 150-160, 20-150, 30-150, 40-150, 50-150, 60-150, 70-150, 80-150, 90-150, 100-150, 110-150, 120-150, 130-150, 140-150, 20-140, 30-140, 40-140, 50-140, 60-140, 70-140, 80-140, 90-140, 100-140, 110-140, 120-140, 130-140, 20-130, 30-130, 40-130, 50-130, 60-130, 70-130, 80-130, 90-130, 100-130, 110-130, 120-130, 20-120, 30-120, 40-120, 50-120, 60-120, 70-120, 80-120, 90-120, 100-120, 110-120, 20-110, 30-110, 40-110, 50-110, 60-110, 70-110, 80-110, 90-110, 100-110, 20-100, 30-100, 40-100, 50-100, 60-100, 70-100, 80-100, 90-100, 20-90, 30-90, 40-90, 50-90, 60-90, 70-90, 80-90, 20-80, 30-80, 40-80, 50-80, 60-80, 70-80, 20-70, 30-70, 40-70, 50-70, 60-70, 20-60, 30-60, 40-60, 50-60, 20-50, 30-50, 40-50, 20-40, 30-40, or 20-30 nucleotides apart. In some embodiments, the first nick and the second nick are 40-100 nucleotides apart.

Without wishing to be bound by theory, it is thought that, for gene modifying systems where a second strand nick is provided and an inward nick orientation is selected, increasing the distance between the first strand nick and second strand nick may be preferred. As is described herein, an inward nick orientation may produce a higher number of DSBs than an outward nick orientation, and may result in a higher amount of undesired insertions and deletions than an outward nick orientation, but increasing the distance between the nicks may mitigate that increase in DSBs, undesired deletions, and/or undesired insertions. In some embodiments, an inward nick orientation wherein the first nick and the second nick are at least a threshold distance apart has an increased level of desired gene modifying system modification outcomes, a decreased level of undesired deletions, and/or a decreased level of undesired insertions relative to an otherwise similar inward nick orientation system where the first nick and the second nick are less than the a threshold distance apart. In some embodiments the threshold distance is given below.

In some embodiments, the first strand nick and the second strand nick are in an inward orientation. In some embodiments, the first strand nick and the second strand nick are in an inward orientation and the first strand nick and second strand nick are at least 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 220, 240, 260, 280, 300, 350, 400, 450, or 500 nucleotides apart, e.g., at least 100 nucleotides apart, (and optionally no more than 500, 400, 300, 200, 190, 180, 170, 160, 150, 140, 130, or 120 nucleotides apart). In some embodiments, the first strand nick and the second strand nick are in an inward orientation and the first strand nick and second strand nick are 100-200, 110-200, 120-200, 130-200, 140-200, 150-200, 160-200, 170-200, 180-

200, 190-200, 100-190, 110-190, 120-190, 130-190, 140-190, 150-190, 160-190, 170-190, 180-190, 100-180, 110-180, 120-180, 130-180, 140-180, 150-180, 160-180, 170-180, 100-170, 110-170, 120-170, 130-170, 140-170, 150-170, 160-170, 100-160, 110-160, 120-160, 130-160, 140-160, 150-160, 100-150, 110-150, 120-150, 130-150, 140-150, 100-140, 110-140, 120-140, 130-140, 100-130, 110-130, 120-130, 100-120, 110-120, or 100-110 nucleotides apart.

Chemically modified nucleic acids and nucleic acid end features

A nucleic acid described herein (e.g., a template nucleic acid, e.g., a template RNA; or a nucleic acid (e.g., mRNA) encoding a gene modifying polypeptide; or a gRNA) can comprise unmodified or modified nucleobases. Naturally occurring RNAs are synthesized from four basic ribonucleotides: ATP, CTP, UTP and GTP, but may contain post-transcriptionally modified nucleotides. Further, approximately one hundred different nucleoside modifications have been identified in RNA (Rozenski, J, Crain, P, and McCloskey, J. (1999). The RNA Modification Database: 1999 update. Nucl Acids Res 27: 196-197). An RNA can also comprise wholly synthetic nucleotides that do not occur in nature.

In some embodiments, the chemical modification is one provided in WO/2016/183482, US Pat. Pub. No. 20090286852, of International Application No. WO/2012/019168, WO/2012/045075, WO/2012/135805, WO/2012/158736, WO/2013/039857, WO/2013/039861, WO/2013/052523, WO/2013/090648, WO/2013/096709, WO/2013/101690, WO/2013/106496, WO/2013/130161, WO/2013/151669, WO/2013/151736, WO/2013/151672, WO/2013/151664, WO/2013/151665, WO/2013/151668, WO/2013/151671, WO/2013/151667, WO/2013/151670, WO/2013/151666, WO/2013/151663, WO/2014/028429, WO/2014/081507, WO/2014/093924, WO/2014/093574, WO/2014/113089, WO/2014/144711, WO/2014/144767, WO/2014/144039, WO/2014/152540, WO/2014/152030, WO/2014/152031, WO/2014/152027, WO/2014/152211, WO/2014/158795, WO/2014/159813, WO/2014/164253, WO/2015/006747, WO/2015/034928, WO/2015/034925, WO/2015/038892, WO/2015/048744, WO/2015/051214, WO/2015/051173, WO/2015/051169, WO/2015/058069, WO/2015/085318, WO/2015/089511, WO/2015/105926, WO/2015/164674, WO/2015/196130, WO/2015/196128, WO/2015/196118, WO/2016/011226, WO/2016/011222, WO/2016/011306, WO/2016/014846, WO/2016/022914, WO/2016/036902, WO/2016/077125, or WO/2016/077123, each of which is herein incorporated by reference in its entirety. It is understood that incorporation of a chemically modified nucleotide into a polynucleotide can result in the modification being incorporated into a nucleobase, the backbone,

or both, depending on the location of the modification in the nucleotide. In some embodiments, the backbone modification is one provided in EP 2813570, which is herein incorporated by reference in its entirety. In some embodiments, the modified cap is one provided in US Pat. Pub. No. 20050287539, which is herein incorporated by reference in its entirety.

In some embodiments, the chemically modified nucleic acid (e.g., RNA, e.g., mRNA) comprises one or more of ARCA: anti-reverse cap analog (m27.3′-OGP3G), GP3G (Unmethylated Cap Analog), m7GP3G (Monomethylated Cap Analog), m32.2.7GP3G (Trimethylated Cap Analog), m5CTP (5′-methyl-cytidine triphosphate), m6ATP (N6-methyl-adenosine-5′-triphosphate), s2UTP (2-thio-uridine triphosphate), and Ψ (pseudouridine triphosphate).

In some embodiments, the chemically modified nucleic acid comprises a 5′ cap, e.g.: a 7-methylguanosine cap (e.g., a O-Me-m7G cap); a hypermethylated cap analog; an NAD+-derived cap analog (e.g., as described in Kiledjian, Trends in Cell Biology 28, 454-464 (2018)); or a modified, e.g., biotinylated, cap analog (e.g., as described in Bednarek et al., Phil Trans R Soc B 373, 20180167 (2018)).

In some embodiments, the chemically modified nucleic acid comprises a 3′ feature selected from one or more of: a polyA tail; a 16-nucleotide long stem-loop structure flanked by unpaired 5 nucleotides (e.g., as described by Mannironi et al., Nucleic Acid Research 17, 9113-9126 (1989)); a triple-helical structure (e.g., as described by Brown et al., PNAS 109, 19202-19207 (2012)); a tRNA, Y RNA, or vault RNA structure (e.g., as described by Labno et al., Biochemica et Biophysica Acta 1863, 3125-3147 (2016)); incorporation of one or more deoxyribonucleotide triphosphates (dNTPs), 2'O-Methylated NTPs, or phosphorothioate-NTPs; a single nucleotide chemical modification (e.g., oxidation of the 3′ terminal ribose to a reactive aldehyde followed by conjugation of the aldehyde-reactive modified nucleotide); or chemical ligation to another nucleic acid molecule.

In some embodiments, the nucleic acid (e.g., template nucleic acid) comprises one or more modified nucleotides, e.g., selected from dihydrouridine, inosine, 7-methylguanosine, 5-methylcytidine (5mC), 5′ Phosphate ribothymidine, 2′-O-methyl ribothymidine, 2′-O-ethyl ribothymidine, 2′-fluoro ribothymidine, C-5 propynyl-deoxycytidine (pdC), C-5 propynyl-deoxyuridine (pdU), C-5 propynyl-cytidine (pC), C-5 propynyl-uridine (pU), 5-methyl cytidine, 5-methyl uridine, 5-methyl deoxycytidine, 5-methyl deoxyuridine methoxy, 2,6-diaminopurine,

5′-Dimethoxytrityl-N4-ethyl-2′-deoxycytidine, C-5 propynyl-f-cytidine (pfC), C-5 propynyl-f-uridine (pfU), 5-methyl f-cytidine, 5-methyl f-uridine, C-5 propynyl-m-cytidine (pmC), C-5 propynyl-f-uridine (pmU), 5-methyl m-cytidine, 5-methyl m-uridine, LNA (locked nucleic acid), MGB (minor groove binder) pseudouridine (Ψ), 1-N-methylpseudouridine (1-Me-Ψ), or 5-methoxyuridine (5-MO-U).

In some embodiments, the nucleic acid comprises a backbone modification, e.g., a modification to a sugar or phosphate group in the backbone. In some embodiments, the nucleic acid comprises a nucleobase modification.

In some embodiments, the nucleic acid comprises one or more chemically modified nucleotides of Table 13, one or more chemical backbone modifications of Table 14, one or more chemically modified caps of Table 15. For instance, in some embodiments, the nucleic acid comprises two or more (e.g., 3, 4, 5, 6, 7, 8, 9, or 10 or more) different types of chemical modifications. As an example, the nucleic acid may comprise two or more (e.g., 3, 4, 5, 6, 7, 8, 9, or 10 or more) different types of modified nucleobases, e.g., as described herein, e.g., in Table 13. Alternatively or in combination, the nucleic acid may comprise two or more (e.g., 3, 4, 5, 6, 7, 8, 9, or 10 or more) different types of backbone modifications, e.g., as described herein, e.g., in Table 14. Alternatively or in combination, the nucleic acid may comprise one or more modified cap, e.g., as described herein, e.g., in Table 15. For instance, in some embodiments, the nucleic acid comprises one or more type of modified nucleobase and one or more type of backbone modification; one or more type of modified nucleobase and one or more modified cap; one or more type of modified cap and one or more type of backbone modification; or one or more type of modified nucleobase, one or more type of backbone modification, and one or more type of modified cap.

In some embodiments, the nucleic acid comprises one or more (e.g., 2, 3, 4, 5, 6, 7, 8, 9, 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250, 300, 350, 400, 450, 500, 600, 700, 800, 900, 1000, or more) modified nucleobases. In some embodiments, all nucleobases of the nucleic acid are modified. In some embodiments, the nucleic acid is modified at one or more (e.g., 2, 3, 4, 5, 6, 7, 8, 9, 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250, 300, 350, 400, 450, 500, 600, 700, 800, 900, 1000, or more) positions in the backbone. In some embodiments, all backbone positions of the nucleic acid are modified.

Table 13. Modified nucleotides

5-aza-uridine	N2-methyl-6-thio-guanosine
2-thio-5-aza-midine	N2,N2-dimethyl-6-thio-guanosine
2-thiouridine	pyridin-4-one ribonucleoside
4-thio-pseudouridine	2-thio-5-aza-uridine
2-thio-pseudouridine	2-thiomidine
5-hydroxyuridine	4-thio-pseudomidine
3-methyluridine	2-thio-pseudowidine
5-carboxymethyl-uridine	3-methylmidine
1-carboxymethyl-pseudouridine	1-propynyl-pseudomidine
5-propynyl-uridine	1-methyl-1-deaza-pseudomidine
1-propynyl-pseudouridine	2-thio-1-methyl-1-deaza-pseudouridine
5-taurinomethyluridine	4-methoxy-pseudomidine
1-taurinomethyl-pseudouridine	5'-O-(1-Thiophosphate)-Adenosine
5-taurinomethyl-2-thio-uridine	5'-O-(1-Thiophosphate)-Cytidine
1-taurinomethyl-4-thio-uridine	5'-O-(1-thiophosphate)-Guanosine
5-methyl-uridine	5'-O-(1-Thiophophate)-Uridine
1-methyl-pseudouridine	5'-O-(1-Thiophosphate)-Pseudouridine
4-thio-1-methyl-pseudouridine	2'-O-methyl-Adenosine
2-thio-1-methyl-pseudouridine	2'-O-methyl-Cytidine
1-methyl-1-deaza-pseudouridine	2'-O-methyl-Guanosine
2-thio-1-methyl-1-deaza-pseudomidine	2'-O-methyl-Uridine
dihydrouridine	2'-O-methyl-Pseudouridine
dihydropseudouridine	2'-O-methyl-Inosine
2-thio-dihydromidine	2-methyladenosine
2-thio-dihydropseudouridine	2-methylthio-N6-methyladenosine
2-methoxyuridine	2-methylthio-N6 isopentenyladenosine
2-methoxy-4-thio-uridine	2-methylthio-N6-(cis-hydroxyisopentenyl)adenosine
4-methoxy-pseudouridine	N6-methyl-N6-threonylcarbamoyladenosine
4-methoxy-2-thio-pseudouridine	N6-hydroxynorvalylcarbamoyladenosine
5-aza-cytidine	2-methylthio-N6-hydroxynorvalyl carbamoyladenosine
pseudoisocytidine	2'-O-ribosyladenosine (phosphate)
3-methyl-cytidine	1,2'-O-dimethylinosine
N4-acetylcytidine	5,2'-O-dimethylcytidine
5-formylcytidine	N4-acetyl-2'-O-methylcytidine
N4-methylcytidine	Lysidine
5-hydroxymethylcytidine	7-methylguanosine
1-methyl-pseudoisocytidine	N2,2'-O-dimethylguanosine
pyrrolo-cytidine	N2,N2,2'-O-trimethylguanosine
pyrrolo-pseudoisocytidine	2'-O-ribosylguanosine (phosphate)
2-thio-cytidine	Wybutosine
2-thio-5-methyl-cytidine	Peroxywybutosine
4-thio-pseudoisocytidine	Hydroxywybutosine
4-thio-1-methyl-pseudoisocytidine	undermodified hydroxywybutosine
4-thio-1-methyl-1-deaza-pseudoisocytidine	
1-methyl-1-deaza-pseudoisocytidine	

zebularine	methylwyosine
5-aza-zebularine	queuosine
5-methyl-zebularine	epoxyqueuosine
5-aza-2-thio-zebularine	galactosyl-queuosine
2-thio-zebularine	mannosyl-queuosine
2-methoxy-cytidine	7-cyano-7-deazaguanosine
2-methoxy-5-methyl-cytidine	7-aminomethyl-7-deazaguanosine
4-methoxy-pseudoisocytidine	archaeosine
4-methoxy-1-methyl-pseudoisocytidine	5,2'-O-dimethyluridine
2-aminopurine	4-thiouridine
2,6-diaminopurine	5-methyl-2-thiouridine
7-deaza-adenine	2-thio-2'-O-methyluridine
7-deaza-8-aza-adenine	3-(3-amino-3-carboxypropyl)uridine
7-deaza-2-aminopurine	5-methoxyuridine
7-deaza-8-aza-2-aminopurine	uridine 5-oxyacetic acid
7-deaza-2,6- diaminopurine	uridine 5-oxyacetic acid methyl ester
7-deaza-8-aza-2,6-diarninopurine	5-(carboxyhydroxymethyl)uridine)
1-methyladenosine	5-(carboxyhydroxymethyl)uridine methyl ester
N6-isopentenyladenosine	5-methoxycarbonylmethyluridine
N6-(cis-hydroxyisopentenyl)adenosine	5-methoxycarbonylmethyl-2'-O-methyluridine
2-methylthio-N6-(cis-hydroxyisopentenyl) adenosine	5-methoxycarbonylmethyl-2-thiouridine
	5-aminomethyl-2-thiouridine
N6-glycinylcarbamoyladenosine	5-methylaminomethyluridine
N6-threonylcarbamoyladenosine	5-methylaminomethyl-2-thiouridine
2-methylthio-N6-threonyl carbamoyladenosine	5-methylaminomethyl-2-selenouridine
	5-carbamoylmethyluridine
N6,N6-dimethyladenosine	5-carbamoylmethyl-2'-O-methyluridine
7-methyladenine	5-carboxymethylaminomethyluridine
2-methylthio-adenine	5-carboxymethylaminomethyl-2'-O-methyluridine
2-methoxy-adenine	
inosine	5-carboxymethylaminomethyl-2-thiouridine
1-methyl-inosine	N4,2'-O-dimethylcytidine
wyosine	5-carboxymethyluridine
wybutosine	N6,2'-O-dimethyladenosine
7-deaza-guanosine	N,N6,O-2'-trimethyladenosine
7-deaza-8-aza-guanosine	N2,7-dimethylguanosine
6-thio-guanosine	N2,N2,7-trimethylguanosine
6-thio-7-deaza-guanosine	3,2'-O-dimethyluridine
6-thio-7-deaza-8-aza-guanosine	5-methyldihydrouridine
7-methyl-guanosine	5-formyl-2'-O-methylcytidine
6-thio-7-methyl-guanosine	1,2'-O-dimethylguanosine
7-methylinosine	4-demethylwyosine
6-methoxy-guanosine	Isowyosine
1-methylguanosine	N6-acetyladenosine
N2-methylguanosine	
N2,N2-dimethylguanosine	

8-oxo-guanosine 7-methyl-8-oxo-guanosine 1-methyl-6-thio-guanosine	

Table 14. Backbone modifications

2'-O-Methyl backbone
Peptide Nucleic Acid (PNA) backbone
phosphorothioate backbone
morpholino backbone
carbamate backbone
siloxane backbone
sulfide backbone
sulfoxide backbone
sulfone backbone
formacetyl backbone
thioformacetyl backbone
methyleneformacetyl backbone
riboacetyl backbone
alkene containing backbone
sulfamate backbone
sulfonate backbone
sulfonamide backbone
methyleneimino backbone
methylenehydrazino backbone
amide backbone

Table 15. Modified caps

m7GpppA
m7GpppC
m2,7GpppG
m2,2,7GpppG
m7Gpppm7G
m7,2'OmeGpppG
m72'dGpppG
m7,3'OmeGpppG
m7,3'dGpppG
GppppG
m7GppppG
m7GppppA
m7GppppC
m2,7GppppG
m2,2,7GppppG
m7Gppppm7G
m7,2'OmeGppppG

m72'dGppppG m7,3'OmeGppppG m7,3'dGppppG

The nucleotides comprising the template of the gene modifying system can be natural or modified bases, or a combination thereof. For example, the template may contain pseudouridine, dihydrouridine, inosine, 7-methylguanosine, or other modified bases. In some embodiments, the template may contain locked nucleic acid nucleotides. In some embodiments, the modified bases used in the template do not inhibit the reverse transcription of the template. In some embodiments, the modified bases used in the template may improve reverse transcription, e.g., specificity or fidelity.

In some embodiments, an RNA component of the system (e.g., a template RNA or a gRNA) comprises one or more nucleotide modifications. In some embodiments, the modification pattern of a gRNA can significantly affect *in vivo* activity compared to unmodified or end-modified guides (e.g., as shown in Figure 1D from Finn et al. *Cell Rep* 22(9):2227-2235 (2018); incorporated herein by reference in its entirety). Without wishing to be bound by theory, this process may be due, at least in part, to a stabilization of the RNA conferred by the modifications. Non-limiting examples of such modifications may include 2'-O-methyl (2'-O-Me), 2'-0-(2-methoxyethyl) (2'-0-MOE), 2'- fluoro (2'-F), phosphorothioate (PS) bond between nucleotides, G-C substitutions, and inverted abasic linkages between nucleotides and equivalents thereof.

In some embodiments, the template RNA (e.g., at the portion thereof that binds a target site) or the guide RNA comprises a 5′ terminus region. In some embodiments, the template RNA or the guide RNA does not comprise a 5′ terminus region. In some embodiments, the 5′ terminus region comprises a gRNA spacer region, e.g., as described with respect to sgRNA in Briner AE et al, Molecular Cell 56: 333-339 (2014) (incorporated herein by reference in its entirety; applicable herein, e.g., to all guide RNAs). In some embodiments, the 5′ terminus region comprises a 5′ end modification. In some embodiments, a 5′ terminus region with or without a spacer region may be associated with a crRNA, trRNA, sgRNA and/or dgRNA. The gRNA spacer region can, in some instances, comprise a guide region, guide domain, or targeting domain.

In some embodiments, the template RNAs (e.g., at the portion thereof that binds a target site) or guide RNAs described herein comprises any of the sequences shown in Table 4 of WO2018107028A1, incorporated herein by reference in its entirety. In some embodiments, where a sequence shows a guide and/or spacer region, the composition may comprise this region or not. In some embodiments, a guide RNA comprises one or more of the modifications of any of the sequences shown in Table 4 of WO2018107028A1, e.g., as identified therein by a SEQ ID NO. In embodiments, the nucleotides may be the same or different, and/or the modification pattern shown may be the same or similar to a modification pattern of a guide sequence as shown in Table 4 of WO2018107028A1. In some embodiments, a modification pattern includes the relative position and identity of modifications of the gRNA or a region of the gRNA (e.g. 5′ terminus region, lower stem region, bulge region, upper stem region, nexus region, hairpin 1 region, hairpin 2 region, 3′ terminus region). In some embodiments, the modification pattern contains at least 50%, 55%, 60%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% of the modifications of any one of the sequences shown in the sequence column of Table 4 of WO2018107028A1, and/or over one or more regions of the sequence. In some embodiments, the modification pattern is at least 50%, 55%, 60%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the modification pattern of any one of the sequences shown in the sequence column of Table 4 of WO2018107028A1. In some embodiments, the modification pattern is at least 50%, 55%, 60%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical over one or more regions of the sequence shown in Table 4 of WO2018107028A1, e.g., in a 5 ' terminus region, lower stem region, bulge region, upper stem region, nexus region, hairpin 1 region, hairpin 2 region, and/or 3′ terminus region. In some embodiments, the modification pattern is least 50%, 55%, 60%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the modification pattern of a sequence over the 5 ' terminus region. In some embodiments, the modification pattern is least 50%, 55%, 60%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical over the lower stem. In some embodiments, the modification pattern is least 50%, 55%, 60%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical over the bulge. In some embodiments, the modification pattern is least 50%, 55%, 60%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical over the upper stem. In some embodiments, the modification pattern is least 50%, 55%, 60%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or

100% identical over the nexus. In some embodiments, the modification pattern is least 50%, 55%, 60%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical over the hairpin 1. In some embodiments, the modification pattern is least 50%, 55%, 60%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical over the hairpin 2. In some embodiments, the modification pattern is least 50%, 55%, 60%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical over the 3 ' terminus. In some embodiments, the modification pattern differs from the modification pattern of a sequence of Table 4 of WO2018107028A1, or a region (e.g. 5′ terminus, lower stem, bulge, upper stem, nexus, hairpin 1, hairpin 2, 3′ terminus) of such a sequence, e.g., at 0, 1, 2, 3, 4, 5, 6, or more nucleotides. In some embodiments, the gRNA comprises modifications that differ from the modifications of a sequence of Table 4 of WO2018107028A1, e.g., at 0, 1, 2, 3, 4, 5, 6, or more nucleotides. In some embodiments, the gRNA comprises modifications that differ from modifications of a region (e.g. 5 ' terminus, lower stem, bulge, upper stem, nexus, hairpin 1, hairpin 2, 3′ terminus) of a sequence of Table 4 of WO2018107028A1, e.g., at 0, 1, 2, 3, 4, 5, 6, or more nucleotides.

In some embodiments, the template RNAs (e.g., at the portion thereof that binds a target site) or the gRNA comprises a 2'-O-methyl (2'-O-Me) modified nucleotide. In some embodiments, the gRNA comprises a 2'-O-(2-methoxy ethyl) (2'-O-moe) modified nucleotide. In some embodiments, the gRNA comprises a 2'-fluoro (2'- F) modified nucleotide. In some embodiments, the gRNA comprises a phosphorothioate (PS) bond between nucleotides. In some embodiments, the gRNA comprises a 5′ end modification, a 3′ end modification, or 5′ and 3′ end modifications. In some embodiments, the 5′ end modification comprises a phosphorothioate (PS) bond between nucleotides. In some embodiments, the 5′ end modification comprises a 2'-O-methyl (2'-O-Me), 2'-O-(2-methoxy ethyl) (2'-O-MOE), and/or 2'-fluoro (2'-F) modified nucleotide. In some embodiments, the 5′ end modification comprises at least one phosphorothioate (PS) bond and one or more of a 2'-O-methyl (2'-O- Me), 2'-O-(2-methoxyethyl) (2'-O-MOE), and/or 2'-fluoro (2'-F) modified nucleotide. The end modification may comprise a phosphorothioate (PS), 2'-O-methyl (2'-O-Me), 2'-O-(2- methoxyethyl) (2'-O-MOE), and/or 2'-fluoro (2'-F) modification. Equivalent end modifications are also encompassed by embodiments described herein. In some embodiments, the template RNA or gRNA comprises an end modification in combination with a modification of one or more regions of the template RNA or gRNA. Additional exemplary modifications and methods for protecting RNA,

e.g., gRNA, and formulae thereof, are described in WO2018126176A1, which is incorporated herein by reference in its entirety.

In some embodiments, a template RNA described herein comprises three phosphorothioate linkages at the 5' end and three phosphorothioate linkages at the 3' end. In some embodiments, a template RNA described herein comprises three 2'-O-methyl ribonucleotides at the 5' end and three 2'-O-methyl ribonucleotides at the 3' end. In some embodiments, the 5' most three nucleotides of the template RNA are 2'-O-methyl ribonucleotides, the 5' most three internucleotide linkages of the template RNA are phosphorothioate linkages, the 3' most three nucleotides of the template RNA are 2'-O-methyl ribonucleotides, and the 3' most three internucleotide linkages of the template RNA are phosphorothioate linkages. In some embodiments, the template RNA comprises alternating blocks of ribonucleotides and 2'-O-methyl ribonucleotides, for instance, blocks of between 12 and 28 nucleotides in length. In some embodiments, the central portion of the template RNA comprises the alternating blocks and the 5' and 3' ends each comprise three 2'-O-methyl ribonucleotides and three phosphorothioate linkages.

In some embodiments, structure-guided and systematic approaches are used to introduce modifications (e.g., 2′-OMe-RNA, 2′-F-RNA, and PS modifications) to a template RNA or guide RNA, for example, as described in Mir et al. *Nat Commun* 9:2641 (2018) (incorporated by reference herein in its entirety). In some embodiments, the incorporation of 2′-F-RNAs increases thermal and nuclease stability of RNA:RNA or RNA:DNA duplexes, e.g., while minimally interfering with C3′-endo sugar puckering. In some embodiments, 2′-F may be better tolerated than 2′-OMe at positions where the 2′-OH is important for RNA:DNA duplex stability. In some embodiments, a crRNA comprises one or more modifications that do not reduce Cas9 activity, e.g., C10, C20, or C21 (fully modified), e.g., as described in Supplementary Table 1 of Mir et al. *Nat Commun* 9:2641 (2018), incorporated herein by reference in its entirety. In some embodiments, a tracrRNA comprises one or more modifications that do not reduce Cas9 activity, e.g., T2, T6, T7, or T8 (fully modified) of Supplementary Table 1 of Mir et al. *Nat Commun* 9:2641 (2018). In some embodiments, a crRNA comprises one or more modifications (e.g., as described herein) may be paired with a tracrRNA comprising one or more modifications, e.g., C20 and T2. In some embodiments, a gRNA comprises a chimera, e.g., of a crRNA and a

tracrRNA (e.g., Jinek et al. *Science* 337(6096):816-821 (2012)). In embodiments, modifications from the crRNA and tracrRNA are mapped onto the single-guide chimera, e.g., to produce a modified gRNA with enhanced stability.

In some embodiments, gRNA molecules may be modified by the addition or subtraction of the naturally occurring structural components, e.g., hairpins. In some embodiments, a gRNA may comprise a gRNA with one or more 3′ hairpin elements deleted, e.g., as described in WO2018106727, incorporated herein by reference in its entirety. In some embodiments, a gRNA may contain an added hairpin structure, e.g., an added hairpin structure in the spacer region, which was shown to increase specificity of a CRISPR-Cas system in the teachings of Kocak et al. *Nat Biotechnol* 37(6):657-666 (2019). Additional modifications, including examples of shortened gRNA and specific modifications improving *in vivo* activity, can be found in US20190316121, incorporated herein by reference in its entirety.

In some embodiments, structure-guided and systematic approaches (e.g., as described in Mir et al. *Nat Commun* 9:2641 (2018); incorporated herein by reference in its entirety) are employed to find modifications for the template RNA. In embodiments, the modifications are identified with the inclusion or exclusion of a guide region of the template RNA. In some embodiments, a structure of polypeptide bound to template RNA is used to determine non-protein-contacted nucleotides of the RNA that may then be selected for modifications, e.g., with lower risk of disrupting the association of the RNA with the polypeptide. Secondary structures in a template RNA can also be predicted *in silico* by software tools, e.g., the RNAstructure tool available at rna.urmc.rochester.edu/RNAstructureWeb (Bellaousov et al. *Nucleic Acids Res* 41:W471-W474 (2013); incorporated by reference herein in its entirety), e.g., to determine secondary structures for selecting modifications, e.g., hairpins, stems, and/or bulges.

Production of Compositions and Systems

As will be appreciated by one of skill, methods of designing and constructing nucleic acid constructs and proteins or polypeptides (such as the systems, constructs and polypeptides described herein) are routine in the art. Generally, recombinant methods may be used. See, in general, Smales & James (Eds.), *Therapeutic Proteins: Methods and Protocols* (Methods in Molecular Biology), Humana Press (2005); and Crommelin, Sindelar & Meibohm (Eds.), *Pharmaceutical Biotechnology: Fundamentals and Applications*, Springer (2013). Methods of

designing, preparing, evaluating, purifying and manipulating nucleic acid compositions are described in Green and Sambrook (Eds.), *Molecular Cloning: A Laboratory Manual* (Fourth Edition), Cold Spring Harbor Laboratory Press (2012).

The disclosure provides, in part, a nucleic acid, e.g., vector, encoding a gene modifying polypeptide described herein, a template nucleic acid described herein, or both. In some embodiments, a vector comprises a selective marker, e.g., an antibiotic resistance marker. In some embodiments, the antibiotic resistance marker is a kanamycin resistance marker. In some embodiments, the antibiotic resistance marker does not confer resistance to beta-lactam antibiotics. In some embodiments, the vector does not comprise an ampicillin resistance marker. In some embodiments, the vector comprises a kanamycin resistance marker and does not comprise an ampicillin resistance marker. In some embodiments, a vector encoding a gene modifying polypeptide is integrated into a target cell genome (e.g., upon administration to a target cell, tissue, organ, or subject). In some embodiments, a vector encoding a gene modifying polypeptide is not integrated into a target cell genome (e.g., upon administration to a target cell, tissue, organ, or subject). In some embodiments, a vector encoding a template nucleic acid (e.g., template RNA) is not integrated into a target cell genome (e.g., upon administration to a target cell, tissue, organ, or subject). In some embodiments, if a vector is integrated into a target site in a target cell genome, the selective marker is not integrated into the genome. In some embodiments, if a vector is integrated into a target site in a target cell genome, genes or sequences involved in vector maintenance (e.g., plasmid maintenance genes) are not integrated into the genome. In some embodiments, if a vector is integrated into a target site in a target cell genome, transfer regulating sequences (e.g., inverted terminal repeats, e.g., from an AAV) are not integrated into the genome. In some embodiments, administration of a vector (e.g., encoding a gene modifying polypeptide described herein, a template nucleic acid described herein, or both) to a target cell, tissue, organ, or subject results in integration of a portion of the vector into one or more target sites in the genome(s) of said target cell, tissue, organ, or subject. In some embodiments, less than 99, 95, 90, 80, 70, 60, 50, 40, 30, 20, 10, 5, 4, 3, 2, or 1% of target sites (e.g., no target sites) comprising integrated material comprise a selective marker (e.g., an antibiotic resistance gene), a transfer regulating sequence (e.g., an inverted terminal repeat, e.g., from an AAV), or both from the vector.

Exemplary methods for producing a therapeutic pharmaceutical protein or polypeptide described herein involve expression in mammalian cells, although recombinant proteins can also be produced using insect cells, yeast, bacteria, or other cells under control of appropriate promoters. Mammalian expression vectors may comprise non-transcribed elements such as an origin of replication, a suitable promoter, and other 5' or 3' flanking non-transcribed sequences, and 5' or 3' non-translated sequences such as necessary ribosome binding sites, a polyadenylation site, splice donor and acceptor sites, and termination sequences. DNA sequences derived from the SV40 viral genome, for example, SV40 origin, early promoter, splice, and polyadenylation sites may be used to provide other genetic elements required for expression of a heterologous DNA sequence. Appropriate cloning and expression vectors for use with bacterial, fungal, yeast, and mammalian cellular hosts are described in Green & Sambrook, *Molecular Cloning: A Laboratory Manual* (Fourth Edition), Cold Spring Harbor Laboratory Press (2012).

Various mammalian cell culture systems can be employed to express and manufacture recombinant protein. Examples of mammalian expression systems include CHO, COS, HEK293, HeLA, and BHK cell lines. Processes of host cell culture for production of protein therapeutics are described in Zhou and Kantardjieff (Eds.), *Mammalian Cell Cultures for Biologics Manufacturing (Advances in Biochemical Engineering/Biotechnology)*, Springer (2014). Compositions described herein may include a vector, such as a viral vector, e.g., a lentiviral vector, encoding a recombinant protein. In some embodiments, a vector, e.g., a viral vector, may comprise a nucleic acid encoding a recombinant protein.

Purification of protein therapeutics is described in Franks, Protein Biotechnology: *Isolation, Characterization, and Stabilization*, Humana Press (2013); and in Cutler, *Protein Purification Protocols (Methods in Molecular Biology)*, Humana Press (2010).

The disclosure also provides compositions and methods for the production of template nucleic acid molecules (e.g., template RNAs) with specificity for a gene modifying polypeptide and/or a genomic target site. In an aspect, the method comprises production of RNA segments including an upstream homology segment, a heterologous object sequence segment, a gene modifying polypeptide binding motif, and a gRNA segment.

Therapeutic Applications

In some embodiments, a gene modifying system as described herein can be used to modify a cell (e.g., an animal cell, plant cell, or fungal cell). In some embodiments, a gene modifying system as described herein can be used to modify a mammalian cell (e.g., a human cell). In some embodiments, a gene modifying system as described herein can be used to modify a cell from a livestock animal (e.g., a cow, horse, sheep, goat, pig, llama, alpaca, camel, yak, chicken, duck, goose, or ostrich). In some embodiments, a gene modifying system as described herein can be used as a laboratory tool or a research tool, or used in a laboratory method or research method, e.g., to modify an animal cell, e.g., a mammalian cell (e.g., a human cell), a plant cell, or a fungal cell.

By integrating coding genes into a RNA sequence template, the gene modifying system can address therapeutic needs, for example, by providing expression of a therapeutic transgene in individuals with loss-of-function mutations, by replacing gain-of-function mutations with normal transgenes, by providing regulatory sequences to eliminate gain-of-function mutation expression, and/or by controlling the expression of operably linked genes, transgenes and systems thereof. In certain embodiments, the RNA sequence template encodes a promotor region specific to the therapeutic needs of the host cell, for example a tissue specific promotor or enhancer. In still other embodiments, a promotor can be operably linked to a coding sequence.

Accordingly, provided herein are methods for treating sickle cell disease (SCD) (e.g., sickle cell anemia) in a subject in need thereof. In some embodiments, treatment results in amelioration of one or more symptoms associated with SCD.

In some embodiments, a system herein is used to treat a subject having a mutation in E6 (e.g., E6V).

In some embodiments, treatment with a system disclosed herein results in correction of the E6V mutation in between about 60-70% (e.g., about 60-65% or about 65-70%) of cells. In some embodiments, treatment with a system disclosed herein results in correction of the E6V mutation in between about 60-70% (e.g., about 60-65% or about 65-70%) of DNA isolated from the treated cells.

In some embodiments, treatment with a gene modifying system described herein results in one or more of:

(a) a reduction in the number of sickle-shaped cells;

(b) a reduction in production of an abnormal version of beta-globulin (e.g., hemoglobulin S);

(c) a reduction of pain and/or organ damage associated with sickle cell-related blood vessel blockage; and/or

(d) an increase in normal blood flow,

as compared to a subject having SCD that has not been treated with a gene modifying system described herein.

Administration and Delivery

The compositions and systems described herein may be used *in vitro* or *in vivo*. In some embodiments the system or components of the system are delivered to cells (e.g., mammalian cells, e.g., human cells), e.g., *in vitro* or *in vivo*. In some embodiments, the cells are eukaryotic cells, e.g., cells of a multicellular organism, e.g., an animal, e.g., a mammal (e.g., human, swine, bovine), a bird (e.g., poultry, such as chicken, turkey, or duck), or a fish. In some embodiments, the cells are non-human animal cells (e.g., a laboratory animal, a livestock animal, or a companion animal). In some embodiments, the cell is a stem cell (e.g., a hematopoietic stem cell), a fibroblast, or a T cell. In some embodiments, the cell is an immune cell, e.g., a T cell (e.g., a Treg, CD4, CD8, γδ, or memory T cell), B cell (e.g., memory B cell or plasma cell), or NK cell. In some embodiments, the cell is a non-dividing cell, e.g., a non-dividing fibroblast or non-dividing T cell. In some embodiments, the cell is an HSC and p53 is not upregulated or is upregulated by less than 10%, 5%, 2%, or 1%, e.g., as determined according to the method described in Example 30 of PCT/US2019/048607. The skilled artisan will understand that the components of the gene modifying system may be delivered in the form of polypeptide, nucleic acid (e.g., DNA, RNA), and combinations thereof.

In one embodiment the system and/or components of the system are delivered as nucleic acid. For example, the gene modifying polypeptide may be delivered in the form of a DNA or RNA encoding the polypeptide, and the template RNA may be delivered in the form of RNA or its complementary DNA to be transcribed into RNA. In some embodiments the system or

components of the system are delivered on 1, 2, 3, 4, or more distinct nucleic acid molecules. In some embodiments the system or components of the system are delivered as a combination of DNA and RNA. In some embodiments the system or components of the system are delivered as a combination of DNA and protein. In some embodiments the system or components of the system are delivered as a combination of RNA and protein. In some embodiments the gene modifying polypeptide is delivered as a protein.

In some embodiments the system or components of the system are delivered to cells, e.g. mammalian cells or human cells, using a vector. The vector may be, e.g., a plasmid or a virus. In some embodiments, delivery is *in vivo*, *in vitro*, *ex vivo*, or *in situ*. In some embodiments the virus is an adeno associated virus (AAV), a lentivirus, or an adenovirus. In some embodiments the system or components of the system are delivered to cells with a viral-like particle or a virosome. In some embodiments the delivery uses more than one virus, viral-like particle or virosome.

In one embodiment, the compositions and systems described herein can be formulated in liposomes or other similar vesicles. Liposomes are spherical vesicle structures composed of a uni- or multilamellar lipid bilayer surrounding internal aqueous compartments and a relatively impermeable outer lipophilic phospholipid bilayer. Liposomes may be anionic, neutral or cationic. Liposomes are biocompatible, nontoxic, can deliver both hydrophilic and lipophilic drug molecules, protect their cargo from degradation by plasma enzymes, and transport their load across biological membranes and the blood brain barrier (BBB) (see, e.g., Spuch and Navarro, Journal of Drug Delivery, vol. 2011, Article ID 469679, 12 pages, 2011. doi:10.1155/2011/469679 for review).

Vesicles can be made from several different types of lipids; however, phospholipids are most commonly used to generate liposomes as drug carriers. Methods for preparation of multilamellar vesicle lipids are known in the art (see for example U.S. Pat. No. 6,693,086, the teachings of which relating to multilamellar vesicle lipid preparation are incorporated herein by reference). Although vesicle formation can be spontaneous when a lipid film is mixed with an aqueous solution, it can also be expedited by applying force in the form of shaking by using a homogenizer, sonicator, or an extrusion apparatus (see, e.g., Spuch and Navarro, Journal of Drug Delivery, vol. 2011, Article ID 469679, 12 pages, 2011. doi:10.1155/2011/469679 for review). Extruded lipids can be prepared by extruding through filters of decreasing size, as described in

Templeton et al., Nature Biotech, 15:647-652, 1997, the teachings of which relating to extruded lipid preparation are incorporated herein by reference.

A variety of nanoparticles can be used for delivery, such as a liposome, a lipid nanoparticle, a cationic lipid nanoparticle, an ionizable lipid nanoparticle, a polymeric nanoparticle, a gold nanoparticle, a dendrimer, a cyclodextrin nanoparticle, a micelle, or a combination of the foregoing.

Lipid nanoparticles are an example of a carrier that provides a biocompatible and biodegradable delivery system for the pharmaceutical compositions described herein. Nanostructured lipid carriers (NLCs) are modified solid lipid nanoparticles (SLNs) that retain the characteristics of the SLN, improve drug stability and loading capacity, and prevent drug leakage. Polymer nanoparticles (PNPs) are an important component of drug delivery. These nanoparticles can effectively direct drug delivery to specific targets and improve drug stability and controlled drug release. Lipid–polymer nanoparticles (PLNs), a type of carrier that combines liposomes and polymers, may also be employed. These nanoparticles possess the complementary advantages of PNPs and liposomes. A PLN is composed of a core–shell structure; the polymer core provides a stable structure, and the phospholipid shell offers good biocompatibility. As such, the two components increase the drug encapsulation efficiency rate, facilitate surface modification, and prevent leakage of water-soluble drugs. For a review, see, e.g., Li et al. 2017, Nanomaterials 7, 122; doi:10.3390/nano7060122.

Exosomes can also be used as drug delivery vehicles for the compositions and systems described herein. For a review, see Ha et al. July 2016. Acta Pharmaceutica Sinica B. Volume 6, Issue 4, Pages 287-296; https://doi.org/10.1016/j.apsb.2016.02.001.

Fusosomes interact and fuse with target cells, and thus can be used as delivery vehicles for a variety of molecules. They generally consist of a bilayer of amphipathic lipids enclosing a lumen or cavity and a fusogen that interacts with the amphipathic lipid bilayer. The fusogen component has been shown to be engineerable in order to confer target cell specificity for the fusion and payload delivery, allowing the creation of delivery vehicles with programmable cell specificity (see for example Patent Application WO2020014209, the teachings of which relating to fusosome design, preparation, and usage are incorporated herein by reference).

In some embodiments, the protein component(s) of the gene modifying system may be pre-associated with the template nucleic acid (e.g., template RNA). For example, in some

embodiments, the gene modifying polypeptide may be first combined with the template nucleic acid (e.g., template RNA) to form a ribonucleoprotein (RNP) complex. In some embodiments, the RNP may be delivered to cells via, e.g., transfection, nucleofection, virus, vesicle, LNP, exosome, fusosome.

A gene modifying system can be introduced into cells, tissues and multicellular organisms. In some embodiments the system or components of the system are delivered to the cells via mechanical means or physical means.

Formulation of protein therapeutics is described in Meyer (Ed.), *Therapeutic Protein Drug Products: Practical Approaches to formulation in the Laboratory, Manufacturing, and the Clinic*, Woodhead Publishing Series (2012).

Tissue Specific Activity/Administration

In some embodiments, a system described herein can make use of one or more feature (e.g., a promoter or microRNA binding site) to limit activity in off-target cells or tissues.

In some embodiments, a nucleic acid described herein (e.g., a template RNA or a DNA encoding a template RNA) comprises a promoter sequence, e.g., a tissue specific promoter sequence. In some embodiments, the tissue-specific promoter is used to increase the target-cell specificity of a gene modifying system. For instance, the promoter can be chosen on the basis that it is active in a target cell type but not active in (or active at a lower level in) a non-target cell type. Thus, even if the promoter integrated into the genome of a non-target cell, it would not drive expression (or only drive low level expression) of an integrated gene. A system having a tissue-specific promoter sequence in the template RNA may also be used in combination with a microRNA binding site, e.g., in the template RNA or a nucleic acid encoding a gene modifying protein, e.g., as described herein. A system having a tissue-specific promoter sequence in the template RNA may also be used in combination with a DNA encoding a gene modifying polypeptide, driven by a tissue-specific promoter, e.g., to achieve higher levels of gene modifying protein in target cells than in non-target cells. In some embodiments, e.g., for liver indications, a tissue-specific promoter is selected from Table 3 of WO2020014209, incorporated herein by reference.

In some embodiments, a nucleic acid described herein (e.g., a template RNA or a DNA encoding a template RNA) comprises a microRNA binding site. In some embodiments, the

microRNA binding site is used to increase the target-cell specificity of a gene modifying system. For instance, the microRNA binding site can be chosen on the basis that is recognized by a miRNA that is present in a non-target cell type, but that is not present (or is present at a reduced level relative to the non-target cell) in a target cell type. Thus, when the template RNA is present in a non-target cell, it would be bound by the miRNA, and when the template RNA is present in a target cell, it would not be bound by the miRNA (or bound but at reduced levels relative to the non-target cell). While not wishing to be bound by theory, binding of the miRNA to the template RNA may interfere with its activity, e.g., may interfere with insertion of the heterologous object sequence into the genome. Accordingly, the system would edit the genome of target cells more efficiently than it edits the genome of non-target cells, e.g., the heterologous object sequence would be inserted into the genome of target cells more efficiently than into the genome of non-target cells, or an insertion or deletion is produced more efficiently in target cells than in non-target cells. A system having a microRNA binding site in the template RNA (or DNA encoding it) may also be used in combination with a nucleic acid encoding a gene modifying polypeptide, wherein expression of the gene modifying polypeptide is regulated by a second microRNA binding site, e.g., as described herein. In some embodiments, e.g., for liver indications, a miRNA is selected from Table 4 of WO2020014209, incorporated herein by reference.

In some embodiments, the template RNA comprises a microRNA sequence, an siRNA sequence, a guide RNA sequence, or a piwi RNA sequence.

Promoters

In some embodiments, one or more promoter or enhancer elements are operably linked to a nucleic acid encoding a gene modifying protein or a template nucleic acid, e.g., that controls expression of the heterologous object sequence. In certain embodiments, the one or more promoter or enhancer elements comprise cell-type or tissue specific elements. In some embodiments, the promoter or enhancer is the same or derived from the promoter or enhancer that naturally controls expression of the heterologous object sequence. For example, the ornithine transcarbomylase promoter and enhancer may be used to control expression of the ornithine transcarbomylase gene in a system or method provided by the invention for correcting

ornithine transcarbomylase deficiencies. In some embodiments, the promoter is a promoter of Table 16 or 17 or a functional fragment or variant thereof.

Exemplary tissue specific promoters that are commercially available can be found, for example, at a uniform resource locator (e.g., www.invivogen.com/tissue-specific-promoters). In some embodiments, a promoter is a native promoter or a minimal promoter, e.g., which consists of a single fragment from the 5′ region of a given gene. In some embodiments, a native promoter comprises a core promoter and its natural 5′ UTR. In some embodiments, the 5′ UTR comprises an intron. In other embodiments, these include composite promoters, which combine promoter elements of different origins or were generated by assembling a distal enhancer with a minimal promoter of the same origin.

Exemplary cell or tissue specific promoters are provided in the tables, below, and exemplary nucleic acid sequences encoding them are known in the art and can be readily accessed using a variety of resources, such as the NCBI database, including RefSeq, as well as the Eukaryotic Promoter Database (//epd.epfl.ch//index.php).

Table 16. Exemplary cell or tissue-specific promoters

Promoter	**Target cells**
B29 Promoter	B cells
CD14 Promoter	Monocytic Cells
CD43 Promoter	Leukocytes and platelets
CD45 Promoter	Hematopoeitic cells
CD68 promoter	macrophages
Desmin promoter	muscle cells
Elastase-1 promoter	pancreatic acinar cells
Endoglin promoter	endothelial cells
fibronectin promoter	differentiating cells, healing tissue
Flt-1 promoter	endothelial cells
GFAP promoter	Astrocytes
GPIIB promoter	megakaryocytes
ICAM-2 Promoter	Endothelial cells
INF-Beta promoter	Hematopoeitic cells
Mb promoter	muscle cells
Nphs1 promoter	podocytes

OG-2 promoter	Osteoblasts, Odonblasts
SP-B promoter	Lung
Syn1 promoter	Neurons
WASP promoter	Hematopoeitic cells
SV40/bAlb promoter	Liver
SV40/bAlb promoter	Liver
SV40/Cd3 promoter	Leukocytes and platelets
SV40/CD45 promoter	hematopoeitic cells
NSE/RU5' promoter	Mature Neurons

Table 17. Additional exemplary cell or tissue-specific promoters

Promoter	**Gene Description**	**Gene Specificity**
APOA2	Apolipoprotein A-II	Hepatocytes (from hepatocyte progenitors)
SERPINA 1 (hAAT)	Serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 (also named alpha 1 anti-tryps in)	Hepatocytes (from definitive endoderm stage)
CYP3A	Cytochrome P450, family 3, subfamily A, polypeptide	Mature Hepatocytes
MIR122	MicroRNA 122	Hepatocytes (from early stage embryonic liver cells) and endoderm
Pancreatic specific promoters		
Promoter	**Gene Description**	**Gene Specificity**
INS	Insulin	Pancreatic beta cells (from definitive endoderm stage)
IRS2	Insulin receptor substrate 2	Pancreatic beta cells
Pdx1	Pancreatic and duodenal homeobox 1	Pancreas (from definitive endoderm stage)
Alx3	Aristaless-like homeobox 3	Pancreatic beta cells (from definitive endoderm stage)
Ppy	Pancreatic polypeptide	PP pancreatic cells (gamma cells)

Cardiac specific promoters		
Promoter	**Gene Description**	**Gene Specificity**
Myh6 (aMHC)	Myosin, heavy chain 6, cardiac muscle, alpha	Late differentiation marker of cardiac muscle cells (atrial specificity)
MYL2 (MLC-2v)	Myosin, light chain 2, regulatory, cardiac, slow	Late differentiation marker of cardiac muscle cells (ventricular specificity)
ITNNl3 (cTnl)	Troponin I type 3 (cardiac)	Cardiomyocytes (from immature state)
ITNNl3 (cTnl)	Troponin I type 3 (cardiac)	Cardiomyocytes (from immature state)
NPPA (ANF)	Natriuretic peptide precursor A (also named Atrial Natriuretic Factor)	Atrial specificity in adult cells
Slc8a1 (Ncx1)	Solute carrier family 8 (sodium/calcium exchanger), member 1	Cardiomyocytes from early developmental stages
CNS specific promoters		
Promoter	**Gene Description**	**Gene Specificity**
SYN1 (hSyn)	Synapsin I	Neurons
GFAP	Glial fibrillary acidic protein	Astrocytes
INA	lnternexin neuronal intermediate filament protein, alpha (a-internexin)	Neuroprogenitors
NES	Nestin	Neuroprogenitors and ectoderm
MOBP	Myelin-associated oligodendrocyte basic protein	Oligodendrocytes
MBP	Myelin basic protein	Oligodendrocytes
TH	Tyrosine hydroxylase	Dopaminergic neurons
FOXA2 (HNF3 beta)	Forkhead box A2	Dopaminergic neurons (also used as a marker of endoderm)
Skin specific promoters		
Promoter	**Gene Description**	**Gene Specificity**
FLG	Filaggrin	Keratinocytes from granular layer
K14	Keratin 14	Keratinocytes from granular and basal layers
TGM3	Transglutaminase 3	Keratinocytes from granular layer

Immune cell specific promoters		
Promoter	**Gene Description**	**Gene Specificity**
ITGAM (CD11B)	lntegrin, alpha M (complement component 3 receptor 3 subunit)	Monocytes, macrophages , granulocytes , natural killer cells
Urogential cell specific promoters		
Promoter	**Gene Description**	**Gene Specificity**
Pbsn	Probasin	Prostatic epithelium
Upk2	Uroplakin 2	Bladder
Sbp	Spermine binding protein	Prostate
Fer1l4	Fer-1-like 4	Bladder
Endothelial cell specific promoters		
Promoter	**Gene Description**	**Gene Specificity**
ENG	Endoglin	Endothelial cells
Pluripotent and embryonic cell specific promoters		
Promoter	**Gene Description**	**Gene Specificity**
Oct4 (POU5F1)	POU class 5 homeobox 1	Pluripotent cells (germ cells, ES cells, iPS cells)
NANOG	Nanog homeobox	Pluripotent cells (ES cells, iPS cells)
Synthetic Oct4	Synthetic promoter based on a Oct-4 core enhancer element	Pluripotent cells (ES cells, iPS cells)
T brachyury	Brachyury	Mesoderm
NES	Nestin	Neuroprogenitors and Ectoderm
SOX17	SRY (sex determining region Y)-box 17	Endoderm
FOXA2 (HNFJ beta)	Forkhead box A2	Endoderm (also used as a marker of dopaminergic neurons)
MIR122	MicroRNA 122	Endoderm and hepatocytes (from early stage embryonic liver cells~

Depending on the host/vector system utilized, any of a number of suitable transcription and translation control elements, including constitutive and inducible promoters, transcription enhancer elements, transcription terminators, etc. may be used in the expression vector (see e.g.,

Bitter et al. (1987) *Methods in Enzymology,* 153:516-544; incorporated herein by reference in its entirety).

In some embodiments, a nucleic acid encoding a gene modifying protein or template nucleic acid is operably linked to a control element, e.g., a transcriptional control element, such as a promoter. The transcriptional control element may, in some embodiment, be functional in either a eukaryotic cell, e.g., a mammalian cell; or a prokaryotic cell (e.g., bacterial or archaeal cell). In some embodiments, a nucleotide sequence encoding a polypeptide is operably linked to multiple control elements, e.g., that allow expression of the nucleotide sequence encoding the polypeptide in both prokaryotic and eukaryotic cells.

For illustration purposes, examples of spatially restricted promoters include, but are not limited to, neuron-specific promoters, adipocyte-specific promoters, cardiomyocyte-specific promoters, smooth muscle-specific promoters, photoreceptor-specific promoters, etc. Neuron-specific spatially restricted promoters include, but are not limited to, a neuron-specific enolase (NSE) promoter (see, e.g., EMBL HSENO2, X51956); an aromatic amino acid decarboxylase (AADC) promoter, a neurofilament promoter (see, e.g., GenBank HUMNFL, L04147); a synapsin promoter (see, e.g., GenBank HUMSYNIB, M55301); a thy-1 promoter (see, e.g., Chen et al. (1987) Cell 51:7-19; and Llewellyn, et al. (2010) Nat. Med. 16(10):1161-1166); a serotonin receptor promoter (see, e.g., GenBank S62283); a tyrosine hydroxylase promoter (TH) (see, e.g., Oh et al. (2009) Gene Ther 16:437; Sasaoka et al. (1992) Mol. Brain Res. 16:274; Boundy et al. (1998) J. Neurosci. 18:9989; and Kaneda et al. (1991) Neuron 6:583-594); a GnRH promoter (see, e.g., Radovick et al. (1991) Proc. Natl. Acad. Sci. USA 88:3402-3406); an L7 promoter (see, e.g., Oberdick et al. (1990) Science 248:223-226); a DNMT promoter (see, e.g., Bartge et al. (1988) Proc. Natl. Acad. Sci. USA 85:3648-3652); an enkephalin promoter (see, e.g., Comb et al. (1988) EMBO J. 17:3793-3805); a myelin basic protein (MBP) promoter; a Ca2+-calmodulin-dependent protein kinase II-alpha (CamKIIα) promoter (see, e.g., Mayford et al. (1996) Proc. Natl. Acad. Sci. USA 93:13250; and Casanova et al. (2001) Genesis 31:37); a CMV enhancer/platelet-derived growth factor-β promoter (see, e.g., Liu et al. (2004) Gene Therapy 11:52-60); and the like.

Adipocyte-specific spatially restricted promoters include, but are not limited to, the aP2 gene promoter/enhancer, e.g., a region from −5.4 kb to +21 bp of a human aP2 gene (see, e.g., Tozzo et al. (1997) Endocrinol. 138:1604; Ross et al. (1990) Proc. Natl. Acad. Sci. USA

87:9590; and Pavjani et al. (2005) Nat. Med. 11:797); a glucose transporter-4 (GLUT4) promoter (see, e.g., Knight et al. (2003) Proc. Natl. Acad. Sci. USA 100:14725); a fatty acid translocase (FAT/CD36) promoter (see, e.g., Kuriki et al. (2002) Biol. Pharm. Bull. 25:1476; and Sato et al. (2002) J. Biol. Chem. 277:15703); a stearoyl-CoA desaturase-1 (SCD1) promoter (Tabor et al. (1999) J. Biol. Chem. 274:20603); a leptin promoter (see, e.g., Mason et al. (1998) Endocrinol. 139:1013; and Chen et al. (1999) Biochem. Biophys. Res. Comm. 262:187); an adiponectin promoter (see, e.g., Kita et al. (2005) Biochem. Biophys. Res. Comm. 331:484; and Chakrabarti (2010) Endocrinol. 151:2408); an adipsin promoter (see, e.g., Platt et al. (1989) Proc. Natl. Acad. Sci. USA 86:7490); a resistin promoter (see, e.g., Seo et al. (2003) Molec. Endocrinol. 17:1522); and the like.

Cardiomyocyte-specific spatially restricted promoters include, but are not limited to, control sequences derived from the following genes: myosin light chain-2, α-myosin heavy chain, AE3, cardiac troponin C, cardiac actin, and the like. Franz et al. (1997) Cardiovasc. Res. 35:560-566; Robbins et al. (1995) Ann. N.Y. Acad. Sci. 752:492-505; Linn et al. (1995) Circ. Res. 76:584-591; Parmacek et al. (1994) Mol. Cell. Biol. 14:1870-1885; Hunter et al. (1993) Hypertension 22:608-617; and Sartorelli et al. (1992) Proc. Natl. Acad. Sci. USA 89:4047-4051.

Smooth muscle-specific spatially restricted promoters include, but are not limited to, an SM22α promoter (see, e.g., Akyürek et al. (2000) Mol. Med. 6:983; and U.S. Pat. No. 7,169,874); a smoothelin promoter (see, e.g., WO 2001/018048); an α-smooth muscle actin promoter; and the like. For example, a 0.4 kb region of the SM22α promoter, within which lie two CArG elements, has been shown to mediate vascular smooth muscle cell-specific expression (see, e.g., Kim, et al. (1997) Mol. Cell. Biol. 17, 2266-2278; Li, et al., (1996) J. Cell Biol. 132, 849-859; and Moessler, et al. (1996) Development 122, 2415-2425).

Photoreceptor-specific spatially restricted promoters include, but are not limited to, a rhodopsin promoter; a rhodopsin kinase promoter (Young et al. (2003) Ophthalmol. Vis. Sci. 44:4076); a beta phosphodiesterase gene promoter (Nicoud et al. (2007) J. Gene Med. 9:1015); a retinitis pigmentosa gene promoter (Nicoud et al. (2007) supra); an interphotoreceptor retinoid-binding protein (IRBP) gene enhancer (Nicoud et al. (2007) supra); an IRBP gene promoter (Yokoyama et al. (1992) Exp Eye Res. 55:225); and the like.

In some embodiments, a gene modifying system, e.g., DNA encoding a gene modifying polypeptide, DNA encoding a template RNA, or DNA or RNA encoding a heterologous object

sequence, is designed such that one or more elements is operably linked to a tissue-specific promoter, e.g., a promoter that is active in T-cells. In further embodiments, the T-cell active promoter is inactive in other cell types, e.g., B-cells, NK cells. In some embodiments, the T-cell active promoter is derived from a promoter for a gene encoding a component of the T-cell receptor, e.g., TRAC, TRBC, TRGC, TRDC. In some embodiments, the T-cell active promoter is derived from a promoter for a gene encoding a component of a T-cell-specific cluster of differentiation protein, e.g., CD3, e.g., CD3D, CD3E, CD3G, CD3Z. In some embodiments, T-cell-specific promoters in gene modifying systems are discovered by comparing publicly available gene expression data across cell types and selecting promoters from the genes with enhanced expression in T-cells. In some embodiments, promoters may be selecting depending on the desired expression breadth, e.g., promoters that are active in T-cells only, promoters that are active in NK cells only, promoters that are active in both T-cells and NK cells.

Cell-specific promoters known in the art may be used to direct expression of a gene modifying protein, e.g., as described herein. Nonlimiting exemplary mammalian cell-specific promoters have been characterized and used in mice expressing Cre recombinase in a cell-specific manner. Certain nonlimiting exemplary mammalian cell-specific promoters are listed in Table 1 of US9845481, incorporated herein by reference.

In some embodiments, a vector as described herein comprises an expression cassette. Typically, an expression cassette comprises the nucleic acid molecule of the instant invention operatively linked to a promoter sequence. For example, a promoter is operatively linked with a coding sequence when it is capable of affecting the expression of that coding sequence (e.g., the coding sequence is under the transcriptional control of the promoter). Encoding sequences can be operatively linked to regulatory sequences in sense or antisense orientation. In certain embodiments, the promoter is a heterologous promoter. In certain embodiments, an expression cassette may comprise additional elements, for example, an intron, an enhancer, a polyadenylation site, a woodchuck response element (WRE), and/or other elements known to affect expression levels of the encoding sequence. A promoter typically controls the expression of a coding sequence or functional RNA. In certain embodiments, a promoter sequence comprises proximal and more distal upstream elements and can further comprise an enhancer element. An enhancer can typically stimulate promoter activity and may be an innate element of the promoter or a heterologous element inserted to enhance the level or tissue-specificity of a

promoter. In certain embodiments, the promoter is derived in its entirety from a native gene. In certain embodiments, the promoter is composed of different elements derived from different naturally occurring promoters. In certain embodiments, the promoter comprises a synthetic nucleotide sequence. It will be understood by those skilled in the art that different promoters will direct the expression of a gene in different tissues or cell types, or at different stages of development, or in response to different environmental conditions or to the presence or the absence of a drug or transcriptional co-factor. Ubiquitous, cell-type-specific, tissue-specific, developmental stage-specific, and conditional promoters, for example, drug-responsive promoters (e.g., tetracycline-responsive promoters) are well known to those of skill in the art. Exemplary promoters include, but are not limited to, the phosphoglycerate kinase (PKG) promoter, CAG (composite of the CMV enhancer the chicken beta actin promoter (CBA) and the rabbit beta globin intron), NSE (neuronal specific enolase), synapsin or NeuN promoters, the SV40 early promoter, mouse mammary tumor virus LTR promoter; adenovirus major late promoter (Ad MLP), a herpes simplex virus (HSV) promoter, a cytomegalovirus (CMV) promoter such as the CMV immediate early promoter region (CMVIE), SFFV promoter, rous sarcoma virus (RSV) promoter, synthetic promoters, hybrid promoters, and the like. Other promoters can be of human origin or from other species, including from mice. Common promoters include, e.g., the human cytomegalovirus (CMV) immediate early gene promoter, the SV40 early promoter, the Rous sarcoma virus long terminal repeat, [beta]- actin, rat insulin promoter, the phosphoglycerate kinase promoter, the human alpha-1 antitrypsin (hAAT) promoter, the transthyretin promoter, the TBG promoter and other liver-specific promoters, the desmin promoter and similar muscle-specific promoters, the EF1 -alpha promoter, hybrid promoters with multi-tissue specificity, promoters specific for neurons like synapsin and glyceraldehyde-3 -phosphate dehydrogenase promoter, all of which are promoters well known and readily available to those of skill in the art, can be used to obtain high-level expression of the coding sequence of interest. In addition, sequences derived from non-viral genes, such as the murine metallothionein gene, will also find use herein. Such promoter sequences are commercially available from, e.g., Stratagene (San Diego, CA). Additional exemplary promoter sequences are described, for example, in WO2018213786A1 (incorporated by reference herein in its entirety).

In some embodiments, the apolipoprotein E enhancer (ApoE) or a functional fragment thereof is used, e.g., to drive expression in the liver. In some embodiments, two copies of the ApoE enhancer or a functional fragment thereof are used. In some embodiments, the ApoE enhancer or functional fragment thereof is used in combination with a promoter, e.g., the human alpha-1 antitrypsin (hAAT) promoter.

In some embodiments, the regulatory sequences impart tissue-specific gene expression capabilities. In some cases, the tissue-specific regulatory sequences bind tissue-specific transcription factors that induce transcription in a tissue specific manner. Various tissue-specific regulatory sequences (e.g., promoters, enhancers, etc.) are known in the art. Exemplary tissue-specific regulatory sequences include, but are not limited to, the following tissue-specific promoters: a liver-specific thyroxin binding globulin (TBG) promoter, a insulin promoter, a glucagon promoter, a somatostatin promoter, a pancreatic polypeptide (PPY) promoter, a synapsin-1 (Syn) promoter, a creatine kinase (MCK) promoter, a mammalian desmin (DES) promoter, a α-myosin heavy chain (a-MHC) promoter, or a cardiac Troponin T (cTnT) promoter. Other exemplary promoters include Beta-actin promoter, hepatitis B virus core promoter, Sandig et al., Gene Ther., 3:1002-9 (1996); alpha-fetoprotein (AFP) promoter, Arbuthnot et al., Hum. Gene Ther., 7:1503-14 (1996)), bone osteocalcin promoter (Stein et al., Mol. Biol. Rep., 24:185-96 (1997)); bone sialoprotein promoter (Chen et al., J. Bone Miner. Res., 11:654-64 (1996)), CD2 promoter (Hansal et al., J. Immunol., 161:1063-8 (1998); immunoglobulin heavy chain promoter; T cell receptor α-chain promoter, neuronal such as neuron-specific enolase (NSE) promoter (Andersen et al., Cell. Mol. Neurobiol., 13:503-15 (1993)), neurofilament light-chain gene promoter (Piccioli et al., Proc. Natl. Acad. Sci. USA, 88:5611-5 (1991)), and the neuron-specific vgf gene promoter (Piccioli et al., Neuron, 15:373-84 (1995)), and others. Additional exemplary promoter sequences are described, for example, in U.S. Patent No. 10300146 (incorporated herein by reference in its entirety). In some embodiments, a tissue-specific regulatory element, e.g., a tissue-specific promoter, is selected from one known to be operably linked to a gene that is highly expressed in a given tissue, e.g., as measured by RNA-seq or protein expression data, or a combination thereof. Methods for analyzing tissue specificity by expression are taught in Fagerberg et al. *Mol Cell Proteomics* 13(2):397-406 (2014), which is incorporated herein by reference in its entirety.

In some embodiments, a vector described herein is a multicistronic expression construct. Multicistronic expression constructs include, for example, constructs harboring a first expression cassette, e.g. comprising a first promoter and a first encoding nucleic acid sequence, and a second expression cassette, e.g. comprising a second promoter and a second encoding nucleic acid sequence. Such multicistronic expression constructs may, in some instances, be particularly useful in the delivery of non-translated gene products, such as hairpin RNAs, together with a polypeptide, for example, a gene modifying polypeptide and gene modifying template. In some embodiments, multicistronic expression constructs may exhibit reduced expression levels of one or more of the included transgenes, for example, because of promoter interference or the presence of incompatible nucleic acid elements in close proximity. If a multicistronic expression construct is part of a viral vector, the presence of a self-complementary nucleic acid sequence may, in some instances, interfere with the formation of structures necessary for viral reproduction or packaging.

In some embodiments, the sequence encodes an RNA with a hairpin. In some embodiments, the hairpin RNA is a guide RNA, a template RNA, a shRNA, or a microRNA. In some embodiments, the first promoter is an RNA polymerase I promoter. In some embodiments, the first promoter is an RNA polymerase II promoter. In some embodiments, the second promoter is an RNA polymerase III promoter. In some embodiments, the second promoter is a U6 or H1 promoter.

Without wishing to be bound by theory, multicistronic expression constructs may not achieve optimal expression levels as compared to expression systems containing only one cistron. One of the suggested causes of lower expression levels achieved with multicistronic expression constructs comprising two or more promoter elements is the phenomenon of promoter interference (see, e.g., Curtin J A, Dane A P, Swanson A, Alexander I E, Ginn S L. *Bidirectional promoter interference between two widely used internal heterologous promoters in a late-generation lentiviral construct*. Gene Ther. 2008 March; 15(5):384-90; and Martin-Duque P, Jezzard S, Kaftansis L, Vassaux G. *Direct comparison of the insulating properties of two genetic elements in an adenoviral vector containing two different expression cassettes*. Hum Gene Ther. 2004 October; 15(10):995-1002; both references incorporated herein by reference for disclosure of promoter interference phenomenon). In some embodiments, the problem of promoter interference may be overcome, e.g., by producing multicistronic expression constructs

comprising only one promoter driving transcription of multiple encoding nucleic acid sequences separated by internal ribosomal entry sites, or by separating cistrons comprising their own promoter with transcriptional insulator elements. In some embodiments, single-promoter driven expression of multiple cistrons may result in uneven expression levels of the cistrons. In some embodiments, a promoter cannot efficiently be isolated and isolation elements may not be compatible with some gene transfer vectors, for example, some retroviral vectors.

MicroRNAs

MicroRNAs (miRNAs) and other small interfering nucleic acids generally regulate gene expression via target RNA transcript cleavage/degradation or translational repression of the target messenger RNA (mRNA). miRNAs may, in some instances, be natively expressed, typically as final 19-25 non-translated RNA products. miRNAs generally exhibit their activity through sequence-specific interactions with the 3′ untranslated regions (UTR) of target mRNAs. These endogenously expressed miRNAs may form hairpin precursors that are subsequently processed into an miRNA duplex, and further into a mature single stranded miRNA molecule This mature miRNA generally guides a multiprotein complex, miRISC, which identifies target 3′ UTR regions of target mRNAs based upon their complementarity to the mature miRNA. Useful transgene products may include, for example, miRNAs or miRNA binding sites that regulate the expression of a linked polypeptide. A non-limiting list of miRNA genes; the products of these genes and their homologues are useful as transgenes or as targets for small interfering nucleic acids (e.g., miRNA sponges, antisense oligonucleotides), e.g., in methods such as those listed in US10300146, 22:25-25:48, are herein incorporated by reference. In some embodiments, one or more binding sites for one or more of the foregoing miRNAs are incorporated in a transgene, e.g., a transgene delivered by a rAAV vector, e.g., to inhibit the expression of the transgene in one or more tissues of an animal harboring the transgene. In some embodiments, a binding site may be selected to control the expression of a transgene in a tissue specific manner. For example, binding sites for the liver-specific miR-122 may be incorporated into a transgene to inhibit expression of that transgene in the liver. Additional exemplary miRNA sequences are described, for example, in U.S. Patent No. 10,300,146 (incorporated herein by reference in its entirety).

An miR inhibitor or miRNA inhibitor is generally an agent that blocks miRNA expression and/or processing. Examples of such agents include, but are not limited to, microRNA antagonists, microRNA specific antisense, microRNA sponges, and microRNA oligonucleotides (double-stranded, hairpin, short oligonucleotides) that inhibit miRNA interaction with a Drosha complex. MicroRNA inhibitors, e.g., miRNA sponges, can be expressed in cells from transgenes (e.g., as described in Ebert, M. S. Nature Methods, Epub Aug. 12, 2007; incorporated by reference herein in its entirety). In some embodiments, microRNA sponges, or other miR inhibitors, are used with the AAVs. microRNA sponges generally specifically inhibit miRNAs through a complementary heptameric seed sequence. In some embodiments, an entire family of miRNAs can be silenced using a single sponge sequence. Other methods for silencing miRNA function (derepression of miRNA targets) in cells will be apparent to one of ordinary skill in the art.

In some embodiments, a gene modifying system, template RNA, or polypeptide described herein is administered to or is active in (e.g., is more active in) a target tissue, e.g., a first tissue. In some embodiments, the gene modifying system, template RNA, or polypeptide is not administered to or is less active in (e.g., not active in) a non-target tissue. In some embodiments, a gene modifying system, template RNA, or polypeptide described herein is useful for modifying DNA in a target tissue, e.g., a first tissue, (e.g., and not modifying DNA in a non-target tissue).

In some embodiments, a gene modifying system comprises (a) a polypeptide described herein or a nucleic acid encoding the same, (b) a template nucleic acid (e.g., template RNA) described herein, and (c) one or more first tissue-specific expression-control sequences specific to the target tissue, wherein the one or more first tissue-specific expression-control sequences specific to the target tissue are in operative association with (a), (b), or (a) and (b), wherein, when associated with (a), (a) comprises a nucleic acid encoding the polypeptide.

In some embodiments, the nucleic acid in (b) comprises RNA.

In some embodiments, the nucleic acid in (b) comprises DNA.

In some embodiments, the nucleic acid in (b): (i) is single-stranded or comprises a single-stranded segment, e.g., is single-stranded DNA or comprises a single-stranded segment and one or more double stranded segments; (ii) has inverted terminal repeats; or (iii) both (i) and (ii).

In some embodiments, the nucleic acid in (b) is double-stranded or comprises a double-stranded segment.

In some embodiments, (a) comprises a nucleic acid encoding the polypeptide.

In some embodiments, the nucleic acid in (a) comprises RNA.

In some embodiments, the nucleic acid in (a) comprises DNA.

In some embodiments, the nucleic acid in (a): (i) is single-stranded or comprises a single-stranded segment, e.g., is single-stranded DNA or comprises a single-stranded segment and one or more double stranded segments; (ii) has inverted terminal repeats; or (iii) both (i) and (ii).

In some embodiments, the nucleic acid in (a) is double-stranded or comprises a double-stranded segment.

In some embodiments, the nucleic acid in (a), (b), or (a) and (b) is linear.

In some embodiments, the nucleic acid in (a), (b), or (a) and (b) is circular, e.g., a plasmid or minicircle.

In some embodiments, the heterologous object sequence is in operative association with a first promoter.

In some embodiments, the one or more first tissue-specific expression-control sequences comprises a tissue specific promoter.

In some embodiments, the tissue-specific promoter comprises a first promoter in operative association with: (i) the heterologous object sequence, (ii) a nucleic acid encoding the retroviral RT, or (iii) (i) and (ii).

In some embodiments, the one or more first tissue-specific expression-control sequences comprises a tissue-specific microRNA recognition sequence in operative association with: (i) the heterologous object sequence, (ii) a nucleic acid encoding the retroviral RT domain, or (iii) (i) and (ii).

In some embodiments, a system comprises a tissue-specific promoter, and the system further comprises one or more tissue-specific microRNA recognition sequences, wherein: (i) the tissue specific promoter is in operative association with: (I) the heterologous object sequence, (II) a nucleic acid encoding the retroviral RT domain, or (III) (I) and (II); and/or (ii) the one or more tissue-specific microRNA recognition sequences are in operative association with: (I) the heterologous object sequence, (II) a nucleic acid encoding the retroviral RT, or (III) (I) and (II).

In some embodiments, wherein (a) comprises a nucleic acid encoding the polypeptide, the nucleic acid comprises a promoter in operative association with the nucleic acid encoding the polypeptide.

In some embodiments, the nucleic acid encoding the polypeptide comprises one or more second tissue-specific expression-control sequences specific to the target tissue in operative association with the polypeptide coding sequence.

In some embodiments, the one or more second tissue-specific expression-control sequences comprises a tissue specific promoter.

In some embodiments, the tissue-specific promoter is the promoter in operative association with the nucleic acid encoding the polypeptide.

In some embodiments, the one or more second tissue-specific expression-control sequences comprises a tissue-specific microRNA recognition sequence.

In some embodiments, the promoter in operative association with the nucleic acid encoding the polypeptide is a tissue-specific promoter, the system further comprising one or more tissue-specific microRNA recognition sequences.

In some embodiments, a nucleic acid component of a system provided by the invention is a sequence (e.g., encoding the polypeptide or comprising a heterologous object sequence) flanked by untranslated regions (UTRs) that modify protein expression levels. Various 5′ and 3′ UTRs can affect protein expression. For example, in some embodiments, the coding sequence may be preceded by a 5′ UTR that modifies RNA stability or protein translation. In some embodiments, the sequence may be followed by a 3′ UTR that modifies RNA stability or translation. In some embodiments, the sequence may be preceded by a 5′ UTR and followed by a 3′ UTR that modify RNA stability or translation. In some embodiments, the 5′ and/or 3′ UTR may be selected from the 5′ and 3′ UTRs of complement factor 3 (C3) (CACTCCTCCCCATCCTCTCCCTCTGTCCCTCTGTCCCTCTGACCCTGCACTGTCCCAG CACC; SEQ ID NO: 11,004) or orosomucoid 1 (ORM1) (CAGGACACAGCCTTGGATCAGGACAGAGACTTGGGGGCCATCCTGCCCCTCCAACC CGACATGTGTACCTCAGCTTTTTCCCTCACTTGCATCAATAAAGCTTCTGTGTTTGGA ACAGCTAA; SEQ ID NO: 11,005) (Asrani et al. RNA Biology 2018). In certain embodiments, the 5′ UTR is the 5′ UTR from C3 and the 3′ UTR is the 3′ UTR from ORM1. In certain embodiments, a 5′ UTR and 3′ UTR for protein expression, e.g., mRNA (or DNA encoding the

RNA) for a gene modifying polypeptide or heterologous object sequence, comprise optimized expression sequences. In some embodiments, the 5′ UTR comprises GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUAAGAGCCACC (SEQ ID NO: 11,006) and/or the 3′ UTR comprising UGAUAAUAGGCUGGAGCCUCGGUGGCCAUGCUUCUUGCCCCUUGGGCCUCCCCCC AGCCCCUCCUCCCCUUCCUGCACCCGUACCCCCGUGGUCUUUGAAUAAAGUCUGA (SEQ ID NO: 11,007), e.g., as described in Richner et al. *Cell* 168(6): P1114-1125 (2017), the sequences of which are incorporated herein by reference.In some embodiments, a 5′ and/or 3′ UTR may be selected to enhance protein expression. In some embodiments, a 5′ and/or 3′ UTR may be selected to modify protein expression such that overproduction inhibition is minimized. In some embodiments, UTRs are around a coding sequence, e.g., outside the coding sequence and in other embodiments proximal to the coding sequence. In some embodiments, additional regulatory elements (e.g., miRNA binding sites, cis-regulatory sites) are included in the UTRs.

In some embodiments, an open reading frame of a gene modifying system, e.g., an ORF of an mRNA (or DNA encoding an mRNA) encoding a gene modifying polypeptide or one or more ORFs of an mRNA (or DNA encoding an mRNA) of a heterologous object sequence, is flanked by a 5′ and/or 3′ untranslated region (UTR) that enhances the expression thereof. In some embodiments, the 5′ UTR of an mRNA component (or transcript produced from a DNA component) of the system comprises the sequence 5′-GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUAAGAGCCACC-3′; SEQ ID NO: 11,008). In some embodiments, the 3′ UTR of an mRNA component (or transcript produced from a DNA component) of the system comprises the sequence 5′-UGAUAAUAGGCUGGAGCCUCGGUGGCCAUGCUUCUUGCCCCUUGGGCCUCCCCCC AGCCCCUCCUCCCCUUCCUGCACCCGUACCCCCGUGGUCUUUGAAUAAAGUCUGA-3′ (SEQ ID NO: 11,009). This combination of 5′ UTR and 3′ UTR has been shown to result in desirable expression of an operably linked ORF by Richner et al. *Cell* 168(6): P1114-1125 (2017), the teachings and sequences of which are incorporated herein by reference. In some embodiments, a system described herein comprises a DNA encoding a transcript, wherein the DNA comprises the corresponding 5′ UTR and 3′ UTR sequences, with T substituting for U in the above-listed sequence). In some embodiments, a DNA vector used to produce an RNA component of the system further comprises a promoter upstream of the 5′ UTR for initiating *in*

vitro transcription, e.g, a T7, T3, or SP6 promoter. The 5′ UTR above begins with GGG, which is a suitable start for optimizing transcription using T7 RNA polymerase. For tuning transcription levels and altering the transcription start site nucleotides to fit alternative 5′ UTRs, the teachings of Davidson et al. *Pac Symp Biocomput* 433-443 (2010) describe T7 promoter variants, and the methods of discovery thereof, that fulfill both of these traits.

Viral vectors and components thereof

Viruses are a useful source of delivery vehicles for the systems described herein, in addition to a source of relevant enzymes or domains as described herein, e.g., as sources of polymerases and polymerase functions used herein, e.g., DNA-dependent DNA polymerase, RNA-dependent RNA polymerase, RNA-dependent DNA polymerase, DNA-dependent RNA polymerase, reverse transcriptase. Some enzymes, e.g., reverse transcriptases, may have multiple activities, e.g., be capable of both RNA-dependent DNA polymerization and DNA-dependent DNA polymerization, e.g., first and second strand synthesis. In some embodiments, the virus used as a gene modifying delivery system or a source of components thereof may be selected from a group as described by Baltimore *Bacteriol Rev* 35(3):235-241 (1971).

In some embodiments, the virus is selected from a Group I virus, e.g., is a DNA virus and packages dsDNA into virions. In some embodiments, the Group I virus is selected from, e.g., Adenoviruses, Herpesviruses, Poxviruses.

In some embodiments, the virus is selected from a Group II virus, e.g., is a DNA virus and packages ssDNA into virions. In some embodiments, the Group II virus is selected from, e.g., Parvoviruses. In some embodiments, the parvovirus is a dependoparvovirus, e.g., an adeno-associated virus (AAV).

In some embodiments, the virus is selected from a Group III virus, e.g., is an RNA virus and packages dsRNA into virions. In some embodiments, the Group III virus is selected from, e.g., Reoviruses. In some embodiments, one or both strands of the dsRNA contained in such virions is a coding molecule able to serve directly as mRNA upon transduction into a host cell, e.g., can be directly translated into protein upon transduction into a host cell without requiring any intervening nucleic acid replication or polymerization steps.

In some embodiments, the virus is selected from a Group IV virus, e.g., is an RNA virus and packages ssRNA(+) into virions. In some embodiments, the Group IV virus is selected

from, e.g., Coronaviruses, Picornaviruses, Togaviruses. In some embodiments, the ssRNA(+) contained in such virions is a coding molecule able to serve directly as mRNA upon transduction into a host cell, e.g., can be directly translated into protein upon transduction into a host cell without requiring any intervening nucleic acid replication or polymerization steps.

In some embodiments, the virus is selected from a Group V virus, e.g., is an RNA virus and packages ssRNA(-) into virions. In some embodiments, the Group V virus is selected from, e.g., Orthomyxoviruses, Rhabdoviruses. In some embodiments, an RNA virus with an ssRNA(-) genome also carries an enzyme inside the virion that is transduced to host cells with the viral genome, e.g., an RNA-dependent RNA polymerase, capable of copying the ssRNA(-) into ssRNA(+) that can be translated directly by the host.

In some embodiments, the virus is selected from a Group VI virus, e.g., is a retrovirus and packages ssRNA(+) into virions. In some embodiments, the Group VI virus is selected from, e.g., retroviruses. In some embodiments, the retrovirus is a lentivirus, e.g., HIV-1, HIV-2, SIV, BIV. In some embodiments, the retrovirus is a spumavirus, e.g., a foamy virus, e.g., HFV, SFV, BFV. In some embodiments, the ssRNA(+) contained in such virions is a coding molecule able to serve directly as mRNA upon transduction into a host cell, e.g., can be directly translated into protein upon transduction into a host cell without requiring any intervening nucleic acid replication or polymerization steps. In some embodiments, the ssRNA(+) is first reverse transcribed and copied to generate a dsDNA genome intermediate from which mRNA can be transcribed in the host cell. In some embodiments, an RNA virus with an ssRNA(+) genome also carries an enzyme inside the virion that is transduced to host cells with the viral genome, e.g., an RNA-dependent DNA polymerase, capable of copying the ssRNA(+) into dsDNA that can be transcribed into mRNA and translated by the host. In some embodiments, the reverse transcriptase from a Group VI retrovirus is incorporated as the reverse transcriptase domain of a gene modifying polypeptide.

In some embodiments, the virus is selected from a Group VII virus, e.g., is a retrovirus and packages dsRNA into virions. In some embodiments, the Group VII virus is selected from, e.g., Hepadnaviruses. In some embodiments, one or both strands of the dsRNA contained in such virions is a coding molecule able to serve directly as mRNA upon transduction into a host cell, e.g., can be directly translated into protein upon transduction into a host cell without requiring any intervening nucleic acid replication or polymerization steps. In some

embodiments, one or both strands of the dsRNA contained in such virions is first reverse transcribed and copied to generate a dsDNA genome intermediate from which mRNA can be transcribed in the host cell. In some embodiments, an RNA virus with a dsRNA genome also carries an enzyme inside the virion that is transduced to host cells with the viral genome, e.g., an RNA-dependent DNA polymerase, capable of copying the dsRNA into dsDNA that can be transcribed into mRNA and translated by the host. In some embodiments, the reverse transcriptase from a Group VII retrovirus is incorporated as the reverse transcriptase domain of a gene modifying polypeptide.

In some embodiments, virions used to deliver nucleic acid in this invention may also carry enzymes involved in the process of gene modification. For example, a retroviral virion may contain a reverse transcriptase domain that is delivered into a host cell along with the nucleic acid. In some embodiments, an RNA template may be associated with a gene modifying polypeptide within a virion, such that both are co-delivered to a target cell upon transduction of the nucleic acid from the viral particle. In some embodiments, the nucleic acid in a virion may comprise DNA, e.g., linear ssDNA, linear dsDNA, circular ssDNA, circular dsDNA, minicircle DNA, dbDNA, ceDNA. In some embodiments, the nucleic acid in a virion may comprise RNA, e.g., linear ssRNA, linear dsRNA, circular ssRNA, circular dsRNA. In some embodiments, a viral genome may circularize upon transduction into a host cell, e.g., a linear ssRNA molecule may undergo a covalent linkage to form a circular ssRNA, a linear dsRNA molecule may undergo a covalent linkage to form a circular dsRNA or one or more circular ssRNA. In some embodiments, a viral genome may replicate by rolling circle replication in a host cell. In some embodiments, a viral genome may comprise a single nucleic acid molecule, e.g., comprise a non-segmented genome. In some embodiments, a viral genome may comprise two or more nucleic acid molecules, e.g., comprise a segmented genome. In some embodiments, a nucleic acid in a virion may be associated with one or proteins. In some embodiments, one or more proteins in a virion may be delivered to a host cell upon transduction. In some embodiments, a natural virus may be adapted for nucleic acid delivery by the addition of virion packaging signals to the target nucleic acid, wherein a host cell is used to package the target nucleic acid containing the packaging signals.

In some embodiments, a virion used as a delivery vehicle may comprise a commensal human virus. In some embodiments, a virion used as a delivery vehicle may comprise an

anellovirus, the use of which is described in WO2018232017A1, which is incorporated herein by reference in its entirety.

AAV Administration

In some embodiments, an adeno-associated virus (AAV) is used in conjunction with the system, template nucleic acid, and/or polypeptide described herein. In some embodiments, an AAV is used to deliver, administer, or package the system, template nucleic acid, and/or polypeptide described herein. In some embodiments, the AAV is a recombinant AAV (rAAV).

In some embodiments, a system comprises (a) a polypeptide described herein or a nucleic acid encoding the same, (b) a template nucleic acid (e.g., template RNA) described herein, and (c) one or more first tissue-specific expression-control sequences specific to the target tissue, wherein the one or more first tissue-specific expression-control sequences specific to the target tissue are in operative association with (a), (b), or (a) and (b), wherein, when associated with (a), (a) comprises a nucleic acid encoding the polypeptide.

In some embodiments, a system described herein further comprises a first recombinant adeno-associated virus (rAAV) capsid protein; wherein the at least one of (a) or (b) is associated with the first rAAV capsid protein, wherein at least one of (a) or (b) is flanked by AAV inverted terminal repeats (ITRs).

In some embodiments, (a) and (b) are associated with the first rAAV capsid protein.

In some embodiments, (a) and (b) are on a single nucleic acid.

In some embodiments, the system further comprises a second rAAV capsid protein, wherein at least one of (a) or (b) is associated with the second rAAV capsid protein, and wherein the at least one of (a) or (b) associated with the second rAAV capsid protein is different from the at least one of (a) or (b) is associated with the first rAAV capsid protein.

In some embodiments, the at least one of (a) or (b) is associated with the first or second rAAV capsid protein is dispersed in the interior of the first or second rAAV capsid protein, which first or second rAAV capsid protein is in the form of an AAV capsid particle.

In some embodiments, the system further comprises a nanoparticle, wherein the nanoparticle is associated with at least one of (a) or (b).

In some embodiments, (a) and (b), respectively are associated with: a) a first rAAV capsid protein and a second rAAV capsid protein; b) a nanoparticle and a first rAAV capsid

protein; c) a first rAAV capsid protein; d) a first adenovirus capsid protein; e) a first nanoparticle and a second nanoparticle; or f) a first nanoparticle.

Viral vectors are useful for delivering all or part of a system provided by the invention, e.g., for use in methods provided by the invention. Systems derived from different viruses have been employed for the delivery of polypeptides or nucleic acids; for example: integrase-deficient lentivirus, adenovirus, adeno-associated virus (AAV), herpes simplex virus, and baculovirus (reviewed in Hodge et al. Hum Gene Ther 2017; Narayanavari et al. Crit Rev Biochem Mol Biol 2017; Boehme et al. Curr Gene Ther 2015).

Adenoviruses are common viruses that have been used as gene delivery vehicles given well-defined biology, genetic stability, high transduction efficiency, and ease of large-scale production (see, for example, review by Lee et al. Genes & Diseases 2017). They possess linear dsDNA genomes and come in a variety of serotypes that differ in tissue and cell tropisms. In order to prevent replication of infectious virus in recipient cells, adenovirus genomes used for packaging are deleted of some or all endogenous viral proteins, which are provided in trans in viral production cells. This renders the genomes helper-dependent, meaning they can only be replicated and packaged into viral particles in the presence of the missing components provided by so-called helper functions. A helper-dependent adenovirus system with all viral ORFs removed may be compatible with packaging foreign DNA of up to ~37 kb (Parks et al. J Virol 1997). In some embodiments, an adenoviral vector is used to deliver DNA corresponding to the polypeptide or template component of the gene modifying system, or both are contained on separate or the same adenoviral vector. In some embodiments, the adenovirus is a helper-dependent adenovirus (HD-AdV) that is incapable of self-packaging. In some embodiments, the adenovirus is a high-capacity adenovirus (HC-AdV) that has had all or a substantial portion of endogenous viral ORFs deleted, while retaining the necessary sequence components for packaging into adenoviral particles. For this type of vector, the only adenoviral sequences required for genome packaging are noncoding sequences: the inverted terminal repeats (ITRs) at both ends and the packaging signal at the 5′-end (Jager et al. Nat Protoc 2009). In some embodiments, the adenoviral genome also comprises stuffer DNA to meet a minimal genome size for optimal production and stability (see, for example, Hausl et al. Mol Ther 2010). In some embodiments, an adenovirus is used to deliver a gene modifying system to the liver.

In some embodiments, an adenovirus is used to deliver a gene modifying system to HSCs, e.g., HDAd5/35++. HDAd5/35++ is an adenovirus with modified serotype 35 fibers that de-target the vector from the liver (Wang et al. Blood Adv 2019). In some embodiments, the adenovirus that delivers a gene modifying system to HSCs utilizes a receptor that is expressed specifically on primitive HSCs, e.g., CD46.

Adeno-associated viruses (AAV) belong to the parvoviridae family and more specifically constitute the dependoparvovirus genus. The AAV genome is composed of a linear single-stranded DNA molecule which contains approximately 4.7 kilobases (kb) and consists of two major open reading frames (ORFs) encoding the non-structural Rep (replication) and structural Cap (capsid) proteins. A second ORF within the cap gene was identified that encodes the assembly-activating protein (AAP). The DNAs flanking the AAV coding regions are two cis-acting inverted terminal repeat (ITR) sequences, approximately 145 nucleotides in length, with interrupted palindromic sequences that can be folded into energetically stable hairpin structures that function as primers of DNA replication. In addition to their role in DNA replication, the ITR sequences have been shown to be involved in viral DNA integration into the cellular genome, rescue from the host genome or plasmid, and encapsidation of viral nucleic acid into mature virions (Muzyczka, (1992) Curr. Top. Micro. Immunol. 158:97-129). In some embodiments, one or more gene modifying nucleic acid components is flanked by ITRs derived from AAV for viral packaging. See, e.g., WO2019113310.

In some embodiments, one or more components of the gene modifying system are carried via at least one AAV vector. In some embodiments, the at least one AAV vector is selected for tropism to a particular cell, tissue, organism. In some embodiments, the AAV vector is pseudotyped, e.g., AAV2/8, wherein AAV2 describes the design of the construct but the capsid protein is replaced by that from AAV8. It is understood that any of the described vectors could be pseudotype derivatives, wherein the capsid protein used to package the AAV genome is derived from that of a different AAV serotype. Without wishing to be limited in vector choice, a list of exemplary AAV serotypes can be found in Table 18. In some embodiments, an AAV to be employed for gene modifying may be evolved for novel cell or tissue tropism as has been demonstrated in the literature (e.g., Davidsson et al. Proc Natl Acad Sci U S A 2019).

In some embodiments, the AAV delivery vector is a vector which has two AAV inverted terminal repeats (ITRs) and a nucleotide sequence of interest (for example, a sequence coding for

a gene modifying polypeptideor a DNA template, or both), each of said ITRs having an interrupted (or noncontiguous) palindromic sequence, i.e., a sequence composed of three segments: a first segment and a last segment that are identical when read 5'→ 3' but hybridize when placed against each other, and a segment that is different that separates the identical segments. See, for example, WO2012123430.

Conventionally, AAV virions with capsids are produced by introducing a plasmid or plasmids encoding the rAAV or scAAV genome, Rep proteins, and Cap proteins (Grimm et al, 1998). Upon introduction of these helper plasmids in trans, the AAV genome is "rescued" (i.e., released and subsequently recovered) from the host genome, and is further encapsidated to produce infectious AAV. In some embodiments, one or more gene modifying nucleic acids are packaged into AAV particles by introducing the ITR-flanked nucleic acids into a packaging cell in conjunction with the helper functions.

In some embodiments, the AAV genome is a so called self-complementary genome (referred to as scAAV), such that the sequence located between the ITRs contains both the desired nucleic acid sequence (e.g., DNA encoding the gene modifying polypeptide or template, or both) in addition to the reverse complement of the desired nucleic acid sequence, such that these two components can fold over and self-hybridize. In some embodiments, the self-complementary modules are separated by an intervening sequence that permits the DNA to fold back on itself, e.g., forms a stem-loop. An scAAV has the advantage of being poised for transcription upon entering the nucleus, rather than being first dependent on ITR priming and second-strand synthesis to form dsDNA. In some embodiments, one or more gene modifying components is designed as an scAAV, wherein the sequence between the AAV ITRs contains two reverse complementing modules that can self-hybridize to create dsDNA.

In some embodiments, nucleic acid (e.g., encoding a polypeptide, or a template, or both) delivered to cells is closed-ended, linear duplex DNA (CELiD DNA or ceDNA). In some embodiments, ceDNA is derived from the replicative form of the AAV genome (Li et al. PLoS One 2013). In some embodiments, the nucleic acid (e.g., encoding a polypeptide, or a template DNA, or both) is flanked by ITRs, e.g., AAV ITRs, wherein at least one of the ITRs comprises a terminal resolution site and a replication protein binding site (sometimes referred to as a replicative protein binding site). In some embodiments, the ITRs are derived from an adeno-

associated virus, e.g., AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAV9, AAV10, AAV11, AAV12, or a combination thereof. In some embodiments, the ITRs are symmetric. In some embodiments, the ITRs are asymmetric. In some embodiments, at least one Rep protein is provided to enable replication of the construct. In some embodiments, the at least one Rep protein is derived from an adeno-associated virus, e.g., AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAV9, AAV10, AAV11, AAV12, or a combination thereof. In some embodiments, ceDNA is generated by providing a production cell with (i) DNA flanked by ITRs, e.g., AAV ITRs, and (ii) components required for ITR-dependent replication, e.g., AAV proteins Rep78 and Rep52 (or nucleic acid encoding the proteins). In some embodiments, ceDNA is free of any capsid protein, e.g., is not packaged into an infectious AAV particle. In some embodiments, ceDNA is formulated into LNPs (see, for example, WO2019051289A1).

In some embodiments, the ceDNA vector consists of two self-complementary sequences, e.g., asymmetrical or symmetrical or substantially symmetrical ITRs as defined herein, flanking said expression cassette, wherein the ceDNA vector is not associated with a capsid protein. In some embodiments, the ceDNA vector comprises two self-complementary sequences found in an AAV genome, where at least one ITR comprises an operative Rep-binding element (RBE) (also sometimes referred to herein as "RBS") and a terminal resolution site (trs) of AAV or a functional variant of the RBE. See, for example, WO2019113310.

In some embodiments, the AAV genome comprises two genes that encode four replication proteins and three capsid proteins, respectively. In some embodiments, the genes are flanked on either side by 145-bp inverted terminal repeats (ITRs). In some embodiments, the virion comprises up to three capsid proteins (Vp1, Vp2, and/or Vp3), e.g., produced in a 1:1:10 ratio. In some embodiments, the capsid proteins are produced from the same open reading frame and/or from differential splicing (Vp1) and alternative translational start sites (Vp2 and Vp3, respectively). Generally, Vp3 is the most abundant subunit in the virion and participates in receptor recognition at the cell surface defining the tropism of the virus. In some embodiments, Vp1 comprises a phospholipase domain, e.g., which functions in viral infectivity, in the N-terminus of Vp1.

In some embodiments, packaging capacity of the viral vectors limits the size of the gene modifying system that can be packaged into the vector. For example, the packaging capacity of

the AAVs can be about 4.5 kb (e.g., about 3.0, 3.5, 4.0, 4.5, 5.0, 5.5, or 6.0 kb), e.g., including one or two inverted terminal repeats (ITRs), e.g., 145 base ITRs.

In some embodiments, recombinant AAV (rAAV) comprises cis-acting 145-bp ITRs flanking vector transgene cassettes, e.g., providing up to 4.5 kb for packaging of foreign DNA. Subsequent to infection, rAAV can, in some instances, express a fusion protein of the invention and persist without integration into the host genome by existing episomally in circular head-to-tail concatemers. rAAV can be used, for example, *in vitro* and *in vivo*. In some embodiments, AAV-mediated gene delivery requires that the length of the coding sequence of the gene is equal or greater in size than the wild-type AAV genome.

AAV delivery of genes that exceed this size and/or the use of large physiological regulatory elements can be accomplished, for example, by dividing the protein(s) to be delivered into two or more fragments. In some embodiments, the N-terminal fragment is fused to an intein-N sequence. In some embodiments, the C- terminal fragment is fused to an intein-C sequence. In embodiments, the fragments are packaged into two or more AAV vectors.

In some embodiments, dual AAV vectors are generated by splitting a large transgene expression cassette in two separate halves (5′ and 3′ ends, or head and tail), e.g., wherein each half of the cassette is packaged in a single AAV vector (of <5 kb). The re-assembly of the full-length transgene expression cassette can, in some embodiments, then be achieved upon co-infection of the same cell by both dual AAV vectors. In some embodiments, co-infection is followed by one or more of: (1) homologous recombination (HR) between 5′ and 3′ genomes (dual AAV overlapping vectors); (2) ITR-mediated tail-to-head concatemerization of 5′ and 3′ genomes (dual AAV trans-splicing vectors); and/or (3) a combination of these two mechanisms (dual AAV hybrid vectors). In some embodiments, the use of dual AAV vectors *in vivo* results in the expression of full-length proteins. In some embodiments, the use of the dual AAV vector platform represents an efficient and viable gene transfer strategy for transgenes of greater than about 4.0, 4.1, 4.2, 4.3, 4.4, 4.5, 4.6, 4.7, 4.8, 4.9, or 5.0 kb in size. In some embodiments, AAV vectors can also be used to transduce cells with target nucleic acids, e.g., in the *in vitro* production of nucleic acids and peptides. In some embodiments, AAV vectors can be used for *in vivo* and *ex vivo* gene therapy procedures (see, e.g., West et al., Virology 160:38-47 (1987); U.S. Patent No. 4,797,368; WO 93/24641; Kotin, Human Gene Therapy 5:793-801 (1994); Muzyczka, J. Clin. Invest.94:1351 (1994); each of which is incorporated herein by reference in

their entirety). The construction of recombinant AAV vectors is described in a number of publications, including U.S. Patent No.5,173,414; Tratschin et al., Mol. Cell. Biol.5:3251- 3260 (1985); Tratschin, et al., Mol. Cell. Biol.4:2072-2081 (1984); Hermonat & Muzyczka, PNAS 81:6466-6470 (1984); and Samulski et al., J. Virol.63:03822-3828 (1989) (incorporated by reference herein in their entirety).

In some embodiments, a gene modifying polypeptide described herein (e.g., with or without one or more guide nucleic acids) can be delivered using AAV, lentivirus, adenovirus or other plasmid or viral vector types, in particular, using formulations and doses from, for example, U.S. Patent No. 8,454,972 (formulations, doses for adenovirus), U.S. Patent No.8,404,658 (formulations, doses for AAV) and U.S. Patent No.5,846,946 (formulations, doses for DNA plasmids) and from clinical trials and publications regarding the clinical trials involving lentivirus, AAV and adenovirus. For example, for AAV, the route of administration, formulation and dose can be as described in U.S. Patent No.8,454,972 and as in clinical trials involving AAV. For adenovirus, the route of administration, formulation and dose can be as described in U.S. Patent No.8,404,658 and as in clinical trials involving adenovirus. For plasmid delivery, the route of administration, formulation and dose can be as described in U.S. Patent No.5,846,946 and as in clinical studies involving plasmids. Doses can be based on or extrapolated to an average 70 kg individual (e.g. a male adult human), and can be adjusted for patients, subjects, mammals of different weight and species. Frequency of administration is within the ambit of the medical or veterinary practitioner (e.g., physician, veterinarian), depending on usual factors including the age, sex, general health, other conditions of the patient or subject and the particular condition or symptoms being addressed. In some embodiments, the viral vectors can be injected into the tissue of interest. For cell-type specific gene modifying, the expression of the gene modifying polypeptide and optional guide nucleic acid can, in some embodiments, be driven by a cell-type specific promoter.

In some embodiments, AAV allows for low toxicity, for example, due to the purification method not requiring ultracentrifugation of cell particles that can activate the immune response. In some embodiments, AAV allows low probability of causing insertional mutagenesis, for example, because it does not substantially integrate into the host genome.

In some embodiments, AAV has a packaging limit of about 4.4, 4.5, 4.6, 4.7, or 4.75 kb. In some embodiments, a gene modifying polypeptide-encoding sequence, promoter, and

transcription terminator can fit into a single viral vector. SpCas9 (4.1 kb) may, in some instances, be difficult to package into AAV. Therefore, in some embodiments, a gene modifying polypeptide coding sequence is used that is shorter in length than other gene modifying polypeptide coding sequences or base editors. In some embodiments, the gene modifying polypeptide encoding sequences are less than about 4.5 kb, 4.4 kb, 4.3 kb, 4.2 kb, 4.1 kb, 4 kb, 3.9 kb, 3.8 kb, 3.7 kb, 3.6 kb, 3.5 kb, 3.4 kb, 3.3 kb, 3.2 kb, 3.1 kb, 3 kb, 2.9 kb, 2.8 kb, 2.7 kb, 2.6 kb, 2.5 kb, 2 kb, or 1.5 kb.

An AAV can be AAV1, AAV2, AAV5 or any combination thereof. In some embodiments, the type of AAV is selected with respect to the cells to be targeted; e.g., AAV serotypes 1, 2, 5 or a hybrid capsid AAV1, AAV2, AAV5 or any combination thereof can be selected for targeting brain or neuronal cells; or AAV4 can be selected for targeting cardiac tissue. In some embodiments, AAV8 is selected for delivery to the liver. Exemplary AAV serotypes as to these cells are described, for example, in Grimm, D. et al, J. Virol.82: 5887-5911 (2008) (incorporated herein by reference in its entirety). In some embodiments, AAV refers all serotypes, subtypes, and naturally-occurring AAV as well as recombinant AAV. AAV may be used to refer to the virus itself or a derivative thereof. In some embodiments, AAV includes AAV1, AAV2, AAV3, AAV3B, AAV4, AAV5, AAV6, AAV6.2, AAV7, AAVrh.64Rl, AAVhu.37, AAVrh.8, AAVrh.32.33, AAV8, AAV9, AAV-DJ, AAV2/8, AAVrhlO, AAVLK03, AV10, AAV11, AAV 12, rhlO, and hybrids thereof, avian AAV, bovine AAV, canine AAV, equine AAV, primate AAV, non-primate AAV, and ovine AAV. The genomic sequences of various serotypes of AAV, as well as the sequences of the native terminal repeats (TRs), Rep proteins, and capsid subunits are known in the art. Such sequences may be found in the literature or in public databases such as GenBank. Additional exemplary AAV serotypes are listed in Table 18.

Table 18. Exemplary AAV serotypes.

Target Tissue	Vehicle	Reference
Liver	AAV (AAV8[1], AAVrh.8[1], AAVhu.37[1], AAV2/8, AAV2/rh10[2], AAV9, AAV2,	1. Wang *et al.*, *Mol. Ther.* **18**, 118–25 (2010)

	NP40[3], NP59[2,3], AAV3B[5], AAV-DJ[4], AAV-LK01[4], AAV-LK02[4], AAV-LK03[4], AAV-LK19[4], AAV5[7] Adenovirus (Ad5, HC-AdV[6])	2. Ginn *et al.*, *JHEP Reports*, 100065 (2019) 3. Paulk *et al.*, *Mol. Ther.* **26**, 289–303 (2018). 4. L. Lisowski *et al.*, *Nature*. **506**, 382–6 (2014). 5. L. Wang *et al.*, *Mol. Ther.* **23**, 1877–87 (2015). 6. Hausl *Mol Ther* (2010) 7. Davidoff *et al.*, *Mol. Ther.* 11, 875-88 (2005)
Lung	AAV (AAV4, AAV5, AAV6[1], AAV9, H22[2]) Adenovirus (Ad5, Ad3, Ad21, Ad14)[3]	1. Duncan *et al.*, *Mol Ther Methods Clin Dev* (2018) 2. Cooney *et al.*, Am J Respir Cell Mol Biol (2019) 3. Li *et al.*, *Mol Ther Methods Clin Dev* (2019)
Skin	AAV (AAV6[1], AAV-LK19[2])	1. Petek et al., *Mol. Ther.* (2010) 2. L. Lisowski *et al.*, *Nature*. **506**, 382–6 (2014).
HSCs	Adenovirus (HDAd5/35^{++})	Wang et al. *Blood Adv* (2019)

In some embodiments, a pharmaceutical composition (e.g., comprising an AAV as described herein) has less than 10% empty capsids, less than 8% empty capsids, less than 7% empty capsids, less than 5% empty capsids, less than 3% empty capsids, or less than 1 % empty

capsids. In some embodiments, the pharmaceutical composition has less than about 5% empty capsids. In some embodiments, the number of empty capsids is below the limit of detection. In some embodiments, it is advantageous for the pharmaceutical composition to have low amounts of empty capsids, e.g., because empty capsids may generate an adverse response (e.g., immune response, inflammatory response, liver response, and/or cardiac response), e.g., with little or no substantial therapeutic benefit.

In some embodiments, the residual host cell protein (rHCP) in the pharmaceutical composition is less than or equal to 100 ng/ml rHCP per 1 x 10^{13} vg/ml, e.g., less than or equal to 40 ng/ml rHCP per 1 x 10^{13} vg/ml or 1-50 ng/ml rHCP per 1 x 10^{13} vg/ml. In some embodiments, the pharmaceutical composition comprises less than 10 ng rHCP per 1.0 x 10^{13} vg, or less than 5 ng rHCP per 1.0 x 10^{13} vg, less than 4 ng rHCP per 1.0 x 10^{13} vg, or less than 3 ng rHCP per 1.0 x 10^{13} vg, or any concentration in between. In some embodiments, the residual host cell DNA (hcDNA) in the pharmaceutical composition is less than or equal to 5 x 10^{6} pg/ml hcDNA per 1 x 10^{13} vg/ml, less than or equal to 1.2 x 10^{6} pg/ml hcDNA per 1 x 10^{13} vg/ml, or 1 x 10^{5} pg/ml hcDNA per 1 x 10^{13} vg/ml. In some embodiments, the residual host cell DNA in said pharmaceutical composition is less than 5.0 x 10^{5} pg per 1 x 10^{13} vg, less than 2.0 x 10^{5} pg per 1.0 x 10^{13} vg, less than 1.1 x 10^{5} pg per 1.0 x 10^{13} vg, less than 1.0 x 10^{5} pg hcDNA per 1.0 x 10^{13} vg, less than 0.9 x 10^{5} pg hcDNA per 1.0 x 10^{13} vg, less than 0.8 x 10^{5} pg hcDNA per 1.0 x 10^{13} vg, or any concentration in between.

In some embodiments, the residual plasmid DNA in the pharmaceutical composition is less than or equal to 1.7 x 10^{5} pg/ml per 1.0 x 10^{13} vg/ml, or 1 x 10^{5} pg/ml per 1 x 1.0 x 10^{13} vg/ml, or 1.7 x 10^{6} pg/ml per 1.0 x 10^{13} vg/ml. In some embodiments, the residual DNA plasmid in the pharmaceutical composition is less than 10.0 x 10^{5} pg by 1.0 x 10^{13} vg, less than 8.0 x 10^{5} pg by 1.0 x 10^{13} vg or less than 6.8 x 10^{5} pg by 1.0 x 10^{13} vg. In embodiments, the pharmaceutical composition comprises less than 0.5 ng per 1.0 x 10^{13} vg, less than 0.3 ng per 1.0 x 10^{13} vg, less than 0.22 ng per 1.0 x 10^{13} vg or less than 0.2 ng per 1.0 x 10^{13} vg or any intermediate concentration of bovine serum albumin (BSA). In embodiments, the benzonase in the pharmaceutical composition is less than 0.2 ng by 1.0 x 10^{13} vg, less than 0.1 ng by 1.0 x 10^{13} vg, less than 0.09 ng by 1.0 x 10^{13} vg, less than 0.08 ng by 1.0 x 10^{13} vg or any intermediate concentration. In embodiments, Poloxamer 188 in the pharmaceutical composition is about 10 to 150 ppm, about 15 to 100 ppm or about 20 to 80 ppm. In embodiments, the cesium in the

pharmaceutical composition is less than 50 pg / g (ppm), less than 30 pg / g (ppm) or less than 20 pg / g (ppm) or any intermediate concentration.

In embodiments, the pharmaceutical composition comprises total impurities, e.g., as determined by SDS-PAGE, of less than 10%, less than 8%, less than 7%, less than 6%, less than 5%, less than 4%, less than 3%, less than 2%, or any percentage in between. In embodiments, the total purity, e.g., as determined by SDS-PAGE, is greater than 90%, greater than 92%, greater than 93%, greater than 94%, greater than 95%, greater than 96%, greater than 97%, greater than 98%, or any percentage in between. In embodiments, no single unnamed related impurity, e.g., as measured by SDS-PAGE, is greater than 5%, greater than 4%, greater than 3% or greater than 2%, or any percentage in between. In embodiments, the pharmaceutical composition comprises a percentage of filled capsids relative to total capsids (e.g., peak 1 + peak 2 as measured by analytical ultracentrifugation) of greater than 85%, greater than 86%, greater than 87%, greater than 88%, greater than 89%, greater than 90%, greater than 91%, greater than 91.9%, greater than 92%, greater than 93%, or any percentage in between. In embodiments of the pharmaceutical composition, the percentage of filled capsids measured in peak 1 by analytical ultracentrifugation is 20-80%, 25-75%, 30-75%, 35-75%, or 37.4-70.3%. In embodiments of the pharmaceutical composition, the percentage of filled capsids measured in peak 2 by analytical ultracentrifugation is 20-80%, 20-70%, 22-65%, 24-62%, or 24.9-60.1%.

In one embodiment, the pharmaceutical composition comprises a genomic titer of 1.0 to 5.0×10^{13} vg / mL, 1.2 to 3.0×10^{13} vg / mL or 1.7 to 2.3×10^{13} vg / ml. In one embodiment, the pharmaceutical composition exhibits a biological load of less than 5 CFU / mL, less than 4 CFU / mL, less than 3 CFU / mL, less than 2 CFU / mL or less than 1 CFU / mL or any intermediate contraction. In embodiments, the amount of endotoxin according to USP, for example, USP <85> (incorporated by reference in its entirety) is less than 1.0 EU / mL, less than 0.8 EU / mL or less than 0.75 EU / mL. In embodiments, the osmolarity of a pharmaceutical composition according to USP, for example, USP <785> (incorporated by reference in its entirety) is 350 to 450 mOsm / kg, 370 to 440 mOsm / kg or 390 to 430 mOsm / kg. In embodiments, the pharmaceutical composition contains less than 1200 particles that are greater than 25 μm per container, less than 1000 particles that are greater than 25 μm per container, less than 500 particles that are greater than 25 μm per container or any intermediate value. In embodiments, the pharmaceutical composition contains less than 10,000 particles that are greater than 10 μm

per container, less than 8000 particles that are greater than 10 μm per container or less than 600 particles that are greater than 10 pm per container.

In one embodiment, the pharmaceutical composition has a genomic titer of 0.5 to 5.0 x 10^{13} vg / mL, 1.0 to 4.0 x 10^{13} vg / mL, 1.5 to 3.0 x 10^{13} vg / ml or 1.7 to 2.3 x 10^{13} vg / ml. In one embodiment, the pharmaceutical composition described herein comprises one or more of the following: less than about 0.09 ng benzonase per 1.0 x 10^{13} vg, less than about 30 pg / g (ppm) of cesium, about 20 to 80 ppm Poloxamer 188, less than about 0.22 ng BSA per 1.0 x 10^{13} vg, less than about 6.8 x 10^{5} pg of residual DNA plasmid per 1.0 x 10^{13} vg, less than about 1.1 x 10^{5} pg of residual hcDNA per 1.0 x 10^{13} vg, less than about 4 ng of rHCP per 1.0 x 10^{13} vg, pH 7.7 to 8.3, about 390 to 430 mOsm / kg, less than about 600 particles that are > 25 μm in size per container, less than about 6000 particles that are > 10 μm in size per container, about 1.7 x 10^{13} - 2.3 x 10^{13} vg / mL genomic titer, infectious titer of about 3.9 x 10^{8} to 8.4 x 10^{10} IU per 1.0 x 10^{13} vg, total protein of about 100-300 pg per 1.0 x 10^{13} vg, mean survival of >24 days in A7SMA mice with about 7.5 x 10^{13} vg / kg dose of viral vector, about 70 to 130% relative potency based on an *in vitro* cell based assay and / or less than about 5% empty capsid. In various embodiments, the pharmaceutical compositions described herein comprise any of the viral particles discussed here, retain a potency of between ± 20%, between ± 15%, between ± 10% or within ± 5% of a reference standard. In some embodiments, potency is measured using a suitable *in vitro* cell assay or *in vivo* animal model.

Additional methods of preparation, characterization, and dosing AAV particles are taught in WO2019094253, which is incorporated herein by reference in its entirety.

Additional rAAV constructs that can be employed consonant with the invention include those described in Wang et al 2019, available at: //doi.org/10.1038/s41573-019-0012-9, including Table 1 thereof, which is incorporated by reference in its entirety.

Lipid Nanoparticles

The methods and systems provided herein may employ any suitable carrier or delivery modality, including, in certain embodiments, lipid nanoparticles (LNPs). Lipid nanoparticles, in some embodiments, comprise one or more ionic lipids, such as non-cationic lipids (e.g., neutral or anionic, or zwitterionic lipids); one or more conjugated lipids (such as PEG-conjugated lipids or lipids conjugated to polymers described in Table 5 of WO2019217941; incorporated herein by

reference in its entirety); one or more sterols (e.g., cholesterol); and, optionally, one or more targeting molecules (e.g., conjugated receptors, receptor ligands, antibodies); or combinations of the foregoing.

Lipids that can be used in nanoparticle formations (e.g., lipid nanoparticles) include, for example those described in Table 4 of WO2019217941, which is incorporated by reference—e.g., a lipid-containing nanoparticle can comprise one or more of the lipids in Table 4 of WO2019217941. Lipid nanoparticles can include additional elements, such as polymers, such as the polymers described in Table 5 of WO2019217941, incorporated by reference.

In some embodiments, conjugated lipids, when present, can include one or more of PEG-diacylglycerol (DAG) (such as l-(monomethoxy-polyethyleneglycol)-2,3- dimyristoylglycerol (PEG-DMG)), PEG-dialkyloxypropyl (DAA), PEG-phospholipid, PEG- ceramide (Cer), a pegylated phosphatidylethanoloamine (PEG-PE), PEG succinate diacylglycerol (PEGS-DAG) (such as 4-0-(2',3'-di(tetradecanoyloxy)propyl-l-0-(w- methoxy(polyethoxy)ethyl) butanedioate (PEG-S-DMG)), PEG dialkoxypropylcarbam, N- (carbonyl-methoxypoly ethylene glycol 2000)-1 ,2-distearoyl-sn-glycero-3-phosphoethanolamine sodium salt, and those described in Table 2 of WO2019051289 (incorporated by reference), and combinations of the foregoing.

In some embodiments, sterols that can be incorporated into lipid nanoparticles include one or more of cholesterol or cholesterol derivatives, such as those in W02009/127060 or US2010/0130588, which are incorporated by reference. Additional exemplary sterols include phytosterols, including those described in Eygeris et al (2020), dx.doi.org/10.1021/acs.nanolett.0c01386, incorporated herein by reference.

In some embodiments, the lipid particle comprises an ionizable lipid, a non-cationic lipid, a conjugated lipid that inhibits aggregation of particles, and a sterol. The amounts of these components can be varied independently and to achieve desired properties. For example, in some embodiments, the lipid nanoparticle comprises an ionizable lipid is in an amount from about 20 mol % to about 90 mol % of the total lipids (in other embodiments it may be 20-70% (mol), 30-60% (mol) or 40-50% (mol); about 50 mol % to about 90 mol % of the total lipid present in the lipid nanoparticle), a non-cationic lipid in an amount from about 5 mol % to about 30 mol % of the total lipids, a conjugated lipid in an amount from about 0.5 mol % to about 20 mol % of the total lipids, and a sterol in an amount from about 20 mol % to about 50 mol % of the total lipids. The ratio of total lipid to nucleic acid (e.g., encoding the gene modifying

polypeptide or template nucleic acid) can be varied as desired. For example, the total lipid to nucleic acid (mass or weight) ratio can be from about 10: 1 to about 30: 1.

In some embodiments, an ionizable lipid may be a cationic lipid, an ionizable cationic lipid, e.g., a cationic lipid that can exist in a positively charged or neutral form depending on pH, or an amine-containing lipid that can be readily protonated. In some embodiments, the cationic lipid is a lipid capable of being positively charged, e.g., under physiological conditions. Exemplary cationic lipids include one or more amine group(s) which bear the positive charge. In some embodiments, the lipid particle comprises a cationic lipid in formulation with one or more of neutral lipids, ionizable amine-containing lipids, biodegradable alkyn lipids, steroids, phospholipids including polyunsaturated lipids, structural lipids (e.g., sterols), PEG, cholesterol and polymer conjugated lipids. In some embodiments, the cationic lipid may be an ionizable cationic lipid. An exemplary cationic lipid as disclosed herein may have an effective pKa over 6.0. In embodiments, a lipid nanoparticle may comprise a second cationic lipid having a different effective pKa (e.g., greater than the first effective pKa), than the first cationic lipid. A lipid nanoparticle may comprise between 40 and 60 mol percent of a cationic lipid, a neutral lipid, a steroid, a polymer conjugated lipid, and a therapeutic agent, e.g., a nucleic acid (e.g., RNA) described herein (e.g., a template nucleic acid or a nucleic acid encoding a gene modifying polypeptide), encapsulated within or associated with the lipid nanoparticle. In some embodiments, the nucleic acid is co-formulated with the cationic lipid. The nucleic acid may be adsorbed to the surface of an LNP, e.g., an LNP comprising a cationic lipid. In some embodiments, the nucleic acid may be encapsulated in an LNP, e.g., an LNP comprising a cationic lipid. In some embodiments, the lipid nanoparticle may comprise a targeting moiety, e.g., coated with a targeting agent. In embodiments, the LNP formulation is biodegradable. In some embodiments, a lipid nanoparticle comprising one or more lipid described herein, e.g., Formula (i), (ii), (ii), (vii) and/or (ix) encapsulates at least 1%, at least 5%, at least 10%, at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 92%, at least 95%, at least 97%, at least 98% or 100% of an RNA molecule, e.g., template RNA and/or a mRNA encoding the gene modifying polypeptide.

In some embodiments, the lipid to nucleic acid ratio (mass/mass ratio; w/w ratio) can be in the range of from about 1 : 1 to about 25: 1, from about 10: 1 to about 14: 1, from about 3 : 1 to about 15: 1, from about 4: 1 to about 10: 1, from about 5: 1 to about 9: 1, or about 6: 1 to

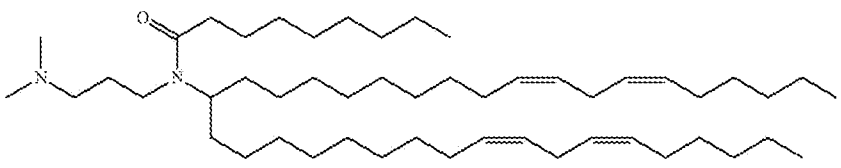
about 9: 1. The amounts of lipids and nucleic acid can be adjusted to provide a desired N/P ratio, for example, N/P ratio of 3, 4, 5, 6, 7, 8, 9, 10 or higher. Generally, the lipid nanoparticle formulation's overall lipid content can range from about 5 mg/ml to about 30 mg/mL.

Exemplary ionizable lipids that can be used in lipid nanoparticle formulations include, without limitation, those listed in Table 1 of WO2019051289, incorporated herein by reference. Additional exemplary lipids include, without limitation, one or more of the following formulae: X of US2016/0311759; I of US20150376115 or in US2016/0376224; I, II or III of US20160151284; I, IA, II, or IIA of US20170210967; I-c of US20150140070; A of US2013/0178541; I of US2013/0303587 or US2013/0123338; I of US2015/0141678; II, III, IV, or V of US2015/0239926; I of US2017/0119904; I or II of WO2017/117528; A of US2012/0149894; A of US2015/0057373; A of WO2013/116126; A of US2013/0090372; A of US2013/0274523; A of US2013/0274504; A of US2013/0053572; A of W02013/016058; A of W02012/162210; I of US2008/042973; I, II, III, or IV of US2012/01287670; I or II of US2014/0200257; I, II, or III of US2015/0203446; I or III of US2015/0005363; I, IA, IB, IC, ID, II, IIA, IIB, IIC, IID, or III-XXIV of US2014/0308304; of US2013/0338210; I, II, III, or IV of W02009/132131; A of US2012/01011478; I or XXXV of US2012/0027796; XIV or XVII of US2012/0058144; of US2013/0323269; I of US2011/0117125; I, II, or III of US2011/0256175; I, II, III, IV, V, VI, VII, VIII, IX, X, XI, XII of US2012/0202871; I, II, III, IV, V, VI, VII, VIII, X, XII, XIII, XIV, XV, or XVI of US2011/0076335; I or II of US2006/008378; I of US2013/0123338; I or X-A-Y-Z of US2015/0064242; XVI, XVII, or XVIII of US2013/0022649; I, II, or III of US2013/0116307; I, II, or III of US2013/0116307; I or II of US2010/0062967; I-X of US2013/0189351; I of US2014/0039032; V of US2018/0028664; I of US2016/0317458; I of US2013/0195920; 5, 6, or 10 of US10,221,127; III-3 of WO2018/081480; I-5 or I-8 of WO2020/081938; 18 or 25 of US9,867,888; A of US2019/0136231; II of WO2020/219876; 1 of US2012/0027803; OF-02 of US2019/0240349; 23 of US10,086,013; cKK-E12/A6 of Miao et al (2020); C12-200 of WO2010/053572; 7C1 of Dahlman et al (2017); 304-O13 or 503-O13 of Whitehead et al; TS-P4C2 of US9,708,628; I of WO2020/106946; I of WO2020/106946.

In some embodiments, the ionizable lipid is MC3 (6Z,9Z,28Z,3 lZ)-heptatriaconta-6,9,28,3 l-tetraen-l9-yl-4-(dimethylamino) butanoate (DLin-MC3-DMA or MC3), e.g., as described in Example 9 of WO2019051289A9 (incorporated by reference herein in its entirety).

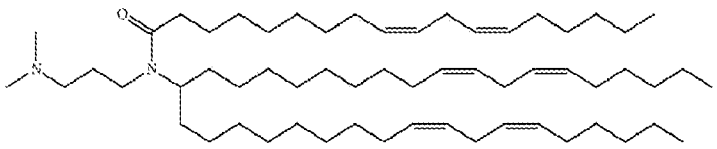
In some embodiments, the ionizable lipid is the lipid ATX-002, e.g., as described in Example 10 of WO2019051289A9 (incorporated by reference herein in its entirety). In some embodiments, the ionizable lipid is (l3Z,l6Z)-A,A-dimethyl-3- nonyldocosa-l3, l6-dien-l-amine (Compound 32), e.g., as described in Example 11 of WO2019051289A9 (incorporated by reference herein in its entirety). In some embodiments, the ionizable lipid is Compound 6 or Compound 22, e.g., as described in Example 12 of WO2019051289A9 (incorporated by reference herein in its entirety). In some embodiments, the ionizable lipid is heptadecan-9-yl 8-((2-hydroxyethyl)(6-oxo-6-(undecyloxy)hexyl)amino)octanoate (SM-102); e.g., as described in Example 1 of US9,867,888(incorporated by reference herein in its entirety). In some embodiments, the ionizable lipid is 9Z,12Z)-3-((4,4-bis(octyloxy)butanoyl)oxy)-2-((((3-(diethylamino)propoxy)carbonyl)oxy)methyl)propyl octadeca-9,12-dienoate (LP01) e.g., as synthesized in Example 13 of WO2015/095340(incorporated by reference herein in its entirety). In some embodiments, the ionizable lipid is Di((Z)-non-2-en-1-yl) 9-((4-dimethylamino)butanoyl)oxy)heptadecanedioate (L319), e.g. as synthesized in Example 7, 8, or 9 of US2012/0027803(incorporated by reference herein in its entirety). In some embodiments, the ionizable lipid is 1,1'-((2-(4-(2-((2-(Bis(2-hydroxydodecyl)amino)ethyl)(2-hydroxydodecyl) amino)ethyl)piperazin-1-yl)ethyl)azanediyl)bis(dodecan-2-ol) (C12-200), e.g., as synthesized in Examples 14 and 16 of WO2010/053572(incorporated by reference herein in its entirety). In some embodiments, the ionizable lipid is; Imidazole cholesterol ester (ICE) lipid (3S, 10R, 13R, 17R)-10, 13-dimethyl-17- ((R)-6-methylheptan-2-yl)-2, 3, 4, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17-tetradecahydro-lH- cyclopenta[a]phenanthren-3-yl 3-(1H-imidazol-4-yl)propanoate, e.g., Structure (I) from WO2020/106946 (incorporated by reference herein in its entirety).

Some non-limiting examples of lipid compounds that may be used (e.g., in combination with other lipid components) to form lipid nanoparticles for the delivery of compositions described herein, e.g., nucleic acid (e.g., RNA) described herein (e.g., a template nucleic acid or a nucleic acid encoding a gene modifying polypeptide) includes,



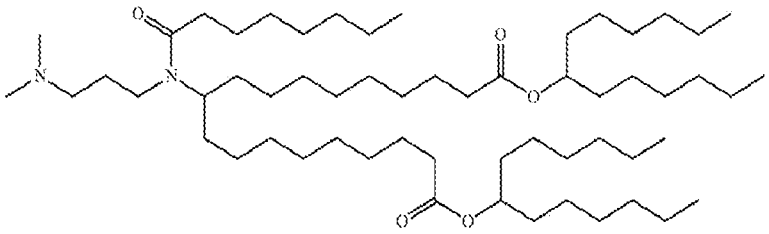
(i)

In some embodiments an LNP comprising Formula (i) is used to deliver a gene modifying composition described herein to the liver and/or hepatocyte cells.



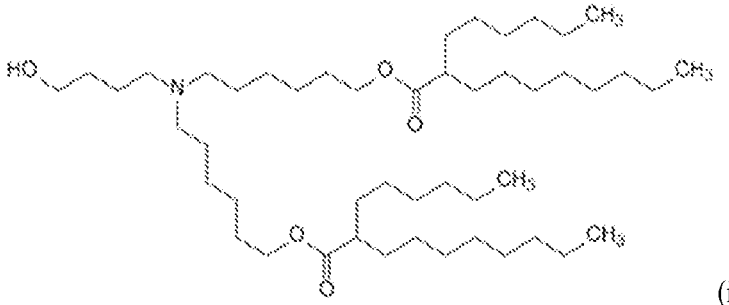
(ii)

In some embodiments an LNP comprising Formula (ii) is used to deliver a gene modifying composition described herein to the liver and/or hepatocyte cells.

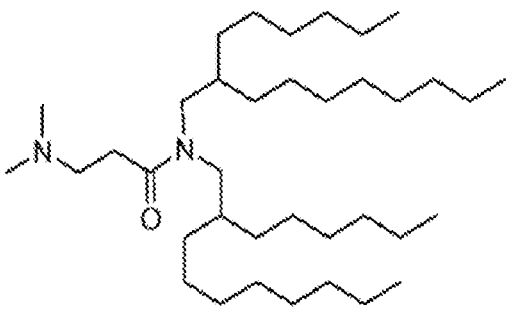


(iii)

In some embodiments an LNP comprising Formula (iii) is used to deliver a gene modifying composition described herein to the liver and/or hepatocyte cells.

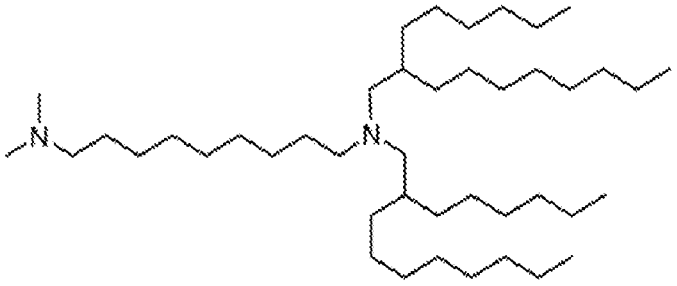


(iv)



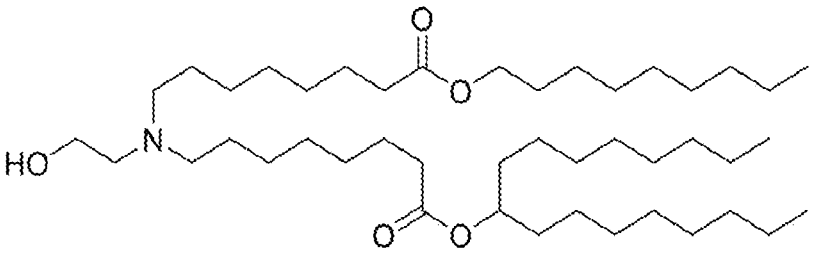
(v)

In some embodiments an LNP comprising Formula (v) is used to deliver a gene modifying composition described herein to the liver and/or hepatocyte cells.

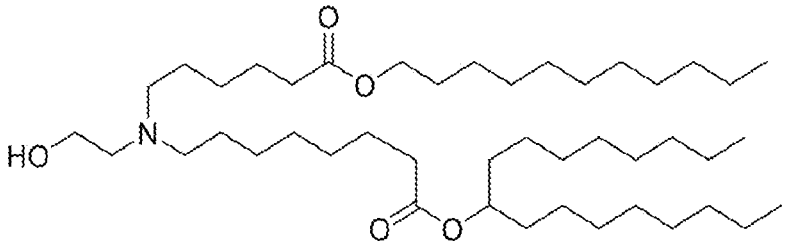


(vi)

In some embodiments an LNP comprising Formula (vi) is used to deliver a gene modifying composition described herein to the liver and/or hepatocyte cells.

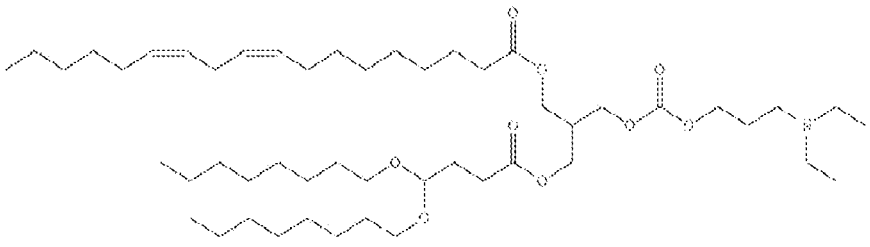


(vii)



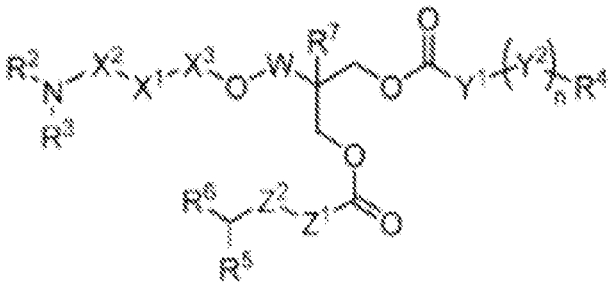
(viii)

In some embodiments an LNP comprising Formula (viii) is used to deliver a gene modifying composition described herein to the liver and/or hepatocyte cells.



(ix)

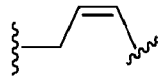
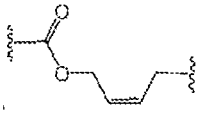
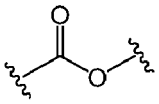
In some embodiments an LNP comprising Formula (ix) is used to deliver a gene modifying composition described herein to the liver and/or hepatocyte cells.



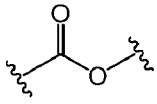
(x)

wherein

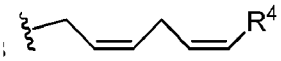
X^1 is O, NR^1, or a direct bond, X^2 is C2-5 alkylene, X^3 is C(=0) or a direct bond, R^1 is H or Me, R^3 is Ci-3 alkyl, R^2 is Ci-3 alkyl, or R^2 taken together with the nitrogen atom to which it is attached and 1-3 carbon atoms of X^2 form a 4-, 5-, or 6-membered ring, or X^1 is NR^1, R^1 and R^2 taken together with the nitrogen atoms to which they are attached form a 5- or 6-membered ring, or R^2 taken together with R^3 and the nitrogen atom to which they are attached form a 5-, 6-, or 7-membered ring, Y^1 is C2-12 alkylene, Y^2 is selected from

 (in either orientation),  (in either orientation),  (in either orientation),

n is 0 to 3, R^4 is Ci-15 alkyl, Z^1 is Ci-6 alkylene or a direct bond,

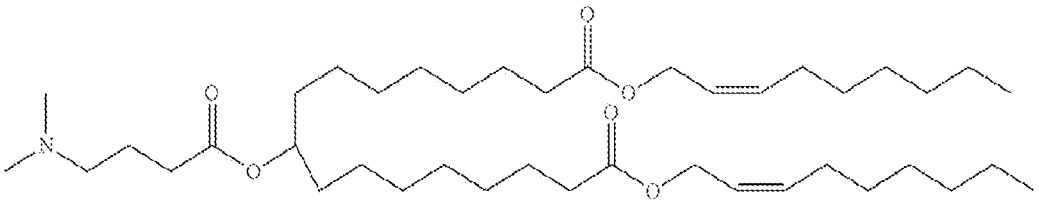
Z^2 is  (in either orientation) or absent, provided that if Z^1 is a direct bond, Z^2 is absent;

R^5 is C5-9 alkyl or C6-10 alkoxy, R^6 is C5-9 alkyl or C6-10 alkoxy, W is methylene or a direct bond, and R^7 is H or Me, or a salt thereof, provided that if R^3 and R^2 are C2 alkyls, X^1 is O, X^2 is linear C3 alkylene, X^3 is C(=0), Y^1 is linear Ce alkylene, (Y^2)n-R^4 is



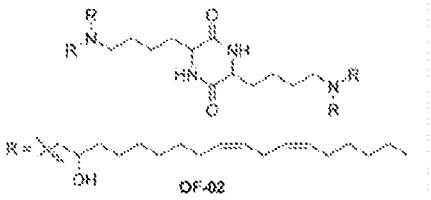
, R^4 is linear C5 alkyl, Z^1 is C2 alkylene, Z^2 is absent, W is methylene, and R^7 is H, then R^5 and R^6 are not Cx alkoxy.

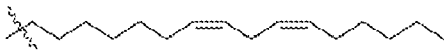
In some embodiments an LNP comprising Formula (xii) is used to deliver a gene modifying composition described herein to the liver and/or hepatocyte cells.



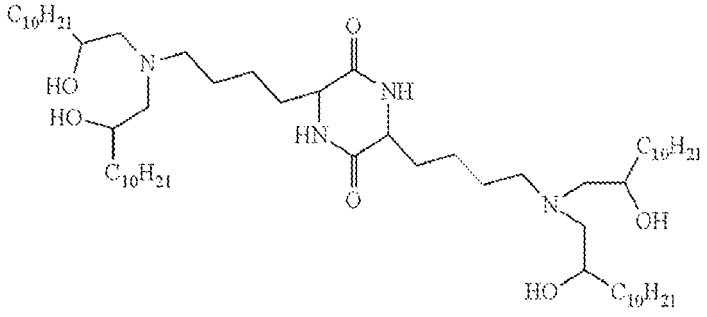
(xi)

In some embodiments an LNP comprising Formula (xi) is used to deliver a gene modifying composition described herein to the liver and/or hepatocyte cells.

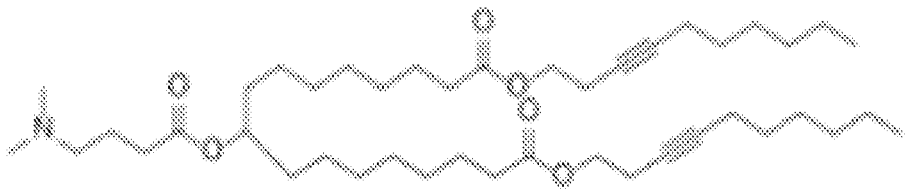


where R= 

(xii)

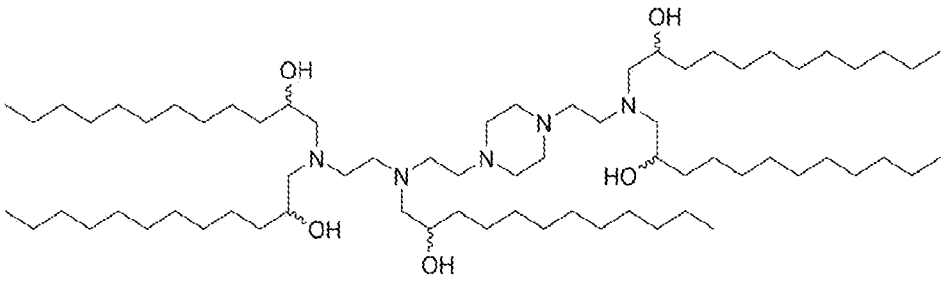


(xiii)



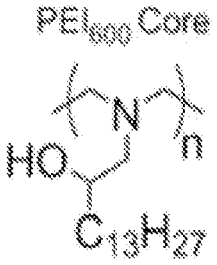
(xiv)

In some embodiments an LNP comprises a compound of Formula (xiii) and a compound of Formula (xiv).



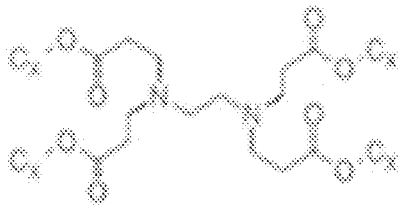
(xv)

In some embodiments an LNP comprising Formula (xv) is used to deliver a gene modifying composition described herein to the liver and/or hepatocyte cells.

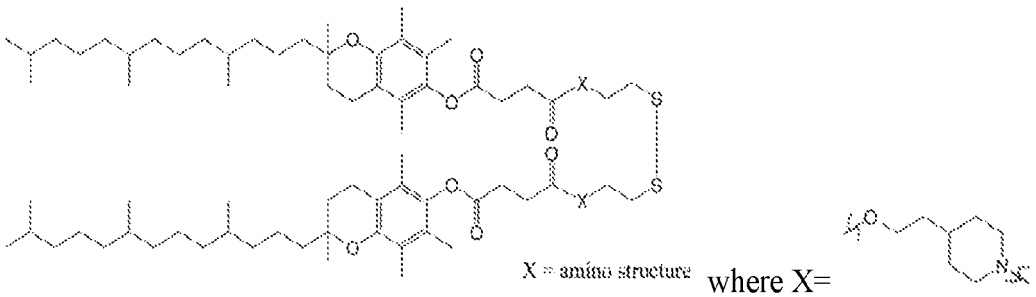


(xvi)

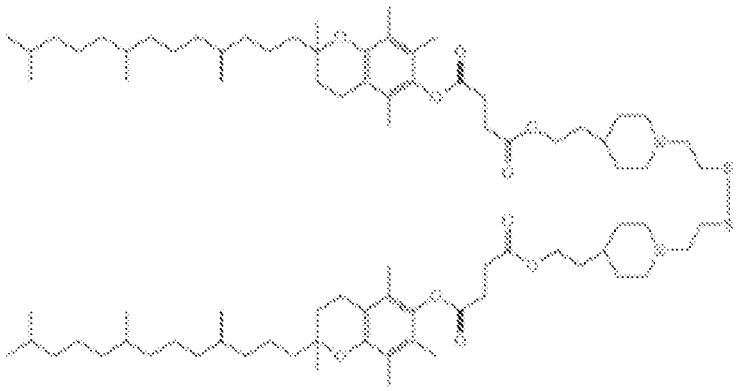
In some embodiments an LNP comprising a formulation of Formula (xvi) is used to deliver a gene modifying composition described herein to the lung endothelial cells.



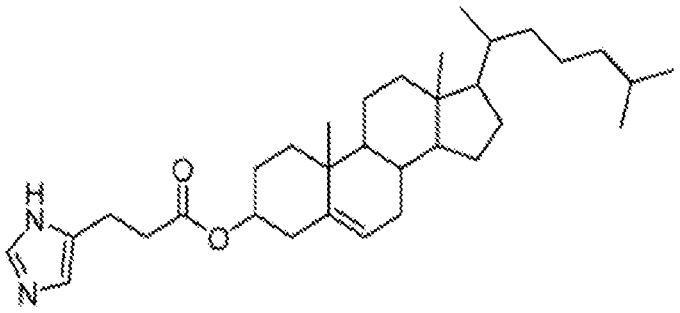
(xvii)



(xviii) (a)

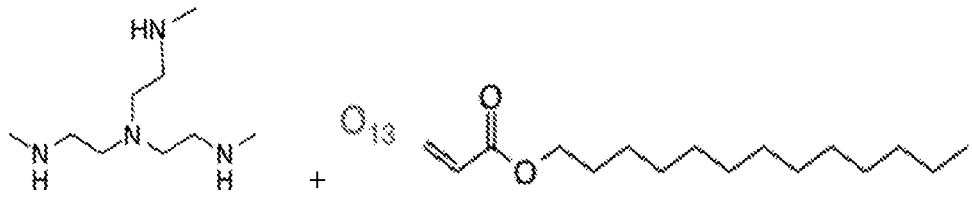


(xviii)(b)

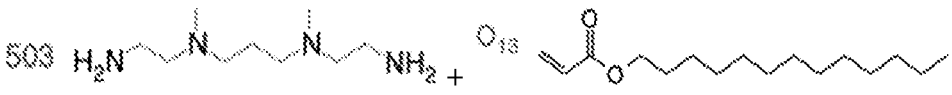


(xix)

In some embodiments, a lipid compound used to form lipid nanoparticles for the delivery of compositions described herein, e.g., nucleic acid (e.g., RNA) described herein (e.g., a template nucleic acid or a nucleic acid encoding a gene modifying polypeptide) is made by one of the following reactions:



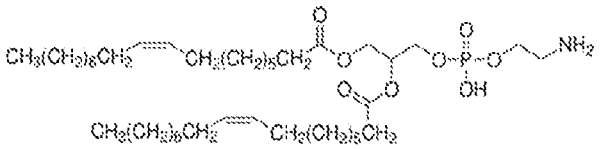
(xx) (a)



(xx)(b)

Exemplary non-cationic lipids include, but are not limited to, distearoyl-sn-glycero-phosphoethanolamine, distearoylphosphatidylcholine (DSPC), dioleoylphosphatidylcholine (DOPC), dipalmitoylphosphatidylcholine (DPPC), dioleoylphosphatidylglycerol (DOPG),

dipalmitoylphosphatidylglycerol (DPPG), dioleoyl-phosphatidylethanolamine (DOPE), 1,2-dioleoyl-sn-glycero-3-phosphoethanolamine (DOPE), palmitoyloleoylphosphatidylcholine (POPC), palmitoyloleoylphosphatidylethanolamine (POPE), dioleoyl-phosphatidylethanolamine 4-(N-maleimidomethyl)-cyclohexane- 1 - carboxylate (DOPE-mal), dipalmitoyl phosphatidyl ethanolamine (DPPE), dimyristoylphosphoethanolamine (DMPE), distearoyl-phosphatidyl-ethanolamine (DSPE), monomethyl-phosphatidylethanolamine (such as 16-O-monomethyl PE), dimethyl- phosphatidylethanolamine (such as 16-O-dimethyl PE), l8-l-trans PE, l-stearoyl-2-oleoyl- phosphatidyethanolamine (SOPE), hydrogenated soy phosphatidylcholine (HSPC), egg phosphatidylcholine (EPC), dioleoylphosphatidylserine (DOPS), sphingomyelin (SM), dimyristoyl phosphatidylcholine (DMPC), dimyristoyl phosphatidylglycerol (DMPG), distearoylphosphatidylglycerol (DSPG), dierucoylphosphatidylcholine (DEPC), palmitoyloleyolphosphatidylglycerol (POPG), dielaidoyl-phosphatidylethanolamine (DEPE), lecithin, phosphatidylethanolamine, lysolecithin, lysophosphatidylethanolamine, phosphatidylserine, phosphatidylinositol, sphingomyelin, egg sphingomyelin (ESM), cephalin, cardiolipin, phosphatidicacid,cerebrosides, dicetylphosphate, lysophosphatidylcholine, dilinoleoylphosphatidylcholine, or mixtures thereof. It is understood that other diacylphosphatidylcholine and diacylphosphatidylethanolamine phospholipids can also be used. The acyl groups in these lipids are preferably acyl groups derived from fatty acids having C10-C24 carbon chains, e.g., lauroyl, myristoyl, paimitoyl, stearoyl, or oleoyl. Additional exemplary lipids, in certain embodiments, include, without limitation, those described in Kim et al. (2020) dx.doi.org/10.1021/acs.nanolett.0c01386, incorporated herein by reference. Such lipids include, in some embodiments, plant lipids found to improve liver transfection with mRNA (e.g., DGTS). In some embodiments, the non-cationic lipid may have the following structure,



(xxi)

Other examples of non-cationic lipids suitable for use in the lipid nanopartieles include, without limitation, nonphosphorous lipids such as, e.g., stearylamine, dodeeylamine, hexadecylamine, acetyl palmitate, glycerol ricinoleate, hexadecyl stereate, isopropyl myristate,

amphoteric acrylic polymers, triethanolamine-lauryl sulfate, alkyl-aryl sulfate polyethyloxylated fatty acid amides, dioctadecyl dimethyl ammonium bromide, ceramide, sphingomyelin, and the like. Other non-cationic lipids are described in WO2017/099823 or US patent publication US2018/0028664, the contents of which is incorporated herein by reference in their entirety.

In some embodiments, the non-cationic lipid is oleic acid or a compound of Formula I, II, or IV of US2018/0028664, incorporated herein by reference in its entirety. The non-cationic lipid can comprise, for example, 0-30% (mol) of the total lipid present in the lipid nanoparticle. In some embodiments, the non-cationic lipid content is 5-20% (mol) or 10-15% (mol) of the total lipid present in the lipid nanoparticle. In embodiments, the molar ratio of ionizable lipid to the neutral lipid ranges from about 2:1 to about 8:1 (e.g., about 2:1, 3:1, 4:1, 5:1, 6:1, 7:1, or 8:1).

In some embodiments, the lipid nanoparticles do not comprise any phospholipids.

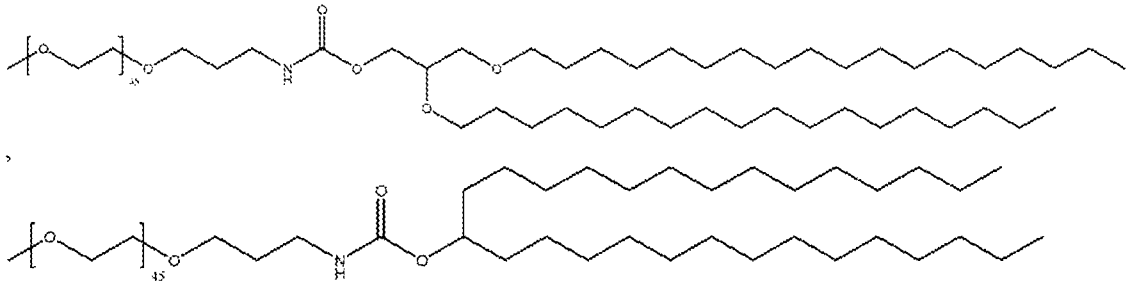
In some aspects, the lipid nanoparticle can further comprise a component, such as a sterol, to provide membrane integrity. One exemplary sterol that can be used in the lipid nanoparticle is cholesterol and derivatives thereof. Non-limiting examples of cholesterol derivatives include polar analogues such as 5a-choiestanol, 53-coprostanol, choiesteryl-(2·-hydroxy)-ethyl ether, choiesteryl-(4'- hydroxy)-butyl ether, and 6-ketocholestanol; non-polar analogues such as 5a-cholestane, cholestenone, 5a-cholestanone, 5p-cholestanone, and cholesteryl decanoate; and mixtures thereof. In some embodiments, the cholesterol derivative is a polar analogue, e.g., choiesteryl-(4'-hydroxy)-buty1 ether. Exemplary cholesterol derivatives are described in PCT publication W02009/127060 and US patent publication US2010/0130588, each of which is incorporated herein by reference in its entirety.

In some embodiments, the component providing membrane integrity, such as a sterol, can comprise 0-50% (mol) (e.g., 0-10%, 10-20%, 20-30%, 30-40%, or 40-50%) of the total lipid present in the lipid nanoparticle. In some embodiments, such a component is 20-50% (mol) 30-40% (mol) of the total lipid content of the lipid nanoparticle.

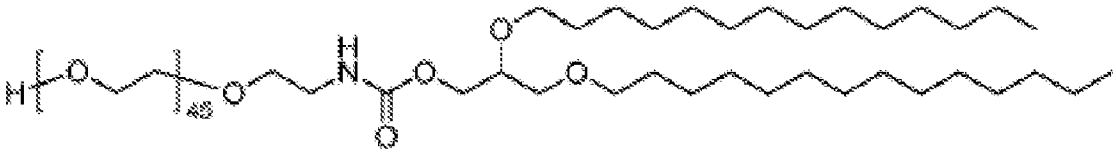
In some embodiments, the lipid nanoparticle can comprise a polyethylene glycol (PEG) or a conjugated lipid molecule. Generally, these are used to inhibit aggregation of lipid nanoparticles and/or provide steric stabilization. Exemplary conjugated lipids include, but are not limited to, PEG-lipid conjugates, polyoxazoline (POZ)-lipid conjugates, polyamide-lipid conjugates (such as ATTA-lipid conjugates), cationic-polymer lipid (CPL) conjugates, and

mixtures thereof. In some embodiments, the conjugated lipid molecule is a PEG-lipid conjugate, for example, a (methoxy polyethylene glycol)-conjugated lipid.

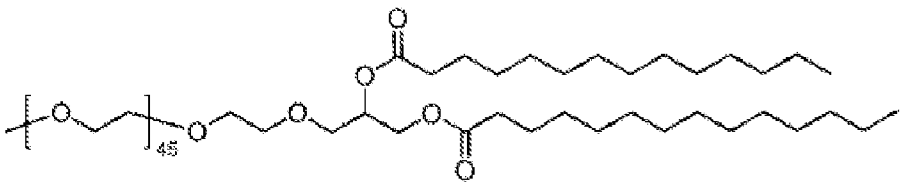
Exemplary PEG-lipid conjugates include, but are not limited to, PEG-diacylglycerol (DAG) (such as l-(monomethoxy-polyethyleneglycol)-2,3-dimyristoylglycerol (PEG-DMG)), PEG-dialkyloxypropyl (DAA), PEG-phospholipid, PEG-ceramide (Cer), a pegylated phosphatidylethanoloamine (PEG-PE), 1,2-dimyristoyl-sn-glycerol, methoxypoly ethylene glycol (DMG-PEG-2K), PEG succinate diacylglycerol (PEGS-DAG) (such as 4-0-(2',3'-di(tetradecanoyloxy)propyl-l-0-(w-methoxy(polyethoxy)ethyl) butanedioate (PEG-S-DMG)), PEG dialkoxypropylcarbam, N-(carbonyl-methoxypolyethylene glycol 2000)-l,2-distearoyl-sn-glycero-3-phosphoethanolamine sodium salt, or a mixture thereof. Additional exemplary PEG-lipid conjugates are described, for example, in US5,885,6l3, US6,287,59l, US2003/0077829, US2003/0077829, US2005/0175682, US2008/0020058, US2011/0117125, US2010/0130588, US2016/0376224, US2017/0119904, and US/099823, the contents of all of which are incorporated herein by reference in their entirety. In some embodiments, a PEG-lipid is a compound of Formula III, III-a-I, III-a-2, III-b-1, III-b-2, or V of US2018/0028664, the content of which is incorporated herein by reference in its entirety. In some embodiments, a PEG-lipid is of Formula II of US20150376115 or US2016/0376224, the content of both of which is incorporated herein by reference in its entirety. In some embodiments, the PEG-DAA conjugate can be, for example, PEG-dilauryloxypropyl, PEG- dimyristyloxypropyl, PEG-dipalmityloxypropyl, or PEG-distearyloxypropyl. The PEG-lipid can be one or more of PEG-DMG, PEG-dilaurylglycerol, PEG-dipalmitoylglycerol, PEG- disterylglycerol, PEG-dilaurylglycamide, PEG-dimyristylglycamide, PEG- dipalmitoylglycamide, PEG-disterylglycamide, PEG-cholesterol (l-[8'-(Cholest-5-en-3[beta]- oxy)carboxamido-3',6'-dioxaoctanyl] carbamoyl-[omega]-methyl-poly(ethylene glycol), PEG- DMB (3,4-Ditetradecoxylbenzyl- [omega]-methyl-poly(ethylene glycol) ether), and 1,2- dimyristoyl-sn-glycero-3-phosphoethanolamine-N-[methoxy(polyethylene glycol)-2000]. In some embodiments, the PEG-lipid comprises PEG-DMG, 1,2- dimyristoyl-sn-glycero-3-phosphoethanolamine-N-[methoxy(polyethylene glycol)-2000]. In some embodiments, the PEG-lipid comprises a structure selected from:



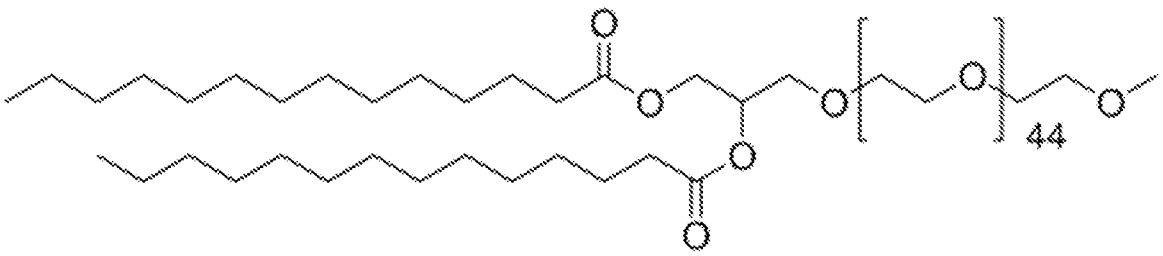
(xxii),



(xxiii),



(xxiv), and



(xxv).

In some embodiments, lipids conjugated with a molecule other than a PEG can also be used in place of PEG-lipid. For example, polyoxazoline (POZ)-lipid conjugates, polyamide-lipid conjugates (such as ATTA-lipid conjugates), and cationic-polymer lipid (GPL) conjugates can be used in place of or in addition to the PEG-lipid.

Exemplary conjugated lipids, i.e., PEG-lipids, (POZ)-lipid conjugates, ATTA-lipid conjugates and cationic polymer-lipids are described in the PCT and LIS patent applications listed in Table 2 of WO2019051289A9 and in WO2020106946A1, the contents of all of which are incorporated herein by reference in their entirety.

In some embodiments an LNP comprises a compound of Formula (xix), a compound of Formula (xxi) and a compound of Formula (xxv). In some embodiments an LNP comprising a formulation of Formula (xix), Formula (xxi) and Formula (xxv)is used to deliver a gene modifying composition described herein to the lung or pulmonary cells.

In some embodiments, a lipid nanoparticle may comprise one or more cationic lipids selected from Formula (i), Formula (ii), Formula (iii), Formula (vii), and Formula (ix). In some embodiments, the LNP may further comprise one or more neutral lipid, e.g., DSPC, DPPC, DMPC, DOPC, POPC, DOPE, SM, a steroid, e.g., cholesterol, and/or one or more polymer conjugated lipid, e.g., a pegylated lipid, e.g., PEG-DAG, PEG-PE, PEG-S-DAG, PEG-cer or a PEG dialkyoxypropylcarbamate.

In some embodiments, the PEG or the conjugated lipid can comprise 0-20% (mol) of the total lipid present in the lipid nanoparticle. In some embodiments, PEG or the conjugated lipid content is 0.5- 10% or 2-5% (mol) of the total lipid present in the lipid nanoparticle. Molar ratios of the ionizable lipid, non-cationic-lipid, sterol, and PEG/conjugated lipid can be varied as needed. For example, the lipid particle can comprise 30-70% ionizable lipid by mole or by total weight of the composition, 0-60% cholesterol by mole or by total weight of the composition, 0-30% non-cationic-lipid by mole or by total weight of the composition and 1-10% conjugated lipid by mole or by total weight of the composition. Preferably, the composition comprises 30-40% ionizable lipid by mole or by total weight of the composition, 40-50% cholesterol by mole or by total weight of the composition, and 10- 20% non-cationic-lipid by mole or by total weight of the composition. In some other embodiments, the composition is 50-75% ionizable lipid by mole or by total weight of the composition, 20-40% cholesterol by mole or by total weight of the composition, and 5 to 10% non-cationic-lipid, by mole or by total weight of the composition and 1-10% conjugated lipid by mole or by total weight of the composition. The composition may contain 60-70% ionizable lipid by mole or by total weight of the composition, 25-35% cholesterol by mole or by total weight of the composition, and 5-10% non-cationic-lipid by mole or by total weight of the composition. The composition may also contain up to 90% ionizable lipid by mole or by total weight of the composition and 2 to 15% non-cationic lipid by mole or by total weight of the composition. The formulation may also be a lipid nanoparticle formulation, for example comprising 8-30% ionizable lipid by mole or by total weight of the composition, 5-

30% non- cationic lipid by mole or by total weight of the composition, and 0-20% cholesterol by mole or by total weight of the composition; 4-25% ionizable lipid by mole or by total weight of the composition, 4-25% non-cationic lipid by mole or by total weight of the composition, 2 to 25% cholesterol by mole or by total weight of the composition, 10 to 35% conjugate lipid by mole or by total weight of the composition, and 5% cholesterol by mole or by total weight of the composition; or 2-30% ionizable lipid by mole or by total weight of the composition, 2-30% non-cationic lipid by mole or by total weight of the composition, 1 to 15% cholesterol by mole or by total weight of the composition, 2 to 35% conjugate lipid by mole or by total weight of the composition, and 1-20% cholesterol by mole or by total weight of the composition; or even up to 90% ionizable lipid by mole or by total weight of the composition and 2-10% non-cationic lipids by mole or by total weight of the composition, or even 100% cationic lipid by mole or by total weight of the composition. In some embodiments, the lipid particle formulation comprises ionizable lipid, phospholipid, cholesterol and a PEG-ylated lipid in a molar ratio of 50: 10:38.5: 1.5. In some other embodiments, the lipid particle formulation comprises ionizable lipid, cholesterol and a PEG-ylated lipid in a molar ratio of 60:38.5: 1.5.

In some embodiments, the lipid particle comprises ionizable lipid, non-cationic lipid (e.g. phospholipid), a sterol (e.g., cholesterol) and a PEG-ylated lipid, where the molar ratio of lipids ranges from 20 to 70 mole percent for the ionizable lipid, with a target of 40-60, the mole percent of non-cationic lipid ranges from 0 to 30, with a target of 0 to 15, the mole percent of sterol ranges from 20 to 70, with a target of 30 to 50, and the mole percent of PEG-ylated lipid ranges from 1 to 6, with a target of 2 to 5.

In some embodiments, the lipid particle comprises ionizable lipid / non-cationic- lipid / sterol / conjugated lipid at a molar ratio of 50: 10:38.5: 1.5.

In an aspect, the disclosure provides a lipid nanoparticle formulation comprising phospholipids, lecithin, phosphatidylcholine and phosphatidylethanolamine.

In some embodiments, one or more additional compounds can also be included. Those compounds can be administered separately or the additional compounds can be included in the lipid nanoparticles of the invention. In other words, the lipid nanoparticles can contain other compounds in addition to the nucleic acid or at least a second nucleic acid, different than the first. Without limitations, other additional compounds can be selected from the group consisting of small or large organic or inorganic molecules, monosaccharides, disaccharides, trisaccharides,

oligosaccharides, polysaccharides, peptides, proteins, peptide analogs and derivatives thereof, peptidomimetics, nucleic acids, nucleic acid analogs and derivatives, an extract made from biological materials, or any combinations thereof.

In some embodiments, a lipid nanoparticle (or a formulation comprising lipid nanoparticles) lacks reactive impurities (e.g., aldehydes or ketones), or comprises less than a preselected level of reactive impurities (e.g., aldehydes or ketones). While not wishing to be bound by theory, in some embodiments, a lipid reagent is used to make a lipid nanoparticle formulation, and the lipid reagent may comprise a contaminating reactive impurity (e.g., an aldehyde or ketone). A lipid regent may be selected for manufacturing based on having less than a preselected level of reactive impurities (e.g., aldehydes or ketones). Without wishing to be bound by theory, in some embodiments, aldehydes can cause modification and damage of RNA, e.g., cross-linking between bases and/or covalently conjugating lipid to RNA (e.g., forming lipid-RNA adducts). This may, in some instances, lead to failure of a reverse transcriptase reaction and/or incorporation of inappropriate bases, e.g., at the site(s) of lesion(s), e.g., a mutation in a newly synthesized target DNA.

In some embodiments, a lipid nanoparticle formulation is produced using a lipid reagent comprising less than 5%, 4%, 3%, 2%, 1%, 0.9%, 0.8%, 0.7%, 0.6%, 0.5%, 0.4%, 0.3%, 0.2%, or 0.1% total reactive impurity (e.g., aldehyde) content. In some embodiments, a lipid nanoparticle formulation is produced using a lipid reagent comprising less than 5%, 4%, 3%, 2%, 1%, 0.9%, 0.8%, 0.7%, 0.6%, 0.5%, 0.4%, 0.3%, 0.2%, or 0.1% of any single reactive impurity (e.g., aldehyde) species. In some embodiments, a lipid nanoparticle formulation is produced using a lipid reagent comprising: (i) less than 5%, 4%, 3%, 2%, 1%, 0.9%, 0.8%, 0.7%, 0.6%, 0.5%, 0.4%, 0.3%, 0.2%, or 0.1% total reactive impurity (e.g., aldehyde) content; and (ii) less than 5%, 4%, 3%, 2%, 1%, 0.9%, 0.8%, 0.7%, 0.6%, 0.5%, 0.4%, 0.3%, 0.2%, or 0.1% of any single reactive impurity (e.g., aldehyde) species. In some embodiments, the lipid nanoparticle formulation is produced using a plurality of lipid reagents, and each lipid reagent of the plurality independently meets one or more criterion described in this paragraph. In some embodiments, each lipid reagent of the plurality meets the same criterion, e.g., a criterion of this paragraph.

In some embodiments, the lipid nanoparticle formulation comprises less than 5%, 4%, 3%, 2%, 1%, 0.9%, 0.8%, 0.7%, 0.6%, 0.5%, 0.4%, 0.3%, 0.2%, or 0.1% total reactive impurity (e.g., aldehyde) content. In some embodiments, the lipid nanoparticle formulation comprises

less than 5%, 4%, 3%, 2%, 1%, 0.9%, 0.8%, 0.7%, 0.6%, 0.5%, 0.4%, 0.3%, 0.2%, or 0.1% of any single reactive impurity (e.g., aldehyde) species. In some embodiments, the lipid nanoparticle formulation comprises: (i) less than 5%, 4%, 3%, 2%, 1%, 0.9%, 0.8%, 0.7%, 0.6%, 0.5%, 0.4%, 0.3%, 0.2%, or 0.1% total reactive impurity (e.g., aldehyde) content; and (ii) less than 5%, 4%, 3%, 2%, 1%, 0.9%, 0.8%, 0.7%, 0.6%, 0.5%, 0.4%, 0.3%, 0.2%, or 0.1% of any single reactive impurity (e.g., aldehyde) species.

In some embodiments, one or more, or optionally all, of the lipid reagents used for a lipid nanoparticle as described herein or a formulation thereof comprise less than 5%, 4%, 3%, 2%, 1%, 0.9%, 0.8%, 0.7%, 0.6%, 0.5%, 0.4%, 0.3%, 0.2%, or 0.1% total reactive impurity (e.g., aldehyde) content. In some embodiments, one or more, or optionally all, of the lipid reagents used for a lipid nanoparticle as described herein or a formulation thereof comprise less than 5%, 4%, 3%, 2%, 1%, 0.9%, 0.8%, 0.7%, 0.6%, 0.5%, 0.4%, 0.3%, 0.2%, or 0.1% of any single reactive impurity (e.g., aldehyde) species. In some embodiments, one or more, or optionally all, of the lipid reagents used for a lipid nanoparticle as described herein or a formulation thereof comprise: (i) less than 5%, 4%, 3%, 2%, 1%, 0.9%, 0.8%, 0.7%, 0.6%, 0.5%, 0.4%, 0.3%, 0.2%, or 0.1% total reactive impurity (e.g., aldehyde) content; and (ii) less than 5%, 4%, 3%, 2%, 1%, 0.9%, 0.8%, 0.7%, 0.6%, 0.5%, 0.4%, 0.3%, 0.2%, or 0.1% of any single reactive impurity (e.g., aldehyde) species.

In some embodiments, total aldehyde content and/or quantity of any single reactive impurity (e.g., aldehyde) species is determined by liquid chromatography (LC), e.g., coupled with tandem mass spectrometry (MS/MS), e.g., according to the method described in Example 40 of PCT/US21/20948. In some embodiments, reactive impurity (e.g., aldehyde) content and/or quantity of reactive impurity (e.g., aldehyde) species is determined by detecting one or more chemical modifications of a nucleic acid molecule (e.g., an RNA molecule, e.g., as described herein) associated with the presence of reactive impurities (e.g., aldehydes), e.g., in the lipid reagents. In some embodiments, reactive impurity (e.g., aldehyde) content and/or quantity of reactive impurity (e.g., aldehyde) species is determined by detecting one or more chemical modifications of a nucleotide or nucleoside (e.g., a ribonucleotide or ribonucleoside, e.g., comprised in or isolated from a template nucleic acid, e.g., as described herein) associated with the presence of reactive impurities (e.g., aldehydes), e.g., in the lipid reagents, e.g., according to the method described in Example 41 of PCT/US21/20948. In embodiments, chemical

modifications of a nucleic acid molecule, nucleotide, or nucleoside are detected by determining the presence of one or more modified nucleotides or nucleosides, e.g., using LC-MS/MS analysis, e.g., according to the method described in Example 41 of PCT/US21/20948.

In some embodiments, a nucleic acid (e.g., RNA) described herein (e.g., a template nucleic acid or a nucleic acid encoding a gene modifying polypeptide) does not comprise an aldehyde modification, or comprises less than a preselected amount of aldehyde modifications. In some embodiments, on average, a nucleic acid has less than 50, 20, 10, 5, 2, or 1 aldehyde modifications per 1000 nucleotides, e.g., wherein a single cross-linking of two nucleotides is a single aldehyde modification. In some embodiments, the aldehyde modification is an RNA adduct (e.g., a lipid-RNA adduct). In some embodiments, the aldehyde-modified nucleotide is cross-linking between bases . In some embodiments, a nucleic acid (e.g., RNA) described herein comprises less than 50, 20, 10, 5, 2, or 1 cross-links between nucleotide.

In some embodiments, LNPs are directed to specific tissues by the addition of targeting domains. For example, biological ligands may be displayed on the surface of LNPs to enhance interaction with cells displaying cognate receptors, thus driving association with and cargo delivery to tissues wherein cells express the receptor. In some embodiments, the biological ligand may be a ligand that drives delivery to the liver, e.g., LNPs that display GalNAc result in delivery of nucleic acid cargo to hepatocytes that display asialoglycoprotein receptor (ASGPR). The work of Akinc et al. *Mol Ther* 18(7):1357-1364 (2010) teaches the conjugation of a trivalent GalNAc ligand to a PEG-lipid (GalNAc-PEG-DSG) to yield LNPs dependent on ASGPR for observable LNP cargo effect (see, e.g., Figure 6 therein). Other ligand-displaying LNP formulations, e.g., incorporating folate, transferrin, or antibodies, are discussed in WO2017223135, which is incorporated herein by reference in its entirety, in addition to the references used therein, namely Kolhatkar et al., Curr Drug Discov Technol. 2011 8:197-206; Musacchio and Torchilin, Front Biosci. 2011 16:1388-1412; Yu et al., Mol Membr Biol. 2010 27:286-298; Patil et al., Crit Rev Ther Drug Carrier Syst. 2008 25:1-61 ; Benoit et al., Biomacromolecules. 2011 12:2708-2714; Zhao et al., Expert Opin Drug Deliv. 2008 5:309-319; Akinc et al., Mol Ther. 2010 18:1357-1364; Srinivasan et al., Methods Mol Biol. 2012 820:105-116; Ben-Arie et al., Methods Mol Biol. 2012 757:497-507; Peer 2010 J Control Release. 20:63-68; Peer et al., Proc Natl Acad Sci U S A. 2007 104:4095-4100; Kim et al., Methods Mol Biol.

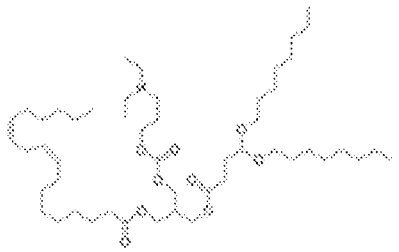
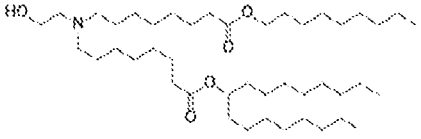
2011 721:339-353; Subramanya et al., Mol Ther. 2010 18:2028-2037; Song et al., Nat Biotechnol. 2005 23:709-717; Peer et al., Science. 2008 319:627-630; and Peer and Lieberman, Gene Ther. 2011 18:1127-1133.

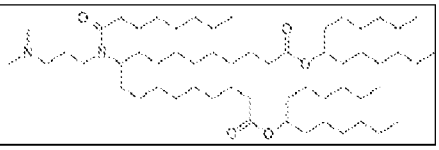
In some embodiments, LNPs are selected for tissue-specific activity by the addition of a Selective ORgan Targeting (SORT) molecule to a formulation comprising traditional components, such as ionizable cationic lipids, amphipathic phospholipids, cholesterol and poly(ethylene glycol) (PEG) lipids. The teachings of Cheng et al. Nat Nanotechnol 15(4):313-320 (2020) demonstrate that the addition of a supplemental "SORT" component precisely alters the *in vivo* RNA delivery profile and mediates tissue-specific (e.g., lungs, liver, spleen) gene delivery and editing as a function of the percentage and biophysical property of the SORT molecule.

In some embodiments, the LNPs comprise biodegradable, ionizable lipids. In some embodiments, the LNPs comprise (9Z,l2Z)-3-((4,4-bis(octyloxy)butanoyl)oxy)-2-((((3-(diethylamino)propoxy)carbonyl)oxy)methyl)propyl octadeca-9,l2-dienoate, also called 3- ((4,4-bis(octyloxy)butanoyl)oxy)-2-((((3-(diethylamino)propoxy)carbonyl)oxy)methyl)propyl (9Z,l2Z)-octadeca-9,l2-dienoate) or another ionizable lipid. See, e.g, lipids of WO2019/067992, WO/2017/173054, WO2015/095340, and WO2014/136086, as well as references provided therein. In some embodiments, the term cationic and ionizable in the context of LNP lipids is interchangeable, e.g., wherein ionizable lipids are cationic depending on the pH.

In some embodiments, an LNP described herein comprises a lipid described in Table 19.

Table 19: Exemplary Lipids

LIPID ID	Chemical Name	Molecular Weight	Structure
LIPIDV003	(9Z,12Z)-3-((4,4-bis(octyloxy)butanoyl)oxy)-2-((((3-(diethylamino)propoxy)carbonyl)oxy)methyl)propyl octadeca-9,12-dienoate	852.29	
LIPIDV004	Heptadecan-9-yl 8-((2-hydroxyethyl)(8-(nonyloxy)-8-oxooctyl)amino)octanoate	710.18	

LIPIDV005		919.56	

In some embodiments, multiple components of a gene modifying system may be prepared as a single LNP formulation, e.g., an LNP formulation comprises mRNA encoding for the gene modifying polypeptide and an RNA template. Ratios of nucleic acid components may be varied in order to maximize the properties of a therapeutic. In some embodiments, the ratio of RNA template to mRNA encoding a gene modifying polypeptide is about 1:1 to 100:1, e.g., about 1:1 to 20:1, about 20:1 to 40:1, about 40:1 to 60:1, about 60:1 to 80:1, or about 80:1 to 100:1, by molar ratio. In other embodiments, a system of multiple nucleic acids may be prepared by separate formulations, e.g., one LNP formulation comprising a template RNA and a second LNP formulation comprising an mRNA encoding a gene modifying polypeptide. In some embodiments, the system may comprise more than two nucleic acid components formulated into LNPs. In some embodiments, the system may comprise a protein, e.g., a gene modifying polypeptide, and a template RNA formulated into at least one LNP formulation.

In some embodiments, the average LNP diameter of the LNP formulation may be between 10s of nm and 100s of nm, e.g., measured by dynamic light scattering (DLS). In some embodiments, the average LNP diameter of the LNP formulation may be from about 40 nm to about 150 nm, such as about 40 nm, 45 nm, 50 nm, 55 nm, 60 nm, 65 nm, 70 nm, 75 nm, 80 nm, 85 nm, 90 nm, 95 nm, 100 nm, 105 nm, 110 nm, 115 nm, 120 nm, 125 nm, 130 nm, 135 nm, 140 nm, 145 nm, or 150 nm. In some embodiments, the average LNP diameter of the LNP formulation may be from about 50 nm to about 100 nm, from about 50 nm to about 90 nm, from about 50 nm to about 80 nm, from about 50 nm to about 70 nm, from about 50 nm to about 60 nm, from about 60 nm to about 100 nm, from about 60 nm to about 90 nm, from about 60 nm to about 80 nm, from about 60 nm to about 70 nm, from about 70 nm to about 100 nm, from about 70 nm to about 90 nm, from about 70 nm to about 80 nm, from about 80 nm to about 100 nm, from about 80 nm to about 90 nm, or from about 90 nm to about 100 nm. In some embodiments, the average LNP diameter of the LNP formulation may be from about 70 nm to about 100 nm. In a particular embodiment, the average LNP diameter of the LNP formulation may be about 80 nm. In some embodiments, the average LNP diameter of the LNP formulation may be about 100 nm. In some embodiments, the average LNP diameter of the LNP formulation ranges from

about l mm to about 500 mm, from about 5 mm to about 200 mm, from about 10 mm to about 100 mm, from about 20 mm to about 80 mm, from about 25 mm to about 60 mm, from about 30 mm to about 55 mm, from about 35 mm to about 50 mm, or from about 38 mm to about 42 mm.

An LNP may, in some instances, be relatively homogenous. A polydispersity index may be used to indicate the homogeneity of an LNP, e.g., the particle size distribution of the lipid nanoparticles. A small (e.g., less than 0.3) polydispersity index generally indicates a narrow particle size distribution. An LNP may have a polydispersity index from about 0 to about 0.25, such as 0.01, 0.02, 0.03, 0.04, 0.05, 0.06, 0.07, 0.08, 0.09, 0.10, 0.11, 0.12, 0.13, 0.14, 0.15, 0.16, 0.17, 0.18, 0.19, 0.20, 0.21, 0.22, 0.23, 0.24, or 0.25. In some embodiments, the polydispersity index of an LNP may be from about 0.10 to about 0.20.

The zeta potential of an LNP may be used to indicate the electrokinetic potential of the composition. In some embodiments, the zeta potential may describe the surface charge of an LNP. Lipid nanoparticles with relatively low charges, positive or negative, are generally desirable, as more highly charged species may interact undesirably with cells, tissues, and other elements in the body. In some embodiments, the zeta potential of an LNP may be from about -10 mV to about +20 mV, from about -10 mV to about +15 mV, from about -10 mV to about +10 mV, from about -10 mV to about +5 mV, from about -10 mV to about 0 mV, from about -10 mV to about -5 mV, from about -5 mV to about +20 mV, from about -5 mV to about +15 mV, from about -5 mV to about +10 mV, from about -5 mV to about +5 mV, from about -5 mV to about 0 mV, from about 0 mV to about +20 mV, from about 0 mV to about +15 mV, from about 0 mV to about +10 mV, from about 0 mV to about +5 mV, from about +5 mV to about +20 mV, from about +5 mV to about +15 mV, or from about +5 mV to about +10 mV.

The efficiency of encapsulation of a protein and/or nucleic acid, e.g., gene modifying polypeptide or mRNA encoding the polypeptide, describes the amount of protein and/or nucleic acid that is encapsulated or otherwise associated with an LNP after preparation, relative to the initial amount provided. The encapsulation efficiency is desirably high (e.g., close to 100%). The encapsulation efficiency may be measured, for example, by comparing the amount of protein or nucleic acid in a solution containing the lipid nanoparticle before and after breaking up the lipid nanoparticle with one or more organic solvents or detergents. An anion exchange resin may be used to measure the amount of free protein or nucleic acid (e.g., RNA) in a solution. Fluorescence may be used to measure the amount of free protein and/or nucleic acid (e.g., RNA)

in a solution. For the lipid nanoparticles described herein, the encapsulation efficiency of a protein and/or nucleic acid may be at least 50%, for example 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100%. In some embodiments, the encapsulation efficiency may be at least 80%. In some embodiments, the encapsulation efficiency may be at least 90%. In some embodiments, the encapsulation efficiency may be at least 95%.

An LNP may optionally comprise one or more coatings. In some embodiments, an LNP may be formulated in a capsule, film, or table having a coating. A capsule, film, or tablet including a composition described herein may have any useful size, tensile strength, hardness or density.

Additional exemplary lipids, formulations, methods, and characterization of LNPs are taught by WO2020061457, which is incorporated herein by reference in its entirety.

In some embodiments, *in vitro* or *ex vivo* cell lipofections are performed using Lipofectamine MessengerMax (Thermo Fisher) or TransIT-mRNA Transfection Reagent (Mirus Bio). In certain embodiments, LNPs are formulated using the GenVoy_ILM ionizable lipid mix (Precision NanoSystems). In certain embodiments, LNPs are formulated using 2,2-dilinoleyl-4-dimethylaminoethyl-[1,3]-dioxolane (DLin-KC2-DMA) or dilinoleylmethyl-4-dimethylaminobutyrate (DLin-MC3-DMA or MC3), the formulation and *in vivo* use of which are taught in Jayaraman et al. Angew Chem Int Ed Engl 51(34):8529-8533 (2012), incorporated herein by reference in its entirety.

LNP formulations optimized for the delivery of CRISPR-Cas systems, e.g., Cas9-gRNA RNP, gRNA, Cas9 mRNA, are described in WO2019067992 and WO2019067910, both incorporated by reference.

Additional specific LNP formulations useful for delivery of nucleic acids are described in US8158601 and US8168775, both incorporated by reference, which include formulations used in patisiran, sold under the name ONPATTRO.

Exemplary dosing of gene modifying LNP may include about 0.1, 0.25, 0.3, 0.5, 1, 2, 3, 4, 5, 6, 8, 10, or 100 mg/kg (RNA). Exemplary dosing of AAV comprising a nucleic acid encoding one or more components of the system may include an MOI of about 10^{11}, 10^{12}, 10^{13}, and 10^{14} vg/kg.

Kits, Articles of Manufacture, and Pharmaceutical Compositions

In an aspect the disclosure provides a kit comprising a gene modifying polypeptide or a gene modifying system, e.g., as described herein. In some embodiments, the kit comprises a gene modifying polypeptide (or a nucleic acid encoding the polypeptide) and a template RNA (or DNA encoding the template RNA). In some embodiments, the kit further comprises a reagent for introducing the system into a cell, e.g., transfection reagent, LNP, and the like. In some embodiments, the kit is suitable for any of the methods described herein. In some embodiments, the kit comprises one or more elements, compositions (e.g., pharmaceutical compositions), gene modifying polypeptides, and/or gene modifying systems, or a functional fragment or component thereof, e.g., disposed in an article of manufacture. In some embodiments, the kit comprises instructions for use thereof.

In an aspect, the disclosure provides an article of manufacture, e.g., in which a kit as described herein, or a component thereof, is disposed.

In an aspect, the disclosure provides a pharmaceutical composition comprising a gene modifying polypeptide or a gene modifying system, e.g., as described herein. In some embodiments, the pharmaceutical composition further comprises a pharmaceutically acceptable carrier or excipient. In some embodiments, the pharmaceutical composition comprises a template RNA and/or an RNA encoding the polypeptide. In embodiments, the pharmaceutical composition has one or more (e.g., 1, 2, 3, or 4) of the following characteristics:

(a) less than 1% (e.g., less than 0.5%, 0.4%, 0.3%, 0.2%, or 0.1%) DNA template relative to the template RNA and/or the RNA encoding the polypeptide, e.g., on a molar basis;

(b) less than 1% (e.g., less than 0.5%, 0.4%, 0.3%, 0.2%, or 0.1%) uncapped RNA relative to the template RNA and/or the RNA encoding the polypeptide, e.g., on a molar basis;

(c) less than 1% (e.g., less than 0.5%, 0.4%, 0.3%, 0.2%, or 0.1%) partial length RNAs relative to the template RNA and/or the RNA encoding the polypeptide, e.g., on a molar basis;

(d) substantially lacks unreacted cap dinucleotides.

Chemistry, Manufacturing, and Controls (CMC)

Purification of protein therapeutics is described, for example, in Franks, Protein Biotechnology: *Isolation, Characterization, and Stabilization*, Humana Press (2013); and in Cutler, *Protein Purification Protocols (Methods in Molecular Biology)*, Humana Press (2010).

In some embodiments, a gene modifying system, polypeptide, and/or template nucleic acid (e.g., template RNA) conforms to certain quality standards. In some embodiments, a gene modifying system, polypeptide, and/or template nucleic acid (e.g., template RNA) produced by a method described herein conforms to certain quality standards. Accordingly, the disclosure is directed, in some aspects, to methods of manufacturing a gene modifying system, polypeptide, and/or template nucleic acid (e.g., template RNA) that conforms to certain quality standards, e.g., in which said quality standards are assayed. The disclosure is also directed, in some aspects, to methods of assaying said quality standards in a gene modifying system, polypeptide, and/or template nucleic acid (e.g., template RNA). In some embodiments, quality standards include, but are not limited to, one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12) of the following:

(i) the length of the template RNA, e.g., whether the template RNA has a length that is above a reference length or within a reference length range, e.g., whether at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% of the template RNA present is greater than 100, 125, 150, 175, or 200 nucleotides long;

(ii) the presence, absence, and/or length of a polyA tail on the template RNA, e.g., whether at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% of the template RNA present contains a polyA tail (e.g., a polyA tail that is at least 5, 10, 20, 30, 50, 70, 100 nucleotides in length);

(iii) the presence, absence, and/or type of a 5′ cap on the template RNA, e.g., whether at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% of the template RNA present contains a 5′ cap, e.g., whether that cap is a 7-methylguanosine cap, e.g., a O-Me-m7G cap;

(iv) the presence, absence, and/or type of one or more modified nucleotides (e.g., selected from pseudouridine, dihydrouridine, inosine, 7-methylguanosine, 1-N-methylpseudouridine (1-Me-Ψ), 5-methoxyuridine (5-MO-U), 5-methylcytidine (5mC), or a locked nucleotide) in the template RNA, e.g., whether at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% of the template RNA present contains one or more modified nucleotides;

(v) the stability of the template RNA (e.g., over time and/or under a pre-selected condition), e.g., whether at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% of the template RNA remains intact (e.g., greater than 100, 125, 150, 175, or 200 nucleotides long) after a stability test;

(vi) the potency of the template RNA in a system for modifying DNA, e.g., whether at least 1% of target sites are modified after a system comprising the template RNA is assayed for potency;

(vii) the length of the polypeptide, first polypeptide, or second polypeptide, e.g., whether the polypeptide, first polypeptide, or second polypeptide has a length that is above a reference length or within a reference length range, e.g., whether at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% of the polypeptide, first polypeptide, or second polypeptide present is greater than 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1050, 1100, 1150, 1200, 1250, 1300, 1350, 1400, 1450, 1500, 1600, 1700, 1800, 1900, or 2000 amino acids long (and optionally, no larger than 2500, 2000, 1500, 1400, 1300, 1200, 1100, 1000, 900, 800, 700, or 600 amino acids long);

(viii) the presence, absence, and/or type of post-translational modification on the polypeptide, first polypeptide, or second polypeptide, e.g., whether at least 80, 85, 90, 95, 96, 97, 98, or 99% of the polypeptide, first polypeptide, or second polypeptide contains phosphorylation, methylation, acetylation, myristoylation, palmitoylation, isoprenylation, glipyatyon, or lipoylation, or any combination thereof;

(ix) the presence, absence, and/or type of one or more artificial, synthetic, or non-canonical amino acids (e.g., selected from ornithine, β-alanine, GABA, δ-Aminolevulinic acid, PABA, a D-amino acid (e.g., D-alanine or D-glutamate), aminoisobutyric acid, dehydroalanine, cystathionine, lanthionine, Djenkolic acid, Diaminopimelic acid, Homoalanine, Norvaline, Norleucine, Homonorleucine, homoserine, O-methyl-homoserine and O-ethyl-homoserine, ethionine, selenocysteine, selenohomocysteine, selenomethionine, selenoethionine, tellurocysteine, or telluromethionine) in the polypeptide, first polypeptide, or second polypeptide, e.g., whether at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% of the polypeptide, first polypeptide, or second polypeptide present contains one or more artificial, synthetic, or non-canonical amino acids;

(x) the stability of the polypeptide, first polypeptide, or second polypeptide (e.g., over time and/or under a pre-selected condition), e.g., whether at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% of the polypeptide, first polypeptide, or second polypeptide remains intact (e.g., greater than 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1050, 1100, 1150, 1200, 1250, 1300, 1350, 1400, 1450, 1500, 1600, 1700, 1800, 1900, or 2000 amino acids long (and

optionally, no larger than 2500, 2000, 1500, 1400, 1300, 1200, 1100, 1000, 900, 800, 700, or 600 amino acids long)) after a stability test;

(xi) the potency of the polypeptide, first polypeptide, or second polypeptide in a system for modifying DNA, e.g., whether at least 1% of target sites are modified after a system comprising the polypeptide, first polypeptide, or second polypeptide is assayed for potency; or

(xii) the presence, absence, and/or level of one or more of a pyrogen, virus, fungus, bacterial pathogen, or host cell protein, e.g., whether the system is free or substantially free of pyrogen, virus, fungus, bacterial pathogen, or host cell protein contamination.

In some embodiments, a system or pharmaceutical composition described herein is endotoxin free.

In some embodiments, the presence, absence, and/or level of one or more of a pyrogen, virus, fungus, bacterial pathogen, and/or host cell protein is determined. In embodiments, whether the system is free or substantially free of pyrogen, virus, fungus, bacterial pathogen, and/or host cell protein contamination is determined.

In some embodiments, a pharmaceutical composition or system as described herein has one or more (e.g., 1, 2, 3, or 4) of the following characteristics:

(a) less than 1% (e.g., less than 0.5%, 0.4%, 0.3%, 0.2%, or 0.1%) DNA template relative to the template RNA and/or the RNA encoding the polypeptide, e.g., on a molar basis;

(b) less than 1% (e.g., less than 0.5%, 0.4%, 0.3%, 0.2%, or 0.1%) uncapped RNA relative to the template RNA and/or the RNA encoding the polypeptide, e.g., on a molar basis;

(c) less than 1% (e.g., less than 0.5%, 0.4%, 0.3%, 0.2%, or 0.1%) partial length RNAs relative to the template RNA and/or the RNA encoding the polypeptide, e.g., on a molar basis;

(d) substantially lacks unreacted cap dinucleotides.

EXAMPLES

Example 1: Screening configurations of template RNAs that correct a sickle cell disease associated mutation in a genomic landing pad in human cells

This example describes the use of gene modifying system containing a gene modifying polypeptide and template RNAs comprising varied lengths of heterologous object sequences and PBS sequences to quantify the activity of template RNAs for correction of the *HBB*:E6V mutation (also referred to as E7V or the HbS variant; NC_000011.10:g.5227002T>A). In this example, a template RNA contains:

(1) a gRNA spacer;

(2) a gRNA scaffold;

(3) a heterologous object sequence; and

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

One or more template RNAs described in Tables 1-4 can be tested as described in this example. The heterologous object sequences and PBS sequences were designed to correct the SCD mutation in a landing pad by replacing an "A" nucleotide with a "T" nucleotide at the mutation site via gene editing, to reverse an E6V mutation in the corresponding protein.

A cell line is created to have a "landing pad" or a stable integration that mimics a region of the *HBB* gene that contains the E6V mutation site and flanking sequences. In some embodiments, a cell line used for screening may contain one or more additional SNPs in the *HBB* locus relative to a patient or reference sequence, e.g., the hg38 human genome reference sequence, and a landing pad containing the target mutation is optionally designed to carry the one or more non-pathogenic SNPs to match the endogenous cell line *HBB* locus, e.g., designed to carry a mutation that recapitulates a SNP present in the endogenous *HBB* locus in HEK293T cells. Without wishing to be limited by example, it is understood that template RNA sequences found to successfully edit a target mutation at a site containing an additional SNP relative to a reference sequence would differ from a therapeutic template RNA in any region overlapping the additional SNP. For example, a successful template RNA in a HEK293T-based screening assay where a genomic landing pad contains the target mutation (corresponding to the endogenous E6V mutation caused by DNA substitution NC_000011.10:g.5227002T>A) and an additional

substitution relative to hg38 (corresponding to the NC_000011.10:g.5227013T>C mutation at the endogenous *HBB* locus in HEK293T cells) in the protospacer may provide a candidate composition where the corresponding therapeutic template RNA would thus have a substitution (C>T) in the spacer region relative to the corresponding spacer region of the screening template RNA, in order to enable therapeutic correction of the E6V mutation at a target site lacking the additional substitution, e.g., at a target site comprising the pathogenic E6V mutation but otherwise matching the hg38 reference sequence. In this example, a screening cell line containing a target site landing pad comprising the pathogenic mutation with an additional T>C substitution in the protospacer region might be corrected using a screening template RNA comprising the spacer sequence 5'-CATGGTGCA**C**CTGACTCCTG-3' (SEQ ID NO: 19249) , whereas the corresponding therapeutic template RNA might comprise the spacer sequence 5'-CATGGTGCA**T**CTGACTCCTG-3'(SEQ ID NO: 19250), where the underlined nucleotides indicate the position that is altered to match either the screening cell target sequence or the hg38 target sequence. In some embodiments, the spacer, PBS, and/or RT template regions may need to be adjusted in this manner to account for any discrepancies between screening and reference target sequences. It is further contemplated that a given patient or patient population may possess one or more SNPs relative to hg38 at the target locus in addition to the pathogenic E6V mutation and thus a similar adaptation of candidate template RNA molecules could be used to generate template RNA sequences specific for the patient or patient population.

The DNA for the landing pad is chemically synthesized and cloned into the pLenti-N-tGFP vector. The cloned landing pad sequence in the lentiviral expression vector is confirmed and the sequence is verified by Sanger sequencing of the landing pad. The sequence verified plasmids (9μg) along with the lentiviral packaging mix (9μg, Biosettia) are transfected using Lipofectamine2000™ according to the manufacturer instructions into a packaging cell line, LentiX-293T (Takara Bio). The transfected cells are incubated at 37°C, 5% CO_2 for 48 hours (including one medium change at 24hrs) and the viral particle containing medium is collected from the cell culture dish. The collected medium is filtered through a 0.2 μm filter to remove cell debris and is prepared for transduction of HEK293T cells. The virus-containing medium is diluted in DMEM and mixed with polybrene to prepare a dilution series for transduction of HEK293T cells where the final concentration of polybrene is 8 μg/ml. The HEK293T cells are grown in virus containing medium for 48 hours and then split with fresh medium. The split cells

are grown to confluence and transduction efficiency of the different dilutions of virus is measured by GFP expression via flow cytometry and ddPCR detection of the genomic integrated lentivirus that contained GFP and the *HBB*:E6V landing pads.

A gene modifying system comprising (i) a compatible gene modifying polypeptide described herein, e.g., having: an NLS of Table 11, a compatible Cas9 domain having a sequence of Table 8, a linker of Table 10, an RT sequence of Table 6 (e.g., MLVMS_P03355_PLV919), and a second NLS of Table 11 and (ii) a template RNA of any of Tables 1-4 is transfected into the HEK293T landing pad cell line. The gene modifying polypeptide and the template RNAs are delivered by nucleofection in RNA format. Specifically, 1μg of gene modifying polypeptide mRNA is combined with 10μM template RNAs. The mRNA and template RNAs are added to 25μL SF buffer containing 250,000 HEK293T landing pad cells and cells are nucleofected using program DS-150. After nucleofection, are were grown at 37˚C, 5% CO_2 for 3 days prior to cell lysis and genomic DNA extraction. To analyze gene editing activity, primers flanking the *HBB*:E6V site are used to amplify across the locus. Amplicons are analyzed via short read sequencing using an Illumina MiSeq. In some embodiments, the assay will indicate that at least 10%, 20%, 30%, 40%, 50%, 60%, or 70% of copies of the *HBB* gene in the sample are converted to the desired wild-type sequence.

Example 2: Gene modifying polypeptide selection by pooled screening in HEK293T & U2OS cells

This example describes the use of an RNA gene modifying system for the targeted editing of a coding sequence in the human genome. More specifically, this example describes the infection of HEK293T and U2OS cells with a library of gene modifying candidates, followed by transfection of a template guide RNA (tgRNA) for *in vitro* gene modifying in the cells, e.g., as a means of evaluating a new gene modifying polypeptide for editing activity in human cells by a pooled screening approach.

The gene modifying polypeptide library candidates assayed herein each comprise: 1) a *S. pyogenes* (Spy) Cas9 nickase containing an N863A mutation that inactivates one endonuclease active site; 2) one of the 122 peptide linkers depicted at **Table 10**; and 3) a reverse transcriptase (RT) domain from **Table 6** of retroviral origin. The particular retroviral RT domains utilized were selected if they were expected to function as a monomer. For each selected RT domain, the wild-type sequences were tested, as well as versions with point mutations installed in the primary wild-

type sequence. In particular, 143 RT domains were tested, either wild type or containing various mutations. In total, 17,446 Cas-linker-RT gene modifying polypeptides were tested.

The system described here is a two-component system comprising: 1) an expression plasmid encoding a human codon-optimized gene modifying polypeptide library candidate within a lentiviral cassette, and 2) a tgRNA expression plasmid expressing a non-coding tgRNA sequence that is recognized by Cas and localizes it to the genomic locus of interest, and that also templates reverse transcription of the desired edit into the genome by the RT domain, driven by a U6 promoter. The lentiviral cassette comprises: (i) a CMV promoter for expression in mammalian cells; (ii) a gene modifying polypeptide library candidate as shown; (iii) a self-cleaving T2A polypeptide; (iv) a puromycin resistance gene enabling selection in mammalian cells; and (v) a polyA tail termination signal.

To prepare a pool of cells expressing gene modifying polypeptide library candidates, HEK293T or U2OS cells were transduced with pooled lentiviral preparations of the gene modifying candidate plasmid library. HEK293 Lenti-X cells were seeded in 15 cm plates ($12x10^6$ cells) prior to lentiviral plasmid transfection. Lentiviral plasmid transfection using the Lentiviral Packaging Mix (Biosettia, 27 ug) and the plasmid DNA for the gene modifying candidate library (27 ug) was performed the following day using Lipofectamine 2000 and Opti-MEM media according to the manufacturer's protocol. Extracellular DNA was removed by a full media change the next day and virus-containing media was harvested 48 hours after. Lentiviral media was concentrated using Lenti-X Concentrator (TaKaRa Biosciences) and 5 mL lentiviral aliquots were made and stored at -80°C. Lentiviral titering was performed by enumerating colony forming units post Puromycin selection. HEK293T or U2OS cells carrying a BFP-expressing genomic landing pad were seeded at $6x10^7$ cells in culture plates and transduced at a 0.3 multiplicity of infection (MOI) to minimize multiple infections per cell. Puromycin (2.5 ug/mL) was added 48 hours post infection to allow for selection of infected cells. Cells were kept under puromycin selection for at least 7 days and then scaled up for tgRNA electroporation.

To determine the genome-editing capacity of the gene modifying library candidates in the assay, infected BFP-expressing HEK293T or U2OS cells were then transfected by electroporation of 250,000 cells/well with 200 ng of a tgRNA (either g4 or g10) plasmid, designed to convert BFP to GFP, at sufficient cell count for >1000x coverage per library candidate.

The g4 tgRNA (5′ to 3′) is as follows: 20 nucleotide spacer region (GCCGAAGCACTGCACGCCGT; SEQ ID NO: 11,011), a scaffold region (GTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAA AAGTGGCACCGAGTCGGTGC; SEQ ID NO: 11,012), the template region encoding the single base pair substitution to change BFP to GFP (**bold**) and a PAM inactivation that introduces a synonymous point mutation in the SpyCas9 PAM (NGG to NCG) that prevents re-engagement of the gene modifying polypeptide upon completion of a functional gene modifying reaction (underline) (ACCCTGAC<u>G</u>**T**ACG; SEQ ID NO: 11,013), and the 13 nucleotide PBS (GCGTGCAGTGCTT; SEQ ID NO: 11,014).

Similarly, the g10 tgRNA (5′ to 3′) is as follows: 20 nucleotide spacer region (AGAAGTCGTGCTGCTTCATG; SEQ ID NO: 11,015), a scaffold region (GTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAA AAGTGGCACCGAGTCGGTGC; SEQ ID NO: 11,016), the template region encoding the single base pair substitution to change BFP to GFP (**bold**) and a PAM inactivation that introduces a synonymous point mutation in the SpyCas9 PAM (NGG to NGA) that prevents re-engagement of the gene modifying polypeptide upon completion of a functional gene modifying reaction (<u>underline</u>) (ACCCTGACC<u>T</u>ACGGCGTGCAGTGCTTCGGCCGCTACCCCGA**T**CACAT; SEQ ID NO: 11,017), and 13 nucleotide PBS (GAAGCAGCACGAC; SEQ ID NO: 11,018).

To assess the genome-editing capacity of the various constructs in the assay, cells were sorted by Fluorescence-Activated Cell Sorting (FACS) for GFP expression 6-7 days post-electroporation. Cells were sorted and harvested as distinct populations of unedited (BFP+) cells, edited (GFP+) cells and imperfect edit (BFP-, GFP-) cells. A sample of unsorted cells was also harvested as the input population to determine enrichment during analysis.

To determine which gene modifying library candidates have genome-editing capacity in this assay, genomic DNA (gDNA) was harvested from sorted and unsorted cell populations, and analyzed by sequencing the gene modifying library candidates in each population. Briefly, gene modifying sequences were amplified from the genome using primers specific to the lentiviral cassette, amplified in a second round of PCR to dilute genomic DNA, and then sequenced using Oxford Nanopore Sequencing Technology according to the manufacturer's protocol.

After quality control of sequencing reads, reads of at least 1500 and no more than 3200 nucleotides were mapped to the gene modifying polypeptide library sequences and those containing a minimum of an 80% match to a library sequence were considered to be successfully aligned to a given candidate. To identify gene modifying candidates capable of performing gene editing in the assay, the read count of each library candidate in the edited population was compared to its read count in the initial, unsorted population. For purposes of this pooled screen, gene modifying candidates with genome-editing capacity were selected as those candidates that were enriched in the converted (GFP+) population relative to unsorted (input) cells and wherein the enrichment was determined to be at or above the enrichment level of a reference (Element ID No: 17380).

A large number of gene modifying polypeptide candidates were determined to be enriched in the GFP+ cell populations. For example, of the 17,446 candidates tested, over 3,300 exhibited enrichment in GFP+ sorted populations (relative to unsorted) that was at least equivalent to that of the reference under similar experimental conditions (HEK293T using g4 tgRNA; HEK293T cells using g10 tgRNA; or U2OS cells using g4 tgRNA), shown in Table D. Although the 17,446 candidates were also tested in U2OS cells using g10 tgRNA, the pooled screen did not yield candidates that were enriched in the converted (GFP+) population relative to unsorted (input) cells under that experimental condition; further investigation is required to explain these results.

Table D. Combinations of linker and RT sequences screened. The amino acid sequence of each RT in this table is provided in Table 6.

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
EAAAKGSS	12,001	PERV_Q4VFZ2_3mutA_WS
EAAAKEAAAKEAAAKEAAAK	12,002	MLVMS_P03355_PLV919
PAPEAAAK	12,003	MLVFF_P26809_3mutA
EAAAKPAPGGG	12,004	MLVFF_P26809_3mutA
GSSGSSGSSGSSGSSGSS	12,005	PERV_Q4VFZ2_3mut
PAPGGGEAAAK	12,006	MLVAV_P03356_3mutA
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	12,007	MLVMS_P03355_PLV919
GSSEAAAK	12,008	MLVFF_P26809_3mutA
EAAAKPAPGGS	12,009	MLVFF_P26809_3mutA
GGSGGSGGSGGSGGSGGS	12,010	MLVFF_P26809_3mutA
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	12,011	XMRV6_A1Z651_3mutA

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	12,012	PERV_Q4VFZ2_3mutA_WS
EAAAKEAAAKEAAAK	12,013	MLVFF_P26809_3mutA
PAPEAAAKGSS	12,014	MLVFF_P26809_3mutA
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	12,015	PERV_Q4VFZ2_3mutA_WS
EAAAKEAAAKEAAAK	12,016	PERV_Q4VFZ2_3mutA_WS
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	12,017	AVIRE_P03360_3mutA
PAPAPAPAPAP	12,018	MLVCB_P08361_3mutA
PAPAPAPAPAP	12,019	MLVFF_P26809_3mutA
EAAAKGGSPAP	12,020	PERV_Q4VFZ2_3mutA_WS
PAP	12,021	MLVMS_P03355_PLV919
PAPGGGGSS	12,022	WMSV_P03359_3mutA
SGSETPGTSESATPES	12,023	MLVFF_P26809_3mutA
PAPEAAAKGSS	12,024	XMRV6_A1Z651_3mutA
EAAAKGGSGGG	12,025	MLVMS_P03355_PLV919
GGGGSGGGGS	12,026	MLVFF_P26809_3mutA
GGGPAPGSS	12,027	MLVAV_P03356_3mutA
GGSGGSGGSGGSGGSGGS	12,028	XMRV6_A1Z651_3mut
GGGGSGGGGSGGGGSGGGGSGGGGSGGGGS	12,029	MLVCB_P08361_3mutA
GSSPAP	12,030	AVIRE_P03360_3mutA
EAAAKGSSPAP	12,031	MLVFF_P26809_3mutA
GSSGGGEAAAK	12,032	MLVFF_P26809_3mutA
GGSGGSGGSGGSGGSGGS	12,033	MLVMS_P03355_3mutA_WS
PAPAPAPAP	12,034	MLVFF_P26809_3mutA
EAAAKEAAAKEAAAKEAAAK	12,035	XMRV6_A1Z651_3mutA
EAAAKGGSPAP	12,036	MLVMS_P03355_3mutA_WS
PAPGGSEAAAK	12,037	AVIRE_P03360_3mutA
GGGGSGGGGSGGGGSGGGGSGGGGSGGGGS	12,038	AVIRE_P03360_3mutA
EAAAKGGGGSEAAAK	12,039	MLVCB_P08361_3mutA
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	12,040	WMSV_P03359_3mutA
GSS	12,041	MLVMS_P03355_PLV919
GSSGSSGSSGSS	12,042	MLVMS_P03355_PLV919
GSSPAPEAAAK	12,043	XMRV6_A1Z651_3mutA
GGSPAPEAAAK	12,044	MLVFF_P26809_3mutA
GGGEAAAKGGS	12,045	MLVFF_P26809_3mutA
EAAAKEAAAKEAAAKEAAAKEAAAK	12,046	PERV_Q4VFZ2_3mutA_WS
GGGGGGGG	12,047	PERV_Q4VFZ2_3mut
GGGPAP	12,048	MLVCB_P08361_3mutA
PAPAPAPAPAPAP	12,049	MLVCB_P08361_3mutA
GGSGGSGGSGGSGGSGGS	12,050	MLVCB_P08361_3mutA

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
PAP	12,051	MLVMS_P03355_3mutA_WS
GGSGGSGGSGGSGGSGGS	12,052	PERV_Q4VFZ2_3mutA_WS
PAPAPAPAPAPAP	12,053	MLVMS_P03355_PLV919
EAAAKPAPGSS	12,054	MLVMS_P03355_3mutA_WS
EAAAKEAAAKEAAAKEAAAK	12,055	MLVMS_P03355_3mutA_WS
EAAAKGGS	12,056	MLVMS_P03355_3mutA_WS
GGGGSEAAAKGGGGS	12,057	MLVFF_P26809_3mutA
EAAAKPAPGSS	12,058	MLVFF_P26809_3mutA
GGGGSGGGGSGGGGSGGGGS	12,059	MLVMS_P03355_PLV919
EAAAKGGGGGS	12,060	MLVMS_P03355_PLV919
GGSPAP	12,061	XMRV6_A1Z651_3mutA
EAAAKGGGPAP	12,062	MLVMS_P03355_PLV919
EAAAKEAAAKEAAAKEAAAKEAAAK	12,063	MLVFF_P26809_3mutA
PAP	12,064	MLVCB_P08361_3mutA
EAAAK	12,065	XMRV6_A1Z651_3mutA
GGSGSSPAP	12,066	PERV_Q4VFZ2_3mutA_WS
GSSGSSGSSGSSGSSGSS	12,067	MLVMS_P03355_PLV919
GSSEAAAKGGG	12,068	MLVAV_P03356_3mutA
GGGEAAAKGGS	12,069	XMRV6_A1Z651_3mutA
EAAAKGGGGSEAAAK	12,070	MLVAV_P03356_3mutA
GGGGSGGGGSGGGGS	12,071	MLVFF_P26809_3mutA
GGGGSGGGGSGGGGSGGGGS	12,072	AVIRE_P03360_3mutA
SGSETPGTSESATPES	12,073	AVIRE_P03360_3mutA
GGGEAAAKPAP	12,074	MLVFF_P26809_3mutA
EAAAKGSSGGG	12,075	MLVMS_P03355_3mutA_WS
EAAAKEAAAKEAAAKEAAAKEAAAK	12,076	WMSV_P03359_3mut
GGSGGSGGSGGS	12,077	XMRV6_A1Z651_3mutA
GGSEAAAKPAP	12,078	MLVFF_P26809_3mutA
EAAAKGSSGGG	12,079	XMRV6_A1Z651_3mutA
GGGGS	12,080	MLVFF_P26809_3mutA
GGGEAAAKGSS	12,081	MLVMS_P03355_PLV919
PAPAPAPAPAPAP	12,082	MLVAV_P03356_3mutA
GGGGSGGGGSGGGGSGGGGS	12,083	MLVCB_P08361_3mutA
GGGEAAAKGSS	12,084	MLVCB_P08361_3mutA
PAPGGSGSS	12,085	MLVFF_P26809_3mutA
GSAGSAAGSGEF	12,086	MLVCB_P08361_3mutA
PAPGGSEAAAK	12,087	MLVMS_P03355_3mutA_WS
GGSGSS	12,088	XMRV6_A1Z651_3mutA
PAPGGGGSS	12,089	MLVMS_P03355_PLV919

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
GSSGSSGSS	12,090	XMRV6_A1Z651_3mut
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	12,091	MLVMS_P03355_3mutA_WS
EAAAK	12,092	MLVMS_P03355_PLV919
GSSGSSGSSGSS	12,093	MLVFF_P26809_3mutA
PAPGGGGSS	12,094	MLVCB_P08361_3mutA
GGGEAAAKGGS	12,095	MLVCB_P08361_3mutA
PAPGGGEAAAK	12,096	MLVMS_P03355_PLV919
GGGGGSPAP	12,097	XMRV6_A1Z651_3mutA
EAAAKGGS	12,098	XMRV6_A1Z651_3mutA
EAAAKGSSPAP	12,099	XMRV6_A1Z651_3mut
PAPEAAAK	12,100	MLVAV_P03356_3mutA
GGSGGSGGSGGS	12,101	MLVMS_P03355_3mutA_WS
GGGPAPGGS	12,102	MLVMS_P03355_PLV919
GSSGSSGSSGSS	12,103	PERV_Q4VFZ2_3mutA_WS
EAAAKPAPGGS	12,104	MLVCB_P08361_3mutA
GSSGSS	12,105	MLVFF_P26809_3mutA
EAAAKEAAAKEAAAKEAAAK	12,106	MLVCB_P08361_3mutA
EAAAKEAAAKEAAAKEAAAK	12,107	FLV_P10273_3mutA
GSS	12,108	MLVFF_P26809_3mutA
EAAAKEAAAK	12,109	MLVMS_P03355_3mutA_WS
PAPEAAAKGGG	12,110	MLVAV_P03356_3mutA
GGSGSSEAAAK	12,111	MLVFF_P26809_3mutA
EAAAKEAAAKEAAAKEAAAKEAAAK	12,112	PERV_Q4VFZ2
GSSEAAAKPAP	12,113	AVIRE_P03360_3mutA
EAAAKEAAAKEAAAKEAAAKEAAAK	12,114	MLVCB_P08361_3mutA
EAAAKGGG	12,115	MLVFF_P26809_3mutA
GSSPAPGGG	12,116	MLVCB_P08361_3mutA
GGGPAPGSS	12,117	MLVMS_P03355_PLV919
GGGGGS	12,118	MLVMS_P03355_3mutA_WS
EAAAKEAAAKEAAAKEAAAKEAAAKEAAAK	12,119	PERV_Q4VFZ2_3mut
GGGGSGGGGSGGGGSGGGGSGGGGS	12,120	WMSV_P03359_3mutA
EAAAKEAAAKEAAAK	12,121	PERV_Q4VFZ2_3mut
PAPAPAPAP	12,122	MLVCB_P08361_3mutA
GSSGSSGSSGSSGSS	12,123	PERV_Q4VFZ2_3mut
GGGGSSEAAAK	12,124	MLVMS_P03355_3mutA_WS
GGSGGSGGSGGS	12,125	MLVCB_P08361_3mutA
PAPEAAAKGGS	12,126	MLVCB_P08361_3mutA
EAAAKEAAAKEAAAKEAAAKEAAAKEAAAK	12,127	MLVCB_P08361_3mutA
EAAAKGGGGSEAAAK	12,128	MLVMS_P03355_PLV919

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
EAAAKGGGGSEAAAK	12,129	MLVMS_P03355_3mutA_WS
EAAAKGGGPAP	12,130	XMRV6_A1Z651_3mut
EAAAKEAAAKEAAAKEAAAKEAAAK	12,131	MLVMS_P03355_3mutA_WS
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	12,132	FLV_P10273_3mutA
GGSEAAAKGGG	12,133	MLVMS_P03355_3mutA_WS
GGGGSGGGGSGGGGSGGGGSGGGGSGGGGS	12,134	KORV_Q9TTC1-Pro_3mutA
GGGPAPGGS	12,135	MLVCB_P08361_3mutA
PAPAPAPAPAP	12,136	XMRV6_A1Z651_3mutA
GGSGSSGGG	12,137	XMRV6_A1Z651_3mutA
GGSGSSGGG	12,138	MLVCB_P08361_3mutA
GGGEAAAKGGS	12,139	MLVMS_P03355_3mutA_WS
EAAAK	12,140	MLVCB_P08361_3mutA
GGSPAPGSS	12,141	MLVMS_P03355_3mutA_WS
GGGGSSEAAAK	12,142	PERV_Q4VFZ2_3mut
PAPAPAPAPAP	12,143	MLVBM_Q7SVK7_3mut
EAAAKEAAAKEAAAKEAAAK	12,144	MLVAV_P03356_3mutA
GGGGGSGSS	12,145	MLVCB_P08361_3mutA
EAAAKGSSPAP	12,146	MLVMS_P03355_3mutA_WS
PAPAPAPAPAPAP	12,147	MLVMS_P03355_3mutA_WS
GSSGGGGGS	12,148	MLVMS_P03355_3mutA_WS
PAPGSSGGG	12,149	MLVMS_P03355_PLV919
GGSGGGPAP	12,150	MLVCB_P08361_3mutA
GGGGGGG	12,151	MLVCB_P08361_3mutA
GSSGSSGSSGSSGSSGSS	12,152	MLVCB_P08361_3mutA
GGGPAPGGS	12,153	MLVFF_P26809_3mutA
EAAAKGGSGGG	12,154	PERV_Q4VFZ2_3mut
EAAAKGGGGSS	12,155	MLVMS_P03355_3mutA_WS
GSSGSSGSSGSSGSSGSS	12,156	MLVMS_P03355_3mut
GGGGSGGGGSGGGGSGGGGS	12,157	MLVBM_Q7SVK7_3mutA_WS
PAPAPAPAPAP	12,158	MLVMS_P03355_PLV919
GGGEAAAKGGS	12,159	MLVMS_P03355_PLV919
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	12,160	MLVMS_P03355_3mut
GSAGSAAGSGEF	12,161	MLVMS_P03355_3mutA_WS
GSSGSSGSSGSSGSS	12,162	MLVFF_P26809_3mutA
EAAAKGGSGSS	12,163	MLVFF_P26809_3mutA
PAPGGG	12,164	MLVFF_P26809_3mutA
GGGPAPGSS	12,165	XMRV6_A1Z651_3mutA
PAPEAAAKGGS	12,166	AVIRE_P03360_3mutA
PAPGGGEAAAK	12,167	MLVFF_P26809_3mut

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
GGGGSSEAAAK	12,168	MLVCB_P08361_3mutA
EAAAK	12,169	MLVMS_P03355_PLV919
GGGGSGGGGSGGGGSGGGGSGGGGSGGGGS	12,170	BAEVM_P10272_3mutA
GGSGGGEAAAK	12,171	MLVMS_P03355_PLV919
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	12,172	MLVFF_P26809_3mutA
GSSPAPGGS	12,173	XMRV6_A1Z651_3mutA
GGSGGGPAP	12,174	MLVMS_P03355_PLV919
EAAAK	12,175	AVIRE_P03360_3mutA
GSS	12,176	XMRV6_A1Z651_3mutA
GGSGGSGGS	12,177	MLVFF_P26809_3mutA
EAAAKEAAAKEAAAKEAAAK	12,178	AVIRE_P03360_3mut
PAPEAAAKGGG	12,179	PERV_Q4VFZ2_3mutA_WS
GGGGGSEAAAK	12,180	BAEVM_P10272_3mutA
GGSGSSGGG	12,181	MLVMS_P03355_3mutA_WS
GGGGGGG	12,182	MLVMS_P03355_3mutA_WS
GSSEAAAKPAP	12,183	PERV_Q4VFZ2_3mut
GGGGGSEAAAK	12,184	WMSV_P03359_3mut
GGGGSGGGGSGGGGSGGGGSGGGGS	12,185	MLVFF_P26809_3mut
GGGEAAAKGGS	12,186	AVIRE_P03360_3mutA
GGSPAPGGG	12,187	AVIRE_P03360_3mutA
GSAGSAAGSGEF	12,188	MLVAV_P03356_3mutA
EAAAK	12,189	MLVAV_P03356_3mutA
EAAAKPAPGSS	12,190	WMSV_P03359_3mutA
EAAAKEAAAKEAAAKEAAAKEAAAKEAAAK	12,191	PERV_Q4VFZ2_3mutA_WS
GGSEAAAKPAP	12,192	MLVCB_P08361_3mutA
PAPAPAPAPAPAP	12,193	MLVBM_Q7SVK7_3mutA_WS
GGSPAPGGG	12,194	MLVMS_P03355_3mutA_WS
GGSEAAAKGGG	12,195	MLVMS_P03355_3mut
GGSGGSGGSGGS	12,196	MLVFF_P26809_3mutA
EAAAKEAAAKEAAAKEAAAKEAAAKEAAAK	12,197	MLVFF_P26809_3mutA
GGG	12,198	AVIRE_P03360_3mutA
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	12,199	PERV_Q4VFZ2_3mut
GGSGGSGGSGGS	12,200	MLVMS_P03355_3mutA_WS
GGGEAAAK	12,201	MLVCB_P08361_3mutA
GSSGSSGSSGSSGSSGSS	12,202	MLVMS_P03355_3mutA_WS
GSSGGGPAP	12,203	MLVMS_P03355_3mutA_WS
GSSEAAAKPAP	12,204	MLVFF_P26809_3mutA
EAAAKEAAAK	12,205	MLVMS_P03355_PLV919
GGGGSGGGGSGGGGSGGGGSGGGGSGGGGS	12,206	MLVCB_P08361_3mut

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
GGGGGG	12,207	MLVMS_P03355_3mutA_WS
GGSGSSGGG	12,208	MLVFF_P26809_3mutA
GSSGGGEAAAK	12,209	PERV_Q4VFZ2_3mutA_WS
PAPAPAPAPAP	12,210	PERV_Q4VFZ2_3mut
EAAAKEAAAKEAAAKEAAAKEAAAKEAAAK	12,211	SFV3L_P27401_2mut
EAAAKGGSGGG	12,212	BAEVM_P10272_3mutA
GGGGSSPAP	12,213	PERV_Q4VFZ2_3mutA_WS
GGGEAAAKPAP	12,214	MLVMS_P03355_PLV919
GGSGGGPAP	12,215	BAEVM_P10272_3mutA
PAPGSSGGS	12,216	MLVMS_P03355_PLV919
GGSGGGPAP	12,217	MLVMS_P03355_3mutA_WS
EAAAKGGSPAP	12,218	PERV_Q4VFZ2_3mutA_WS
EAAAKGGSGGG	12,219	MLVMS_P03355_3mutA_WS
PAPGSSGGG	12,220	MLVFF_P26809_3mutA
GSSEAAAKGGS	12,221	MLVFF_P26809_3mutA
PAPGSSEAAAK	12,222	MLVFF_P26809_3mutA
EAAAKGSSPAP	12,223	KORV_Q9TTC1-Pro_3mutA
EAAAKEAAAKEAAAKEAAAKEAAAK	12,224	MLVBM_Q7SVK7_3mutA_WS
PAPGSSEAAAK	12,225	MLVMS_P03355_PLV919
EAAAKGSSGGG	12,226	MLVMS_P03355_3mutA_WS
EAAAKGGGGGS	12,227	AVIRE_P03360_3mutA
EAAAKEAAAKEAAAK	12,228	MLVMS_P03355_PLV919
PAPAPAPAPAPAP	12,229	MLVFF_P26809_3mutA
GGGGSGGGGSGGGGS	12,230	MLVCB_P08361_3mutA
PAPGGSEAAAK	12,231	MLVCB_P08361_3mutA
PAPGSSEAAAK	12,232	MLVBM_Q7SVK7_3mutA_WS
PAPEAAAKGSS	12,233	AVIRE_P03360_3mutA
GGSPAPGSS	12,234	WMSV_P03359_3mutA
PAPGGSGGG	12,235	MLVMS_P03355_PLV919
EAAAKGGSGSS	12,236	MLVMS_P03355_3mutA_WS
GGSGGG	12,237	MLVFF_P26809_3mutA
GGSEAAAKGSS	12,238	KORV_Q9TTC1_3mutA
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	12,239	MLVCB_P08361_3mutA
PAPAPAPAPAPAP	12,240	PERV_Q4VFZ2_3mutA_WS
PAPEAAAK	12,241	MLVMS_P03355_3mutA_WS
GGSEAAAKGGG	12,242	MLVMS_P03355_PLV919
GSSPAP	12,243	MLVMS_P03355_3mutA_WS
GGGGSS	12,244	MLVMS_P03355_PLV919
GGGEAAAKPAP	12,245	AVIRE_P03360_3mutA

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
EAAAKPAPGGS	12,246	MLVAV_P03356_3mutA
EAAAKGGGPAP	12,247	MLVAV_P03356_3mutA
PAPGGSEAAAK	12,248	BAEVM_P10272_3mutA
PAPGGSGSS	12,249	MLVMS_P03355_3mutA_WS
PAPGGSGSS	12,250	AVIRE_P03360_3mutA
GGSGGGPAP	12,251	MLVMS_P03355_3mutA_WS
EAAAKEAAAKEAAAKEAAAK	12,252	BAEVM_P10272_3mutA
GGGGSGGGGSGGGGSGGGGSGGGGS	12,253	MLVMS_P03355_PLV919
GGGGSSPAP	12,254	MLVCB_P08361_3mutA
GSSGGGPAP	12,255	MLVFF_P26809_3mutA
GGGGSSGGS	12,256	MLVMS_P03355_PLV919
GGSGGG	12,257	MLVCB_P08361_3mutA
GSSGGGGGS	12,258	MLVMS_P03355_PLV919
SGGSSGGSSGSETPGTSESATPESSGGSSGGSS	12,259	XMRV6_A1Z651_3mutA
GGGGGSGSS	12,260	KORV_Q9TTC1_3mut
GGGEAAAKGGS	12,261	BAEVM_P10272_3mutA
GGSGGG	12,262	BAEVM_P10272_3mutA
PAPAPAP	12,263	KORV_Q9TTC1-Pro_3mut
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	12,264	SFV3L_P27401_2mutA
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	12,265	MLVBM_Q7SVK7_3mutA_WS
GSSGSSGSSGSSGSS	12,266	MLVMS_P03355_3mutA_WS
GSSGGGEAAAK	12,267	MLVMS_P03355_3mutA_WS
GSSGGSEAAAK	12,268	MLVFF_P26809_3mutA
PAP	12,269	MLVMS_P03355_PLV919
EAAAKGGGGSEAAAK	12,270	MLVBM_Q7SVK7_3mutA_WS
PAPAP	12,271	AVIRE_P03360_3mutA
PAP	12,272	MLVFF_P26809_3mutA
GSSGGG	12,273	MLVMS_P03355_3mut
GSSPAPGGS	12,274	MLVFF_P26809_3mutA
PAPAPAPAP	12,275	XMRV6_A1Z651_3mutA
EAAAKGSSGGS	12,276	PERV_Q4VFZ2_3mut
PAPEAAAKGGG	12,277	KORV_Q9TTC1-Pro_3mutA
PAPGGS	12,278	MLVCB_P08361_3mutA
EAAAKGGG	12,279	MLVCB_P08361_3mutA
GSSEAAAKPAP	12,280	MLVMS_P03355_PLV919
PAPGGS	12,281	MLVFF_P26809_3mutA
EAAAKGGS	12,282	MLVCB_P08361_3mutA
EAAAKEAAAKEAAAKEAAAKEAAAKEAAAK	12,283	FLV_P10273_3mutA
PAPGGSEAAAK	12,284	MLVAV_P03356_3mutA

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
GSS	12,285	MLVCB_P08361_3mutA
GSSGSSGSSGSS	12,286	AVIRE_P03360_3mutA
GSSGSSGSS	12,287	MLVFF_P26809_3mutA
GSSGGG	12,288	MLVMS_P03355_PLV919
EAAAK	12,289	MLVFF_P26809_3mutA
GGSPAPEAAAK	12,290	MLVCB_P08361_3mutA
GGSGSS	12,291	MLVCB_P08361_3mutA
GSSPAPGGG	12,292	MLVMS_P03355_PLV919
EAAAKEAAAKEAAAKEAAAKEAAAK	12,293	MLVAV_P03356_3mutA
EAAAKGSSPAP	12,294	FLV_P10273_3mutA
GGGGSS	12,295	XMRV6_A1Z651_3mutA
GGSPAPGSS	12,296	MLVMS_P03355_PLV919
EAAAKEAAAKEAAAKEAAAKEAAAK	12,297	MLVMS_P03355_3mutA_WS
PAPEAAAKGGG	12,298	FLV_P10273_3mutA
EAAAKPAPGGS	12,299	XMRV6_A1Z651_3mut
PAPAP	12,300	BAEVM_P10272_3mutA
EAAAKEAAAKEAAAKEAAAK	12,301	MLVMS_P03355_PLV919
GSSPAPGGG	12,302	MLVMS_P03355_PLV919
EAAAKGGGPAP	12,303	KORV_Q9TTC1_3mutA
PAPEAAAK	12,304	MLVMS_P03355_PLV919
PAPGGGEAAAK	12,305	PERV_Q4VFZ2_3mutA_WS
EAAAKGSSGGS	12,306	MLVMS_P03355_3mutA_WS
EAAAKEAAAKEAAAK	12,307	MLVMS_P03355_PLV919
GSSEAAAK	12,308	MLVMS_P03355_3mutA_WS
GSSGSSGSSGSS	12,309	MLVMS_P03355_3mutA_WS
GGGGSGGGGSGGGGSGGGGS	12,310	MLVMS_P03355_3mutA_WS
EAAAKGGGGSEAAAK	12,311	MLVMS_P03355_3mut
GGS	12,312	MLVCB_P08361_3mutA
GGGGSGGGGSGGGGSGGGGSGGGGSGGGGS	12,313	XMRV6_A1Z651_3mutA
GGSGSSPAP	12,314	MLVCB_P08361_3mutA
GGGGSGGGGSGGGGS	12,315	XMRV6_A1Z651_3mutA
PAPAPAPAPAP	12,316	BAEVM_P10272_3mutA
PAPAPAPAPAP	12,317	MLVMS_P03355_3mutA_WS
EAAAKEAAAKEAAAKEAAAK	12,318	MLVBM_Q7SVK7_3mut
GGGGSGGGGSGGGGSGGGGSGGGGS	12,319	BAEVM_P10272_3mutA
GGSGGSGGS	12,320	MLVMS_P03355_3mutA_WS
EAAAKPAPGSS	12,321	MLVMS_P03355_PLV919
GSS	12,322	MLVMS_P03355_3mutA_WS
PAPEAAAKGGS	12,323	MLVMS_P03355_3mutA_WS

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
GGGPAPGGS	12,324	MLVMS_P03355_3mutA_WS
EAAAKGGGGSS	12,325	MLVAV_P03356_3mutA
GSSGSSGSSGSSGSS	12,326	MLVFF_P26809_3mut
SGSETPGTSESATPES	12,327	PERV_Q4VFZ2_3mut
GGSEAAAKGGG	12,328	MLVMS_P03355_3mut
GSSGSSGSSGSSGSSGSS	12,329	AVIRE_P03360_3mutA
PAPAPAPAPAPAP	12,330	AVIRE_P03360_3mut
GGSGGS	12,331	XMRV6_A1Z651_3mutA
PAPGSSEAAAK	12,332	MLVCB_P08361_3mut
GGSPAPEAAAK	12,333	PERV_Q4VFZ2_3mut
EAAAKGGGGGS	12,334	MLVCB_P08361_3mutA
GGSGGSGGSGGS	12,335	MLVMS_P03355_PLV919
GGGGSSEAAAK	12,336	MLVMS_P03355_PLV919
GSSEAAAKGGG	12,337	MLVFF_P26809_3mutA
PAPGGS	12,338	MLVMS_P03355_3mutA_WS
EAAAKGGSGGG	12,339	MLVCB_P08361_3mutA
EAAAKGGG	12,340	PERV_Q4VFZ2_3mut
PAPGGS	12,341	XMRV6_A1Z651_3mutA
GSSPAPGGG	12,342	XMRV6_A1Z651_3mutA
PAPEAAAKGGG	12,343	MLVMS_P03355_3mutA_WS
GSSEAAAKGGG	12,344	PERV_Q4VFZ2_3mutA_WS
PAPGGSEAAAK	12,345	XMRV6_A1Z651_3mutA
GGGGGS	12,346	MLVMS_P03355_3mutA_WS
GGSPAPEAAAK	12,347	MLVMS_P03355_3mutA_WS
GGGPAP	12,348	MLVFF_P26809_3mutA
PAPGSSGGG	12,349	XMRV6_A1Z651_3mutA
PAPGSSGGG	12,350	MLVBM_Q7SVK7_3mutA_WS
GGGEAAAKGSS	12,351	MLVMS_P03355_3mutA_WS
GSSEAAAKGGS	12,352	MLVCB_P08361_3mutA
PAPGGSGSS	12,353	MLVCB_P08361_3mutA
EAAAKGGGGSEAAAK	12,354	BAEVM_P10272_3mutA
PAPAPAP	12,355	PERV_Q4VFZ2_3mutA_WS
GGGGGG	12,356	MLVAV_P03356_3mutA
GSSPAPEAAAK	12,357	MLVCB_P08361_3mutA
GGSGGSGGS	12,358	MLVMS_P03355_3mutA_WS
GSSGSSGSSGSSGSS	12,359	XMRV6_A1Z651_3mut
GGGPAPGGS	12,360	XMRV6_A1Z651_3mutA
GGGPAPEAAAK	12,361	BAEVM_P10272_3mutA
GGSGGG	12,362	AVIRE_P03360_3mutA

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
SGSETPGTSESATPES	12,363	PERV_Q4VFZ2_3mutA_WS
EAAAKGSSPAP	12,364	MLVMS_P03355_PLV919
GSSEAAAK	12,365	XMRV6_A1Z651_3mut
GSSGGSGGG	12,366	MLVFF_P26809_3mutA
EAAAKEAAAKEAAAKEAAAKEAAAK	12,367	WMSV_P03359_3mutA
GGGGSEAAAKGGGGS	12,368	MLVMS_P03355_PLV919
PAPGGGGSS	12,369	MLVMS_P03355_3mutA_WS
SGSETPGTSESATPES	12,370	MLVMS_P03355_3mutA_WS
GGSPAPEAAAK	12,371	KORV_Q9TTC1-Pro_3mutA
GSSEAAAKGGG	12,372	MLVMS_P03355_3mutA_WS
GSSEAAAK	12,373	WMSV_P03359_3mutA
GGGGSEAAAKGGGGS	12,374	AVIRE_P03360_3mutA
GSS	12,375	WMSV_P03359_3mutA
PAPGGSEAAAK	12,376	MLVFF_P26809_3mutA
GGGGS	12,377	MLVMS_P03355_3mutA_WS
GGGPAP	12,378	MLVMS_P03355_3mutA_WS
EAAAKEAAAKEAAAKEAAAKEAAAKEAAAK	12,379	MLVMS_P03355_3mutA_WS
EAAAKPAPGSS	12,380	PERV_Q4VFZ2_3mut
EAAAKPAPGSS	12,381	MLVCB_P08361_3mutA
GGGGGG	12,382	WMSV_P03359_3mutA
EAAAKPAPGGS	12,383	MLVMS_P03355_PLV919
PAPGGGEAAAK	12,384	PERV_Q4VFZ2_3mut
EAAAKEAAAKEAAAKEAAAKEAAAK	12,385	AVIRE_P03360_3mutA
GSSEAAAKPAP	12,386	XMRV6_A1Z651_3mutA
PAPGGSEAAAK	12,387	MLVBM_Q7SVK7_3mutA_WS
PAPGSS	12,388	MLVCB_P08361_3mutA
EAAAKGGG	12,389	MLVMS_P03355_3mutA_WS
EAAAKPAP	12,390	MLVCB_P08361_3mutA
PAPEAAAKGGS	12,391	MLVBM_Q7SVK7_3mutA_WS
GGSPAPGGG	12,392	MLVCB_P08361_3mutA
PAPGGSGSS	12,393	WMSV_P03359_3mutA
EAAAKEAAAKEAAAKEAAAKEAAAKEAAAK	12,394	MLVMS_P03355_PLV919
GGSGGGPAP	12,395	MLVMS_P03355_PLV919
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	12,396	MLVMS_P03355
PAPEAAAKGSS	12,397	MLVCB_P08361_3mutA
EAAAKGSS	12,398	MLVMS_P03355_3mutA_WS
GGSGGS	12,399	MLVMS_P03355_3mutA_WS
EAAAKEAAAKEAAAKEAAAKEAAAK	12,400	BAEVM_P10272_3mutA
GGGGSEAAAKGGGGS	12,401	FLV_P10273_3mutA

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
GGSEAAAKGGG	12,402	MLVCB_P08361_3mutA
GSSGSSGSSGSSGSS	12,403	BAEVM_P10272_3mutA
GGGGSGGGGSGGGGSGGGGSGGGGSGGGGS	12,404	MLVFF_P26809_3mutA
EAAAKGGG	12,405	PERV_Q4VFZ2_3mut
GGGGGSEAAAK	12,406	MLVCB_P08361_3mutA
EAAAKPAPGGS	12,407	MLVMS_P03355_3mutA_WS
GGGGGSGSS	12,408	XMRV6_A1Z651_3mutA
PAPGSSEAAAK	12,409	MLVMS_P03355_3mutA_WS
GSSEAAAKPAP	12,410	MLVCB_P08361_3mutA
EAAAKGSSPAP	12,411	MLVAV_P03356_3mutA
GGGPAPGGS	12,412	WMSV_P03359_3mutA
GGSPAP	12,413	MLVMS_P03355_3mutA_WS
GGSEAAAKGGG	12,414	MLVMS_P03355_3mutA_WS
GGGGGGGG	12,415	MLVFF_P26809_3mutA
GGGGSGGGGSGGGGSGGGGSGGGGSGGGGS	12,416	MLVMS_P03355_3mutA_WS
GGGGSGGGGSGGGGSGGGGSGGGGSGGGGS	12,417	MLVBM_Q7SVK7_3mutA_WS
GSSPAPGGG	12,418	MLVAV_P03356_3mutA
GGGGGG	12,419	AVIRE_P03360_3mutA
GSSGGS	12,420	MLVMS_P03355_3mutA_WS
GGSPAPGSS	12,421	MLVFF_P26809_3mutA
PAPEAAAKGGG	12,422	PERV_Q4VFZ2_3mut
EAAAKGGGPAP	12,423	MLVFF_P26809_3mutA
GGGEAAAKGGS	12,424	MLVMS_P03355_PLV919
GGSGSSPAP	12,425	MLVFF_P26809_3mutA
SGSETPGTSESATPES	12,426	WMSV_P03359_3mutA
PAPGGSEAAAK	12,427	MLVBM_Q7SVK7_3mutA_WS
GGSGGG	12,428	MLVMS_P03355_PLV919
GGGGSSPAP	12,429	PERV_Q4VFZ2_3mut
GGGEAAAKGSS	12,430	MLVAV_P03356_3mutA
PAPAPAPAPAPAP	12,431	MLVMS_P03355_3mutA_WS
EAAAKGGGGSEAAAK	12,432	PERV_Q4VFZ2
EAAAKEAAAKEAAAKEAAAKEAAAK	12,433	MLVMS_P03355_PLV919
GGGGGSEAAAK	12,434	PERV_Q4VFZ2_3mut
PAPGSSEAAAK	12,435	MLVCB_P08361_3mutA
GSAGSAAGSGEF	12,436	PERV_Q4VFZ2_3mutA_WS
EAAAKGGGGSEAAAK	12,437	MLVFF_P26809_3mutA
GGSPAPGGG	12,438	PERV_Q4VFZ2_3mutA_WS
GSSEAAAKGGG	12,439	AVIRE_P03360_3mutA
GGGEAAAKPAP	12,440	MLVMS_P03355_3mutA_WS

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
GGGPAP	12,441	AVIRE_P03360_3mutA
GGSEAAAK	12,442	MLVCB_P08361_3mutA
SGGSSGGSSGSETPGTSESATPESSGGSSGGSS	12,443	PERV_Q4VFZ2_3mut
EAAAKPAPGGS	12,444	MLVBM_Q7SVK7_3mutA_WS
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	12,445	XMRV6_A1Z651_3mut
GGGGGGGG	12,446	MLVCB_P08361_3mutA
PAPGSS	12,447	PERV_Q4VFZ2_3mut
EAAAK	12,448	PERV_Q4VFZ2_3mut
GSAGSAAGSGEF	12,449	MLVMS_P03355_3mutA_WS
PAPGGGEAAAK	12,450	PERV_Q4VFZ2_3mut
EAAAKGSSGGS	12,451	MLVFF_P26809_3mut
GGGGSEAAAKGGGGS	12,452	BAEVM_P10272_3mutA
GGGGSGGGGSGGGGS	12,453	MLVMS_P03355_PLV919
EAAAKGGGGSEAAAK	12,454	BAEVM_P10272_3mut
PAPGGGEAAAK	12,455	MLVMS_P03355_3mutA_WS
GGSEAAAKPAP	12,456	MLVMS_P03355_3mutA_WS
PAPAP	12,457	MLVCB_P08361_3mutA
PAPAP	12,458	MLVFF_P26809_3mutA
GGSPAP	12,459	AVIRE_P03360_3mutA
EAAAKGSSGGS	12,460	MLVCB_P08361_3mutA
PAPGSSGGS	12,461	AVIRE_P03360_3mutA
EAAAKGGGGSEAAAK	12,462	XMRV6_A1Z651_3mutA
PAPAPAP	12,463	BAEVM_P10272_3mutA
GGSGGSGGSGGSGGSGGS	12,464	MLVMS_P03355_PLV919
GGGGGSGSS	12,465	MLVMS_P03355_PLV919
PAPGSSEAAAK	12,466	XMRV6_A1Z651_3mut
GGSEAAAKPAP	12,467	XMRV6_A1Z651_3mutA
EAAAKEAAAKEAAAKEAAAK	12,468	XMRV6_A1Z651_3mut
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	12,469	WMSV_P03359_3mut
GGSGGGEAAAK	12,470	XMRV6_A1Z651_3mutA
GGGEAAAK	12,471	XMRV6_A1Z651_3mutA
GGGGSGGGGSGGGGS	12,472	MLVMS_P03355_3mutA_WS
GGSGGSGGSGGSGGS	12,473	MLVFF_P26809_3mutA
GSSGGGGGS	12,474	MLVMS_P03355_3mut
PAPGGSEAAAK	12,475	MLVMS_P03355_3mutA_WS
GSSGGSPAP	12,476	MLVMS_P03355_3mutA_WS
SGSETPGTSESATPES	12,477	XMRV6_A1Z651_3mutA
GGGGSGGGGS	12,478	MLVMS_P03355_PLV919
PAPAPAPAPAP	12,479	MLVMS_P03355_3mut

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
GSSGSS	12,480	XMRV6_A1Z651_3mutA
GSSEAAAKPAP	12,481	PERV_Q4VFZ2_3mut
GGSGSSGGG	12,482	MLVMS_P03355_3mutA_WS
EAAAKEAAAK	12,483	MLVCB_P08361_3mutA
GSSGSSGSSGSS	12,484	MLVMS_P03355_3mutA_WS
GSSPAPGGG	12,485	PERV_Q4VFZ2_3mutA_WS
EAAAKEAAAKEAAAK	12,486	MLVMS_P03355_3mutA_WS
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	12,487	SFV1_P23074_2mutA
GGGGSGGGGSGGGGSGGGGSGGGGSGGGGS	12,488	MLVMS_P03355_PLV919
GSAGSAAGSGEF	12,489	MLVMS_P03355_PLV919
PAPGSSEAAAK	12,490	MLVMS_P03355_3mutA_WS
GGSEAAAK	12,491	MLVMS_P03355_3mutA_WS
GSSGSSGSSGSSGSS	12,492	PERV_Q4VFZ2_3mutA_WS
GGSEAAAKPAP	12,493	PERV_Q4VFZ2_3mutA_WS
GGSGGSGGS	12,494	MLVCB_P08361_3mutA
EAAAKGGSGSS	12,495	MLVCB_P08361_3mutA
GGGGSGGGGSGGGGSGGGGSGGGGS	12,496	FLV_P10273_3mutA
EAAAKEAAAKEAAAKEAAAK	12,497	MLVBM_Q7SVK7_3mutA_WS
GGSGSSPAP	12,498	BAEVM_P10272_3mutA
EAAAKEAAAKEAAAKEAAAKEAAAK	12,499	XMRV6_A1Z651_3mutA
GGGGSGGGGSGGGGSGGGGSGGGGS	12,500	MLVBM_Q7SVK7_3mutA_WS
GGSGSS	12,501	WMSV_P03359_3mutA
PAPEAAAK	12,502	MLVCB_P08361_3mutA
EAAAKPAP	12,503	BAEVM_P10272_3mutA
GSSPAP	12,504	PERV_Q4VFZ2_3mutA_WS
GGGPAP	12,505	PERV_Q4VFZ2_3mutA_WS
EAAAKGGSGSS	12,506	MLVMS_P03355_3mutA_WS
EAAAKGGGGSEAAAK	12,507	AVIRE_P03360_3mutA
GGSGGG	12,508	KORV_Q9TTC1-Pro_3mutA
GSSPAP	12,509	MLVFF_P26809_3mutA
GGSGSSEAAAK	12,510	BAEVM_P10272_3mutA
PAPGSSGGS	12,511	BAEVM_P10272_3mutA
GGGGGG	12,512	MLVFF_P26809_3mutA
PAPGGSEAAAK	12,513	MLVMS_P03355_PLV919
PAPGGS	12,514	MLVMS_P03355_PLV919
GGSGGSGGSGGS	12,515	BAEVM_P10272_3mutA
GSSPAP	12,516	MLVCB_P08361_3mutA
PAPAPAPAP	12,517	MLVMS_P03355_3mutA_WS
GGGGGG	12,518	MLVCB_P08361_3mutA

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
GSSGSSGSSGSSGSSGSS	12,519	KORV_Q9TTC1-Pro_3mutA
GSSEAAAKGGS	12,520	BAEVM_P10272_3mutA
GGSEAAAK	12,521	FLV_P10273_3mutA
GGSGGSGGSGGSGGS	12,522	KORV_Q9TTC1-Pro_3mutA
GSSPAPEAAAK	12,523	PERV_Q4VFZ2_3mut
GSSGSSGSSGSSGSS	12,524	XMRV6_A1Z651_3mutA
EAAAKPAPGGS	12,525	MLVMS_P03355_3mut
SGGSSGGSSGSETPGTSESATPESSGGSSGGSS	12,526	FLV_P10273_3mut
GGSPAPEAAAK	12,527	XMRV6_A1Z651_3mut
EAAAKGGSGGG	12,528	MLVFF_P26809_3mutA
EAAAKEAAAKEAAAKEAAAK	12,529	MLVFF_P26809_3mutA
GSSPAP	12,530	WMSV_P03359_3mutA
PAPAPAPAP	12,531	MLVAV_P03356_3mutA
PAPGGSEAAAK	12,532	KORV_Q9TTC1_3mut
GGSGSSEAAAK	12,533	MLVBM_Q7SVK7_3mutA_WS
GSSGGG	12,534	MLVCB_P08361_3mutA
GGGEAAAKGSS	12,535	PERV_Q4VFZ2_3mut
PAPGGSGGG	12,536	MLVFF_P26809_3mutA
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	12,537	FFV_O93209
PAPGGGGSS	12,538	MLVMS_P03355_3mutA_WS
EAAAKGGS	12,539	MLVAV_P03356_3mutA
EAAAKEAAAKEAAAKEAAAKEAAAKEAAAK	12,540	MLVBM_Q7SVK7_3mutA_WS
GGSGGSGGS	12,541	WMSV_P03359_3mutA
PAPAP	12,542	MLVMS_P03355_3mutA_WS
GSSGGGEAAAK	12,543	MLVAV_P03356_3mutA
GGGGSSEAAAK	12,544	MLVFF_P26809_3mutA
EAAAKGSSGGS	12,545	MLVMS_P03355_PLV919
EAAAKGGGGSEAAAK	12,546	MLVMS_P03355_3mutA_WS
GGGGGGGG	12,547	MLVMS_P03355_PLV919
GSSGSSGSS	12,548	MLVMS_P03355_PLV919
GGGEAAAKPAP	12,549	PERV_Q4VFZ2_3mutA_WS
GGGGGSGSS	12,550	MLVMS_P03355_3mutA_WS
GGGGGGG	12,551	MLVMS_P03355_PLV919
GGS	12,552	MLVMS_P03355_PLV919
GSSGGG	12,553	MLVMS_P03355_3mutA_WS
EAAAKGGSGSS	12,554	PERV_Q4VFZ2_3mutA_WS
PAPGSSEAAAK	12,555	MLVMS_P03355_PLV919
GSSEAAAKPAP	12,556	MLVMS_P03355_PLV919
GGSPAPGSS	12,557	BAEVM_P10272_3mutA

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
GSAGSAAGSGEF	12,558	MLVCB_P08361_3mut
GGSPAPGGG	12,559	PERV_Q4VFZ2_3mut
GGGGSGGGGSGGGGSGGGGS	12,560	MLVMS_P03355_3mut
GSSGSSGSS	12,561	PERV_Q4VFZ2_3mutA_WS
EAAAKEAAAKEAAAKEAAAKEAAAKEAAAK	12,562	PERV_Q4VFZ2_3mut
GGGGSEAAAKGGGGS	12,563	MLVCB_P08361_3mutA
GGSEAAAKGSS	12,564	MLVAV_P03356_3mutA
EAAAKGGGGSEAAAK	12,565	MLVCB_P08361_3mut
EAAAKEAAAKEAAAKEAAAKEAAAKEAAAK	12,566	XMRV6_A1Z651_3mutA
PAPGGGEAAAK	12,567	MLVMS_P03355_3mutA_WS
GSSGGGEAAAK	12,568	PERV_Q4VFZ2_3mutA_WS
GSSGSS	12,569	MLVCB_P08361_3mut
PAPAPAPAPAPAP	12,570	PERV_Q4VFZ2_3mut
GGSPAPGGG	12,571	MLVFF_P26809_3mutA
GGSGGSGGSGGSGGS	12,572	MLVCB_P08361_3mutA
EAAAKEAAAK	12,573	MLVFF_P26809_3mutA
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	12,574	GALV_P21414_3mut
PAPAPAPAPAPAP	12,575	WMSV_P03359_3mutA
GGGEAAAKGGS	12,576	KORV_Q9TTC1_3mutA
EAAAKGGGPAP	12,577	KORV_Q9TTC1_3mut
PAPEAAAKGSS	12,578	MLVBM_Q7SVK7_3mutA_WS
PAPEAAAKGSS	12,579	FLV_P10273_3mutA
PAPGGSEAAAK	12,580	MLVMS_P03355_3mut
GSSPAPGGG	12,581	BAEVM_P10272_3mutA
GGGEAAAKPAP	12,582	KORV_Q9TTC1-Pro_3mutA
GGGGSGGGGS	12,583	MLVMS_P03355_PLV919
GGGEAAAKGSS	12,584	MLVFF_P26809_3mutA
PAPGGGGSS	12,585	MLVBM_Q7SVK7_3mutA_WS
GSSEAAAK	12,586	BAEVM_P10272_3mutA
GGGGGGGG	12,587	MLVMS_P03355_PLV919
PAPGSSGGS	12,588	MLVAV_P03356_3mutA
GGGGSGGGGSGGGGSGGGGS	12,589	BAEVM_P10272_3mutA
PAP	12,590	MLVMS_P03355_3mut
EAAAKGSSPAP	12,591	XMRV6_A1Z651_3mutA
PAPEAAAKGGS	12,592	MLVFF_P26809_3mutA
GSSGGGEAAAK	12,593	BAEVM_P10272_3mutA
PAPAPAP	12,594	MLVMS_P03355_3mutA_WS
GGSEAAAKGGG	12,595	MLVMS_P03355_PLV919
GSSEAAAK	12,596	PERV_Q4VFZ2_3mut

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
GGGG	12,597	MLVMS_P03355_3mutA_WS
GGGGGS	12,598	MLVMS_P03355_3mut
GGGGSSEAAAK	12,599	PERV_Q4VFZ2_3mut
EAAAKEAAAKEAAAKEAAAKEAAAKEAAAK	12,600	SFV3L_P27401-Pro_2mutA
GGSEAAAKGSS	12,601	MLVMS_P03355_3mutA_WS
PAPGSSGGS	12,602	XMRV6_A1Z651_3mutA
GGSPAP	12,603	MLVMS_P03355_3mutA_WS
GGGGSSEAAAK	12,604	BAEVM_P10272_3mut
GGSGGSGGSGGS	12,605	AVIRE_P03360_3mutA
PAPGSSGGS	12,606	MLVFF_P26809_3mutA
GSSPAPGGG	12,607	MLVMS_P03355_3mutA_WS
GGGGGGG	12,608	MLVMS_P03355_3mutA_WS
EAAAKGGGGGS	12,609	MLVMS_P03355_3mutA_WS
EAAAKGGSGGG	12,610	MLVMS_P03355_PLV919
GGGGSSEAAAK	12,611	XMRV6_A1Z651_3mutA
GGGGSEAAAKGGGGS	12,612	MLVBM_Q7SVK7_3mutA_WS
GSSGSS	12,613	MLVMS_P03355_PLV919
GGSGGG	12,614	MLVMS_P03355_PLV919
PAPEAAAKGGG	12,615	AVIRE_P03360_3mutA
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	12,616	FOAMV_P14350-Pro_2mutA
GGGGGSGSS	12,617	PERV_Q4VFZ2_3mut
GSSGSSGSSGSSGSS	12,618	KORV_Q9TTC1-Pro_3mut
GGGGSEAAAKGGGGS	12,619	MLVMS_P03355_3mutA_WS
GGGGGSPAP	12,620	FLV_P10273_3mut
GGGEAAAK	12,621	MLVMS_P03355_3mutA_WS
GGSGGSGGSGGS	12,622	FLV_P10273_3mutA
GGG	12,623	MLVMS_P03355_PLV919
GGSPAPEAAAK	12,624	BAEVM_P10272_3mutA
EAAAKEAAAK	12,625	FLV_P10273_3mutA
GGGEAAAKPAP	12,626	BAEVM_P10272_3mutA
GGGEAAAKGGS	12,627	PERV_Q4VFZ2_3mut
GGSGGSGGS	12,628	PERV_Q4VFZ2_3mut
EAAAKGGGPAP	12,629	XMRV6_A1Z651_3mutA
EAAAK	12,630	MLVBM_Q7SVK7_3mutA_WS
PAPEAAAKGGG	12,631	PERV_Q4VFZ2_3mut
EAAAKGSS	12,632	MLVCB_P08361_3mutA
GGSEAAAKGGG	12,633	MLVBM_Q7SVK7_3mutA_WS
GGGGSGGGGSGGGGSGGGGS	12,634	XMRV6_A1Z651_3mutA
GGGGSGGGGSGGGGSGGGGSGGGGS	12,635	BAEVM_P10272_3mut

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
GGGGSSPAP	12,636	PERV_Q4VFZ2_3mutA_WS
GGSGGSGGSGGSGGSGGS	12,637	PERV_Q4VFZ2_3mut
GGGEAAAKPAP	12,638	PERV_Q4VFZ2_3mut
EAAAKEAAAK	12,639	BAEVM_P10272_3mutA
GGSGSSEAAAK	12,640	XMRV6_A1Z651_3mutA
PAPEAAAKGSS	12,641	WMSV_P03359_3mutA
PAPAPAPAPAP	12,642	XMRV6_A1Z651_3mutA
GSSGGGEAAAK	12,643	MLVMS_P03355_PLV919
GSSPAPGGG	12,644	MLVFF_P26809_3mutA
GGSPAPEAAAK	12,645	MLVFF_P26809_3mut
PAPGGSEAAAK	12,646	PERV_Q4VFZ2_3mut
GGGGSS	12,647	MLVFF_P26809_3mutA
GGSGSSGGG	12,648	BAEVM_P10272_3mutA
GSSGGGEAAAK	12,649	MLVMS_P03355_3mutA_WS
EAAAKGGS	12,650	MLVBM_Q7SVK7_3mutA_WS
GGGPAPGGS	12,651	MLVMS_P03355_PLV919
EAAAKEAAAK	12,652	MLVMS_P03355_PLV919
GSSGSSGSS	12,653	MLVMS_P03355_PLV919
GGGEAAAKPAP	12,654	MLVAV_P03356_3mutA
SGSETPGTSESATPES	12,655	FLV_P10273_3mutA
PAPAPAPAPAP	12,656	KORV_Q9TTC1-Pro_3mut
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	12,657	BAEVM_P10272_3mutA
PAPGSSGGG	12,658	MLVMS_P03355_3mutA_WS
GSSGGGEAAAK	12,659	XMRV6_A1Z651_3mutA
GGGGSGGGGSGGGGSGGGGSGGGGS	12,660	XMRV6_A1Z651_3mutA
GGGGSSPAP	12,661	MLVFF_P26809_3mutA
GGSGGGPAP	12,662	PERV_Q4VFZ2_3mutA_WS
GSS	12,663	PERV_Q4VFZ2_3mut
EAAAKGSSPAP	12,664	MLVMS_P03355_3mut
EAAAKGGG	12,665	XMRV6_A1Z651_3mutA
GSSGSSGSSGSS	12,666	WMSV_P03359_3mutA
PAPEAAAKGSS	12,667	MLVMS_P03355_PLV919
GSSEAAAK	12,668	AVIRE_P03360_3mutA
EAAAKGGSGSS	12,669	AVIRE_P03360_3mutA
GSSEAAAK	12,670	MLVMS_P03355_3mut
GGSGSSEAAAK	12,671	MLVMS_P03355_PLV919
GGSEAAAKGGG	12,672	MLVFF_P26809_3mutA
GGGGSGGGGSGGGGSGGGGS	12,673	MLVAV_P03356_3mutA
PAPAPAPAPAP	12,674	MLVFF_P26809_3mut

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
EAAAKPAPGSS	12,675	KORV_Q9TTC1-Pro_3mut
PAPGSSEAAAK	12,676	MLVAV_P03356_3mutA
GGGGSSPAP	12,677	WMSV_P03359_3mutA
EAAAKGGGGGS	12,678	MLVMS_P03355_3mutA_WS
GGGEAAAKGGS	12,679	MLVMS_P03355_3mut
GGSGSSGGG	12,680	MLVMS_P03355_3mut
GGGPAPGGS	12,681	MLVAV_P03356_3mutA
PAPGGGGGS	12,682	MLVMS_P03355_PLV919
GGGPAPGSS	12,683	PERV_Q4VFZ2_3mut
GGGGGGG	12,684	MLVFF_P26809_3mutA
GGSGGGGSS	12,685	MLVCB_P08361_3mutA
GGGGGG	12,686	FLV_P10273_3mutA
GGSEAAAKGSS	12,687	PERV_Q4VFZ2_3mut
GGSPAPGGG	12,688	BAEVM_P10272_3mutA
GGSPAPGSS	12,689	AVIRE_P03360_3mutA
GGSGGSGGSGGS	12,690	KORV_Q9TTC1_3mut
EAAAKEAAAKEAAAKEAAAKEAAAK	12,691	MLVBM_Q7SVK7_3mut
PAPGSSGGS	12,692	XMRV6_A1Z651_3mut
EAAAKGGGGSS	12,693	PERV_Q4VFZ2_3mutA_WS
GGSGGSGGSGGSGGS	12,694	PERV_Q4VFZ2_3mutA_WS
PAPGGSGGG	12,695	MLVMS_P03355_PLV919
PAPGSSGGG	12,696	PERV_Q4VFZ2_3mutA_WS
GSSGSS	12,697	BAEVM_P10272_3mutA
EAAAKGSS	12,698	MLVFF_P26809_3mutA
GGGPAP	12,699	MLVMS_P03355_PLV919
EAAAKGGGGGS	12,700	MLVFF_P26809_3mutA
EAAAKGGSPAP	12,701	MLVBM_Q7SVK7_3mutA_WS
EAAAKEAAAKEAAAKEAAAKEAAAKEAAAK	12,702	WMSV_P03359_3mutA
GSSPAPGGG	12,703	MLVBM_Q7SVK7_3mutA_WS
GGGEAAAKGSS	12,704	AVIRE_P03360_3mutA
GGGGSSEAAAK	12,705	AVIRE_P03360_3mutA
GGGGGGGG	12,706	PERV_Q4VFZ2_3mutA_WS
PAPGSSEAAAK	12,707	BAEVM_P10272_3mutA
EAAAKGSS	12,708	MLVFF_P26809_3mut
GSSEAAAKGGG	12,709	MLVCB_P08361_3mutA
GGSEAAAK	12,710	MLVBM_Q7SVK7_3mutA_WS
GSSEAAAKGGG	12,711	PERV_Q4VFZ2_3mutA_WS
PAPGGSGGG	12,712	WMSV_P03359_3mutA
GSSGGSGGG	12,713	MLVCB_P08361_3mutA

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
EAAAKGSSGGG	12,714	FLV_P10273_3mutA
GSSEAAAK	12,715	MLVCB_P08361_3mutA
GSSGGGEAAAK	12,716	MLVMS_P03355_3mut
GGGGSGGGGS	12,717	MLVCB_P08361_3mutA
EAAAKGGGGSEAAAK	12,718	MLVBM_Q7SVK7_3mutA_WS
EAAAKGGG	12,719	PERV_Q4VFZ2_3mutA_WS
EAAAKGGSPAP	12,720	MLVMS_P03355_PLV919
GGGPAPGGS	12,721	AVIRE_P03360_3mutA
GSSEAAAK	12,722	MLVBM_Q7SVK7_3mutA_WS
GSSGGGEAAAK	12,723	PERV_Q4VFZ2_3mut
SGSETPGTSESATPES	12,724	MLVMS_P03355_PLV919
GGSGSSPAP	12,725	MLVMS_P03355_3mut
GGGGGG	12,726	MLVBM_Q7SVK7_3mutA_WS
GGSPAPGGG	12,727	XMRV6_A1Z651_3mutA
GGSGSS	12,728	PERV_Q4VFZ2_3mutA_WS
PAP	12,729	MLVBM_Q7SVK7_3mutA_WS
EAAAKPAPGSS	12,730	MLVMS_P03355_PLV919
EAAAKGGG	12,731	MLVMS_P03355_3mut
GSSEAAAKPAP	12,732	PERV_Q4VFZ2_3mutA_WS
GGGGSS	12,733	MLVMS_P03355_3mutA_WS
GGSGSSEAAAK	12,734	PERV_Q4VFZ2_3mut
GGGGSS	12,735	BAEVM_P10272_3mutA
PAPAP	12,736	MLVFF_P26809_3mut
PAPEAAAKGGG	12,737	BAEVM_P10272_3mutA
EAAAKGGS	12,738	MLVMS_P03355_PLV919
PAPAPAPAPAPAP	12,739	PERV_Q4VFZ2_3mutA_WS
GGGGGSEAAAK	12,740	MLVMS_P03355_3mut
PAPGGS	12,741	PERV_Q4VFZ2_3mut
GGGGSS	12,742	MLVCB_P08361_3mutA
GGGGS	12,743	MLVAV_P03356_3mutA
GSSPAPEAAAK	12,744	MLVMS_P03355_PLV919
GGGGSSGGS	12,745	MLVFF_P26809_3mutA
PAPEAAAKGSS	12,746	MLVMS_P03355_PLV919
GGSGSSEAAAK	12,747	MLVMS_P03355_3mutA_WS
EAAAKGGG	12,748	MLVAV_P03356_3mutA
PAPGSSEAAAK	12,749	FLV_P10273_3mutA
EAAAKGSSGGG	12,750	MLVCB_P08361_3mutA
PAPEAAAK	12,751	KORV_Q9TTC1-Pro_3mutA
GGSPAPEAAAK	12,752	KORV_Q9TTC1-Pro_3mut

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
GGSGGSGGSGGSGGSGGS	12,753	MLVAV_P03356_3mutA
GSSEAAAKPAP	12,754	MLVBM_Q7SVK7_3mutA_WS
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	12,755	KORV_Q9TTC1-Pro_3mutA
GSSGGGEAAAK	12,756	XMRV6_A1Z651_3mut
PAPGGSGGG	12,757	AVIRE_P03360_3mutA
PAPGGSEAAAK	12,758	PERV_Q4VFZ2_3mutA_WS
GGGGS	12,759	MLVMS_P03355_3mutA_WS
GGGGSGGGGSGGGGS	12,760	MLVBM_Q7SVK7_3mutA_WS
PAPAPAPAPAP	12,761	PERV_Q4VFZ2_3mutA_WS
EAAAKEAAAKEAAAKEAAAKEAAAK	12,762	MLVMS_P03355_3mut
GSSGGSEAAAK	12,763	MLVMS_P03355_3mutA_WS
GGSGGSGGSGGS	12,764	WMSV_P03359_3mutA
EAAAKGSSGGG	12,765	WMSV_P03359_3mutA
EAAAKGGG	12,766	PERV_Q4VFZ2_3mutA_WS
SGSETPGTSESATPES	12,767	PERV_Q4VFZ2_3mut
PAPGSSGGS	12,768	MLVMS_P03355_3mutA_WS
PAPEAAAKGSS	12,769	PERV_Q4VFZ2_3mut
PAPEAAAK	12,770	AVIRE_P03360_3mutA
GSSEAAAKGGG	12,771	BAEVM_P10272_3mutA
GSSPAP	12,772	MLVAV_P03356_3mutA
EAAAKEAAAKEAAAKEAAAK	12,773	MLVFF_P26809_3mut
PAPGGSGSS	12,774	MLVAV_P03356_3mutA
GGGGSGGGGSGGGGS	12,775	PERV_Q4VFZ2_3mutA_WS
GSSGGSEAAAK	12,776	MLVCB_P08361_3mutA
EAAAKGGS	12,777	KORV_Q9TTC1-Pro_3mutA
EAAAKGGS	12,778	MLVFF_P26809_3mutA
GGSPAP	12,779	MLVMS_P03355_PLV919
GGSGSS	12,780	MLVMS_P03355_PLV919
SGSETPGTSESATPES	12,781	WMSV_P03359_3mut
GGGGGGG	12,782	WMSV_P03359_3mut
GGSPAPGSS	12,783	MLVCB_P08361_3mutA
GGGGSSGGS	12,784	WMSV_P03359_3mut
PAPGGS	12,785	MLVMS_P03355_PLV919
PAPGSSGGS	12,786	MLVCB_P08361_3mutA
EAAAKEAAAKEAAAKEAAAKEAAAK	12,787	MLVFF_P26809_3mut
SGGSSGGSSGSETPGTSESATPESSGGSSGGSS	12,788	PERV_Q4VFZ2_3mut
GGSGGSGGSGGSGGS	12,789	BAEVM_P10272_3mutA
GSSEAAAK	12,790	PERV_Q4VFZ2_3mut
EAAAKEAAAKEAAAKEAAAK	12,791	KORV_Q9TTC1-Pro_3mutA

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
GGSGGSGGSGGSGGS	12,792	MLVMS_P03355_3mut
PAPAPAPAPAPAP	12,793	MLVMS_P03355_3mut
GGSPAPEAAAK	12,794	MLVMS_P03355_PLV919
EAAAK	12,795	WMSV_P03359_3mutA
EAAAKGSSGGS	12,796	MLVBM_Q7SVK7_3mutA_WS
GGSGGGGSS	12,797	MLVMS_P03355_3mutA_WS
GGGEAAAKPAP	12,798	MLVMS_P03355_3mut
EAAAKGGSGGG	12,799	XMRV6_A1Z651_3mutA
GGGGGSEAAAK	12,800	KORV_Q9TTC1-Pro_3mutA
GGGGGG	12,801	BAEVM_P10272_3mutA
GGGGGG	12,802	MLVMS_P03355_3mut
GGGGGGG	12,803	MLVBM_Q7SVK7_3mutA_WS
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	12,804	AVIRE_P03360
PAPGSSGGS	12,805	PERV_Q4VFZ2_3mut
GGGGGS	12,806	XMRV6_A1Z651_3mut
EAAAKPAP	12,807	XMRV6_A1Z651_3mutA
GGG	12,808	MLVMS_P03355_3mutA_WS
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	12,809	FLV_P10273_3mut
EAAAKGSSPAP	12,810	MLVMS_P03355_3mut
SGSETPGTSESATPES	12,811	BAEVM_P10272_3mutA
GGSPAPEAAAK	12,812	MLVMS_P03355_3mut
GSSGSSGSSGSS	12,813	MLVAV_P03356_3mutA
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	12,814	MLVMS_P03355_3mut
GGSPAP	12,815	MLVCB_P08361_3mutA
GGGGGSEAAAK	12,816	MLVMS_P03355_3mutA_WS
GGGGG	12,817	MLVFF_P26809_3mutA
GSSEAAAK	12,818	MLVAV_P03356_3mutA
GGS	12,819	BAEVM_P10272_3mut
EAAAKGGSPAP	12,820	MLVCB_P08361_3mutA
PAPAPAPAP	12,821	FLV_P10273_3mutA
PAPGGGEAAAK	12,822	MLVCB_P08361_3mutA
GGGGSSEAAAK	12,823	MLVMS_P03355_3mutA_WS
GGGGG	12,824	PERV_Q4VFZ2_3mutA_WS
GGSGGSGGSGGSGGSGGS	12,825	PERV_Q4VFZ2_3mut
GGGGG	12,826	MLVMS_P03355_3mut
PAPEAAAKGGG	12,827	MLVBM_Q7SVK7_3mutA_WS
GSSGGGPAP	12,828	XMRV6_A1Z651_3mutA
GSSGSSGSSGSSGSSGSS	12,829	PERV_Q4VFZ2_3mutA_WS
EAAAKGGSPAP	12,830	PERV_Q4VFZ2_3mut

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
GSSGGSEAAAK	12,831	MLVMS_P03355_PLV919
GSS	12,832	PERV_Q4VFZ2_3mut
EAAAKGGS	12,833	WMSV_P03359_3mutA
GGGGGSPAP	12,834	PERV_Q4VFZ2_3mutA_WS
EAAAKGSS	12,835	MLVMS_P03355_PLV919
EAAAKGGGGSS	12,836	KORV_Q9TTC1-Pro_3mutA
PAPGSSGGG	12,837	PERV_Q4VFZ2_3mut
GGGGSSEAAAK	12,838	MLVFF_P26809_3mut
PAPAPAP	12,839	MLVMS_P03355_3mut
GSSGGSEAAAK	12,840	XMRV6_A1Z651_3mut
PAPEAAAKGSS	12,841	MLVMS_P03355_3mutA_WS
GGSGGSGGSGGSGGS	12,842	MLVMS_P03355_3mutA_WS
GGSGSSPAP	12,843	XMRV6_A1Z651_3mutA
GGGGSSPAP	12,844	MLVMS_P03355_PLV919
GGGGS	12,845	MLVCB_P08361_3mutA
EAAAKEAAAKEAAAKEAAAK	12,846	PERV_Q4VFZ2_3mutA_WS
EAAAKEAAAK	12,847	KORV_Q9TTC1_3mutA
PAPGGGEAAAK	12,848	BAEVM_P10272_3mutA
GSSGGSEAAAK	12,849	XMRV6_A1Z651_3mutA
EAAAKEAAAKEAAAKEAAAKEAAAKEAAAK	12,850	FLV_P10273_3mut
GSSEAAAKPAP	12,851	MLVMS_P03355_3mutA_WS
EAAAKPAPGSS	12,852	PERV_Q4VFZ2_3mutA_WS
GSSGGSPAP	12,853	XMRV6_A1Z651_3mutA
GSSEAAAKGGG	12,854	PERV_Q4VFZ2_3mut
GGGEAAAKGGS	12,855	WMSV_P03359_3mutA
GSSEAAAKGGG	12,856	MLVFF_P26809_3mut
PAPAPAP	12,857	KORV_Q9TTC1-Pro_3mutA
EAAAKGGSPAP	12,858	MLVMS_P03355_3mutA_WS
PAPGGSEAAAK	12,859	PERV_Q4VFZ2_3mut
GGGGS	12,860	MLVBM_Q7SVK7_3mutA_WS
EAAAKGSSGGG	12,861	KORV_Q9TTC1_3mut
EAAAKGGGPAP	12,862	MLVCB_P08361_3mutA
EAAAKGSS	12,863	BAEVM_P10272_3mutA
GGSPAPGGG	12,864	MLVBM_Q7SVK7_3mutA_WS
GGGGSEAAAKGGGGS	12,865	MLVMS_P03355_3mutA_WS
GGGEAAAKGGS	12,866	PERV_Q4VFZ2_3mutA_WS
EAAAKGGGGSS	12,867	MLVMS_P03355_3mutA_WS
EAAAKGGGPAP	12,868	MLVFF_P26809_3mut
GSSPAP	12,869	PERV_Q4VFZ2_3mutA_WS

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
EAAAKGGS	12,870	MLVMS_P03355_3mut
GGGGSS	12,871	KORV_Q9TTC1-Pro_3mutA
EAAAKGSSPAP	12,872	MLVMS_P03355_3mutA_WS
GGGPAP	12,873	PERV_Q4VFZ2_3mut
EAAAKGSSGGS	12,874	XMRV6_A1Z651_3mutA
PAPGGG	12,875	MLVAV_P03356_3mutA
GSSPAPEAAAK	12,876	BAEVM_P10272_3mutA
GGGPAP	12,877	MLVBM_Q7SVK7_3mutA_WS
GSSGGGGGS	12,878	AVIRE_P03360_3mutA
SGSETPGTSESATPES	12,879	MLVMS_P03355_PLV919
GGGPAP	12,880	MLVFF_P26809_3mut
EAAAKGGGGSS	12,881	XMRV6_A1Z651_3mutA
GGGGSSPAP	12,882	XMRV6_A1Z651_3mut
GGGGSEAAAKGGGGS	12,883	MLVMS_P03355_3mut
GSSPAP	12,884	MLVBM_Q7SVK7_3mutA_WS
GGSGSSEAAAK	12,885	FLV_P10273_3mutA
SGSETPGTSESATPES	12,886	MLVBM_Q7SVK7_3mutA_WS
PAPGGG	12,887	AVIRE_P03360_3mutA
GGGEAAAKPAP	12,888	MLVMS_P03355_3mutA_WS
EAAAKGGSGSS	12,889	PERV_Q4VFZ2_3mut
GGSPAPGGG	12,890	MLVAV_P03356_3mutA
PAPGGSGSS	12,891	BAEVM_P10272_3mutA
GSSGGSPAP	12,892	MLVFF_P26809_3mutA
EAAAKGSSGGG	12,893	PERV_Q4VFZ2_3mut
GGGGSGGGGS	12,894	PERV_Q4VFZ2_3mutA_WS
GSSGGGGGS	12,895	BAEVM_P10272_3mutA
GGGGSSGGS	12,896	MLVBM_Q7SVK7_3mutA_WS
EAAAKGGS	12,897	PERV_Q4VFZ2_3mutA_WS
GSSGSSGSSGSS	12,898	MLVMS_P03355_3mut
GGS	12,899	MLVMS_P03355_3mutA_WS
GSSGGSEAAAK	12,900	MLVBM_Q7SVK7_3mutA_WS
SGGSSGGSSGSETPGTSESATPESSGGSSGGSS	12,901	XMRV6_A1Z651
GGGGG	12,902	FLV_P10273_3mutA
PAPEAAAKGSS	12,903	PERV_Q4VFZ2_3mut
GGGGGG	12,904	WMSV_P03359_3mut
EAAAKGGG	12,905	BAEVM_P10272_3mutA
GGGGSS	12,906	MLVMS_P03355_3mutA_WS
GSSGGGEAAAK	12,907	KORV_Q9TTC1_3mut
GGSGSS	12,908	AVIRE_P03360_3mutA

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
EAAAKPAP	12,909	MLVMS_P03355_3mut
EAAAKEAAAKEAAAK	12,910	FLV_P10273_3mutA
GGGG	12,911	XMRV6_A1Z651_3mutA
GSSPAPGGS	12,912	BAEVM_P10272_3mutA
GSSGGGGGS	12,913	MLVFF_P26809_3mutA
GGGGSSGGS	12,914	MLVAV_P03356_3mutA
GGS	12,915	PERV_Q4VFZ2_3mut
GGGGG	12,916	WMSV_P03359_3mutA
GSSGSSGSSGSSGSSGSS	12,917	FLV_P10273_3mutA
PAPGGGGSS	12,918	MLVAV_P03356_3mutA
GGGGGGGG	12,919	BAEVM_P10272_3mutA
SGSETPGTSESATPES	12,920	MLVCB_P08361_3mutA
PAPGGG	12,921	BAEVM_P10272_3mutA
GSSGSSGSS	12,922	MLVCB_P08361_3mutA
GGSGSS	12,923	MLVMS_P03355_3mutA_WS
EAAAKGGGGSEAAAK	12,924	WMSV_P03359_3mutA
GGGGGGGG	12,925	FLV_P10273_3mutA
GSSGSS	12,926	MLVMS_P03355_3mutA_WS
PAPEAAAKGGS	12,927	XMRV6_A1Z651_3mutA
EAAAKEAAAK	12,928	MLVMS_P03355_3mut
GGGGSGGGGSGGGGS	12,929	BAEVM_P10272_3mutA
EAAAKGSSPAP	12,930	MLVMS_P03355_PLV919
GGGGSSEAAAK	12,931	MLVMS_P03355_3mut
GGGGSSEAAAK	12,932	BAEVM_P10272_3mutA
PAPGGSGSS	12,933	PERV_Q4VFZ2_3mut
GGSGGGEAAAK	12,934	MLVFF_P26809_3mut
PAPEAAAKGGS	12,935	PERV_Q4VFZ2_3mut
GGGPAPGSS	12,936	AVIRE_P03360_3mut
PAPGGSGGG	12,937	PERV_Q4VFZ2_3mutA_WS
GGGGGGGG	12,938	PERV_Q4VFZ2_3mutA_WS
GSSEAAAK	12,939	MLVMS_P03355_3mutA_WS
GGGGSGGGGSGGGGS	12,940	PERV_Q4VFZ2_3mutA_WS
EAAAKGGS	12,941	MLVMS_P03355_3mut
GGGGGSGSS	12,942	MLVCB_P08361_3mut
GGGPAP	12,943	KORV_Q9TTC1-Pro_3mutA
EAAAKPAPGGG	12,944	MLVCB_P08361_3mut
GSSGGSPAP	12,945	MLVCB_P08361_3mutA
SGGSSGGSSGSETPGTSESATPESSGGSSGGSS	12,946	MLVMS_P03355_3mut
PAPAPAPAP	12,947	MLVMS_P03355_3mut

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
GSSGGS	12,948	XMRV6_A1Z651_3mutA
GSSEAAAKGGG	12,949	MLVMS_P03355_3mut
GGSGSSPAP	12,950	MLVMS_P03355_3mutA_WS
GSSEAAAKGGS	12,951	MLVMS_P03355_PLV919
EAAAKEAAAKEAAAKEAAAKEAAAK	12,952	BAEVM_P10272_3mut
PAPGGGGSS	12,953	KORV_Q9TTC1_3mutA
EAAAKGSS	12,954	MLVMS_P03355_3mutA_WS
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	12,955	FFV_O93209_2mut
GGSGGSGGSGGSGGSGGS	12,956	BAEVM_P10272_3mutA
GGGGGG	12,957	MLVMS_P03355_PLV919
PAPEAAAK	12,958	BAEVM_P10272_3mutA
GGSGSSEAAAK	12,959	MLVAV_P03356_3mutA
GGG	12,960	MLVCB_P08361_3mutA
GGGGG	12,961	MLVCB_P08361_3mutA
GGSGGSGGSGGS	12,962	KORV_Q9TTC1-Pro_3mutA
GSSGSSGSSGSSGSSGSS	12,963	XMRV6_A1Z651_3mutA
GSSEAAAKPAP	12,964	FLV_P10273_3mutA
GGGEAAAKPAP	12,965	MLVCB_P08361_3mutA
GSSGSSGSS	12,966	MLVMS_P03355_3mutA_WS
PAPAPAPAP	12,967	MLVMS_P03355_PLV919
EAAAKGGG	12,968	MLVMS_P03355_PLV919
PAPAPAPAPAPAP	12,969	FLV_P10273_3mutA
EAAAKGGSGSS	12,970	MLVMS_P03355_3mut
GGGGGG	12,971	PERV_Q4VFZ2_3mutA_WS
PAPGGG	12,972	MLVCB_P08361_3mutA
GGGGGSGSS	12,973	KORV_Q9TTC1_3mutA
GGGGSGGGGSGGGGSGGGGS	12,974	XMRV6_A1Z651_3mut
GGSGGSGGS	12,975	KORV_Q9TTC1-Pro_3mutA
EAAAKPAPGGG	12,976	MLVMS_P03355_3mutA_WS
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	12,977	XMRV6_A1Z651
GGGGSGGGGSGGGGSGGGGSGGGGSGGGGS	12,978	FLV_P10273_3mutA
EAAAKGGGGSEAAAK	12,979	PERV_Q4VFZ2_3mutA_WS
GGGPAPGSS	12,980	AVIRE_P03360_3mutA
GGGGG	12,981	MLVMS_P03355_3mutA_WS
GGGGSGGGGSGGGGSGGGGSGGGGSGGGGS	12,982	MLVMS_P03355_3mut
GGGGSGGGGS	12,983	MLVMS_P03355_3mutA_WS
EAAAKGGSPAP	12,984	XMRV6_A1Z651_3mutA
EAAAKGSSPAP	12,985	AVIRE_P03360_3mutA
PAPGGSGSS	12,986	KORV_Q9TTC1-Pro_3mutA

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
GSS	12,987	MLVBM_Q7SVK7_3mutA_WS
GSS	12,988	WMSV_P03359_3mut
GGGPAPGSS	12,989	MLVFF_P26809_3mutA
EAAAKPAP	12,990	MLVMS_P03355_3mut
GSSPAPEAAAK	12,991	FLV_P10273_3mutA
GGSPAPGSS	12,992	MLVBM_Q7SVK7_3mutA_WS
GGGGGSEAAAK	12,993	XMRV6_A1Z651_3mut
PAPEAAAKGGG	12,994	WMSV_P03359_3mutA
PAPGGG	12,995	PERV_Q4VFZ2_3mut
GGSPAPEAAAK	12,996	WMSV_P03359_3mutA
GGSGGGGSS	12,997	PERV_Q4VFZ2_3mut
EAAAKGGGGSS	12,998	PERV_Q4VFZ2_3mut
EAAAKGGSPAP	12,999	AVIRE_P03360_3mut
GGSGGGGSS	13,000	WMSV_P03359_3mutA
PAPGSSEAAAK	13,001	MLVFF_P26809_3mut
GSSEAAAK	13,002	MLVMS_P03355_PLV919
GSAGSAAGSGEF	13,003	AVIRE_P03360_3mutA
EAAAKGGSGSS	13,004	MLVMS_P03355_3mut
GGSEAAAKPAP	13,005	MLVMS_P03355_PLV919
GGGGSGGGGSGGGGSGGGGSGGGGS	13,006	MLVFF_P26809_3mutA
PAPGSSEAAAK	13,007	PERV_Q4VFZ2_3mutA_WS
GGGGSSPAP	13,008	MLVMS_P03355_3mutA_WS
PAPAPAP	13,009	MLVCB_P08361_3mutA
EAAAKPAPGGG	13,010	MLVBM_Q7SVK7_3mutA_WS
GGGPAPGSS	13,011	BAEVM_P10272_3mutA
PAP	13,012	MLVMS_P03355_3mutA_WS
PAPGGSGGG	13,013	MLVMS_P03355_3mutA_WS
GGSGGSGGSGGSGGS	13,014	MLVBM_Q7SVK7_3mutA_WS
PAPAPAPAP	13,015	XMRV6_A1Z651_3mut
GSSPAPGGG	13,016	MLVMS_P03355_3mutA_WS
GSSPAPGGG	13,017	MLVMS_P03355_3mut
PAPGGG	13,018	MLVMS_P03355_PLV919
GGGEAAAKGSS	13,019	WMSV_P03359_3mut
EAAAKGSS	13,020	KORV_Q9TTC1-Pro_3mutA
EAAAKGGS	13,021	PERV_Q4VFZ2_3mut
EAAAKEAAAKEAAAKEAAAKEAAAK	13,022	PERV_Q4VFZ2_3mut
PAPEAAAKGGG	13,023	MLVMS_P03355_PLV919
EAAAKGSSGGG	13,024	MLVFF_P26809_3mut
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	13,025	PERV_Q4VFZ2

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
EAAAKEAAAKEAAAKEAAAKEAAAKEAAAK	13,026	MLVAV_P03356_3mutA
GSSGGSGGG	13,027	MLVFF_P26809_3mut
GSSGSSGSSGSS	13,028	PERV_Q4VFZ2_3mutA_WS
GGSPAPGGG	13,029	MLVMS_P03355_PLV919
GSS	13,030	BAEVM_P10272_3mut
GGGPAPGSS	13,031	MLVMS_P03355_3mutA_WS
GGGGSS	13,032	KORV_Q9TTC1_3mutA
GSSGGSGGG	13,033	BAEVM_P10272_3mutA
EAAAKEAAAKEAAAK	13,034	MLVCB_P08361_3mutA
SGGSSGGSSGSETPGTSESATPESSGGSSGGSS	13,035	FLV_P10273_3mutA
PAPGGGGGS	13,036	PERV_Q4VFZ2_3mut
PAPAPAPAPAP	13,037	KORV_Q9TTC1-Pro_3mutA
EAAAK	13,038	MLVMS_P03355_3mutA_WS
GGG	13,039	MLVCB_P08361_3mut
GGSEAAAKGGG	13,040	BAEVM_P10272_3mutA
GGGGGSGSS	13,041	MLVAV_P03356_3mutA
EAAAKGSSPAP	13,042	MLVBM_Q7SVK7_3mutA_WS
GGSGGSGGS	13,043	XMRV6_A1Z651_3mut
EAAAKPAPGGG	13,044	KORV_Q9TTC1-Pro_3mutA
GGGPAPEAAAK	13,045	FLV_P10273_3mutA
GGSPAPEAAAK	13,046	MLVMS_P03355_3mutA_WS
GGSGGSGGSGGSGGS	13,047	MLVFF_P26809_3mut
EAAAKGGSGSS	13,048	MLVMS_P03355_PLV919
GGGEAAAKGGS	13,049	MLVBM_Q7SVK7_3mutA_WS
PAPAPAPAP	13,050	BAEVM_P10272_3mutA
EAAAKEAAAKEAAAKEAAAK	13,051	MLVMS_P03355_3mut
EAAAKPAP	13,052	XMRV6_A1Z651_3mut
EAAAKEAAAK	13,053	MLVBM_Q7SVK7_3mutA_WS
EAAAKGGG	13,054	BAEVM_P10272_3mut
EAAAKGSS	13,055	MLVAV_P03356_3mutA
EAAAKEAAAKEAAAKEAAAKEAAAKEAAAK	13,056	MLVFF_P26809_3mut
GGGPAPGSS	13,057	PERV_Q4VFZ2_3mutA_WS
GGGG	13,058	PERV_Q4VFZ2_3mut
EAAAKGGSGSS	13,059	MLVMS_P03355_PLV919
GGGGSGGGGSGGGGS	13,060	MLVMS_P03355_3mutA_WS
EAAAK	13,061	MLVMS_P03355_3mutA_WS
GGGGSS	13,062	PERV_Q4VFZ2
PAPEAAAKGGS	13,063	MLVCB_P08361_3mut
GSS	13,064	MLVMS_P03355_3mut

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
GSAGSAAGSGEF	13,065	MLVFF_P26809_3mutA
EAAAKEAAAKEAAAKEAAAKEAAAKEAAAK	13,066	KORV_Q9TTC1-Pro_3mut
GGGGSGGGGS	13,067	AVIRE_P03360_3mutA
EAAAK	13,068	MLVMS_P03355_3mut
GGGPAPGGS	13,069	PERV_Q4VFZ2_3mut
GGGGSGGGGSGGGGS	13,070	MLVMS_P03355_PLV919
PAPGGG	13,071	MLVMS_P03355_3mutA_WS
GGGEAAAKPAP	13,072	PERV_Q4VFZ2_3mutA_WS
EAAAKPAPGSS	13,073	KORV_Q9TTC1-Pro_3mutA
PAPGSS	13,074	KORV_Q9TTC1_3mutA
GSAGSAAGSGEF	13,075	PERV_Q4VFZ2_3mut
PAPGGGGSS	13,076	KORV_Q9TTC1-Pro_3mutA
GSSGGGEAAAK	13,077	MLVCB_P08361_3mutA
GSS	13,078	AVIRE_P03360_3mutA
GSSGSSGSSGSS	13,079	XMRV6_A1Z651_3mutA
PAPEAAAKGGG	13,080	MLVMS_P03355_PLV919
GGGPAPEAAAK	13,081	MLVCB_P08361_3mutA
PAPGGGGGS	13,082	MLVCB_P08361_3mutA
EAAAKEAAAKEAAAKEAAAK	13,083	PERV_Q4VFZ2_3mutA_WS
GGGGGSPAP	13,084	MLVFF_P26809_3mutA
GSSGSSGSSGSSGSS	13,085	PERV_Q4VFZ2
GSSPAPEAAAK	13,086	MLVMS_P03355_PLV919
GSSGSSGSSGSSGSSGSS	13,087	MLVBM_Q7SVK7_3mutA_WS
GSSGSSGSSGSSGSSGSS	13,088	MLVMS_P03355_3mutA_WS
GGSPAPEAAAK	13,089	MLVAV_P03356_3mutA
GSSGGG	13,090	BAEVM_P10272_3mut
EAAAKGSSGGS	13,091	KORV_Q9TTC1-Pro_3mutA
GGSGSSEAAAK	13,092	MLVMS_P03355_3mutA_WS
GGGPAPEAAAK	13,093	MLVFF_P26809_3mutA
GGGPAPGGS	13,094	MLVMS_P03355_3mutA_WS
GGGGG	13,095	MLVMS_P03355_PLV919
GGGEAAAKPAP	13,096	MLVBM_Q7SVK7_3mutA_WS
GGGGSGGGGS	13,097	WMSV_P03359_3mut
GGGPAPEAAAK	13,098	PERV_Q4VFZ2_3mut
GGSGSSEAAAK	13,099	MLVMS_P03355_PLV919
EAAAKGGGPAP	13,100	MLVMS_P03355_3mutA_WS
GSSGSSGSSGSSGSS	13,101	KORV_Q9TTC1-Pro_3mutA
PAPAP	13,102	WMSV_P03359_3mutA
GGSPAPGSS	13,103	MLVAV_P03356_3mutA

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
GGSGGGPAP	13,104	MLVMS_P03355_3mut
GGSPAP	13,105	MLVMS_P03355_PLV919
EAAAKGGSPAP	13,106	PERV_Q4VFZ2_3mut
GSSPAPGGG	13,107	KORV_Q9TTC1-Pro_3mutA
GSAGSAAGSGEF	13,108	MLVMS_P03355_3mut
GGSPAP	13,109	PERV_Q4VFZ2_3mut
GSSGSS	13,110	KORV_Q9TTC1-Pro_3mut
GGGPAPGSS	13,111	MLVMS_P03355_3mutA_WS
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	13,112	FOAMV_P14350
PAPGSSGGG	13,113	MLVMS_P03355_PLV919
GGSEAAAKPAP	13,114	BAEVM_P10272_3mutA
GGGGGS	13,115	MLVCB_P08361_3mutA
PAPEAAAKGGS	13,116	MLVMS_P03355_3mutA_WS
EAAAKEAAAKEAAAKEAAAKEAAAKEAAAK	13,117	BAEVM_P10272_3mutA
GGSEAAAK	13,118	BAEVM_P10272_3mutA
GSSPAPEAAAK	13,119	MLVMS_P03355_3mutA_WS
PAPGGG	13,120	WMSV_P03359_3mut
EAAAKPAP	13,121	PERV_Q4VFZ2_3mut
GSSGSSGSSGSSGSS	13,122	WMSV_P03359_3mut
PAPGGG	13,123	MLVBM_Q7SVK7_3mutA_WS
GGSGGGEAAAK	13,124	BAEVM_P10272_3mutA
PAPGGS	13,125	MLVMS_P03355_3mut
GGSGGSGGSGGS	13,126	MLVBM_Q7SVK7_3mutA_WS
EAAAKEAAAKEAAAKEAAAK	13,127	PERV_Q4VFZ2_3mut
GGSEAAAKGGG	13,128	WMSV_P03359_3mutA
GGGPAP	13,129	BAEVM_P10272_3mutA
GGGGSGGGGSGGGGSGGGGSGGGGSGGGGS	13,130	XMRV6_A1Z651_3mut
GGSPAPGSS	13,131	KORV_Q9TTC1_3mut
GGGPAPGSS	13,132	MLVMS_P03355_3mut
GGGGSSGGS	13,133	BAEVM_P10272_3mutA
GGGEAAAKGSS	13,134	KORV_Q9TTC1-Pro_3mutA
PAPAP	13,135	MLVBM_Q7SVK7_3mutA_WS
GGSPAPGGG	13,136	PERV_Q4VFZ2_3mut
PAPGSS	13,137	PERV_Q4VFZ2_3mutA_WS
GSSGGSPAP	13,138	MLVBM_Q7SVK7_3mutA_WS
EAAAKGGGGSEAAAK	13,139	PERV_Q4VFZ2_3mut
GSSEAAAKGGS	13,140	KORV_Q9TTC1-Pro_3mut
PAPAPAPAP	13,141	KORV_Q9TTC1-Pro_3mutA
GGSEAAAKPAP	13,142	WMSV_P03359_3mutA

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
PAPGGS	13,143	FLV_P10273_3mutA
EAAAKGGGPAP	13,144	PERV_Q4VFZ2_3mut
GGSGSSGGG	13,145	AVIRE_P03360_3mutA
EAAAKGGSGSS	13,146	BAEVM_P10272_3mutA
SGGSSGGSSGSETPGTSESATPESSGGSSGGSS	13,147	MLVCB_P08361_3mutA
GSSEAAAKGGS	13,148	XMRV6_A1Z651_3mutA
GGGGG	13,149	BAEVM_P10272_3mutA
GGGGSGGGGSGGGGSGGGGSGGGGSGGGGS	13,150	SFV3L_P27401_2mutA
GGGEAAAKGSS	13,151	MLVMS_P03355_PLV919
EAAAKGGGGSEAAAK	13,152	KORV_Q9TTC1_3mutA
EAAAKGGG	13,153	AVIRE_P03360_3mut
GGSGGG	13,154	MLVMS_P03355_3mutA_WS
GGSGSSGGG	13,155	MLVMS_P03355_PLV919
GGGGSGGGGSGGGGSGGGGSGGGGSGGGGS	13,156	KORV_Q9TTC1_3mut
GGGGSEAAAKGGGGS	13,157	KORV_Q9TTC1_3mutA
PAPAPAPAPAP	13,158	FLV_P10273_3mutA
GGS	13,159	MLVBM_Q7SVK7_3mutA_WS
GGGGGSEAAAK	13,160	MLVBM_Q7SVK7_3mutA_WS
GSSGSSGSSGSSGSS	13,161	MLVMS_P03355_3mutA_WS
EAAAKEAAAKEAAAKEAAAKEAAAK	13,162	MLVMS_P03355_3mut
GGSGSSGGG	13,163	PERV_Q4VFZ2_3mut
PAP	13,164	MLVFF_P26809_3mut
GSSPAPEAAAK	13,165	MLVAV_P03356_3mutA
EAAAKGGGGSS	13,166	MLVMS_P03355_3mut
GGGEAAAKGGS	13,167	XMRV6_A1Z651_3mut
GGSGGGPAP	13,168	MLVBM_Q7SVK7_3mutA_WS
GSAGSAAGSGEF	13,169	BAEVM_P10272_3mutA
GSSEAAAK	13,170	MLVCB_P08361_3mut
PAPGSS	13,171	MLVMS_P03355_3mut
EAAAKEAAAKEAAAK	13,172	MLVAV_P03356_3mutA
GSAGSAAGSGEF	13,173	XMRV6_A1Z651_3mutA
GSSGSSGSSGSS	13,174	BAEVM_P10272_3mutA
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	13,175	KORV_Q9TTC1-Pro_3mut
GGGGSSEAAAK	13,176	WMSV_P03359_3mut
GSSGGGEAAAK	13,177	MLVBM_Q7SVK7_3mutA_WS
EAAAKPAP	13,178	MLVFF_P26809_3mutA
GGSPAPGGG	13,179	KORV_Q9TTC1_3mutA
PAPEAAAK	13,180	FLV_P10273_3mutA
GSSGSSGSS	13,181	MLVBM_Q7SVK7_3mutA_WS

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
GSSGGGEAAAK	13,182	FLV_P10273_3mutA
GGSPAP	13,183	MLVBM_Q7SVK7_3mutA_WS
GSAGSAAGSGEF	13,184	KORV_Q9TTC1-Pro_3mutA
PAPGGSEAAAK	13,185	MLVMS_P03355_PLV919
GGSPAPEAAAK	13,186	MLVBM_Q7SVK7_3mutA_WS
GGGGGSPAP	13,187	MLVBM_Q7SVK7_3mutA_WS
EAAAKGSSPAP	13,188	WMSV_P03359_3mut
EAAAKGGGPAP	13,189	MLVBM_Q7SVK7_3mutA_WS
PAPGSS	13,190	KORV_Q9TTC1-Pro_3mutA
GGSGSSGGG	13,191	BAEVM_P10272_3mut
SGGSSGGSSGSETPGTSESATPESSGGSSGGSS	13,192	FFV_O93209-Pro_2mut
GGSGGSGGSGGSGGSGGS	13,193	WMSV_P03359_3mutA
GGSGGSGGS	13,194	PERV_Q4VFZ2_3mutA_WS
GGGGG	13,195	PERV_Q4VFZ2_3mutA_WS
GGGPAP	13,196	FLV_P10273_3mutA
PAPGGSGGG	13,197	XMRV6_A1Z651_3mutA
GGGGSEAAAKGGGGS	13,198	XMRV6_A1Z651_3mut
EAAAKGSSGGG	13,199	KORV_Q9TTC1-Pro_3mutA
GSSGGSEAAAK	13,200	WMSV_P03359_3mut
EAAAKGGSGSS	13,201	PERV_Q4VFZ2_3mut
PAPAPAPAPAP	13,202	PERV_Q4VFZ2_3mut
GGGGSGGGGSGGGGSGGGGSGGGGSGGGGS	13,203	MLVMS_P03355_3mutA_WS
GGGGGGG	13,204	KORV_Q9TTC1_3mutA
EAAAK	13,205	KORV_Q9TTC1-Pro_3mutA
GGGEAAAKGGS	13,206	KORV_Q9TTC1-Pro_3mutA
GGGEAAAKGGS	13,207	PERV_Q4VFZ2_3mutA_WS
GGGGGSPAP	13,208	XMRV6_A1Z651_3mut
GGGGSGGGGSGGGGSGGGGS	13,209	MLVFF_P26809_3mut
GGGGGGG	13,210	MLVFF_P26809_3mut
PAPAPAPAPAPAP	13,211	AVIRE_P03360_3mutA
GSSPAPGGG	13,212	FLV_P10273_3mutA
GGGGGSPAP	13,213	MLVMS_P03355_3mutA_WS
GGGGSGGGGSGGGGS	13,214	MLVMS_P03355_3mut
GGGGSGGGGSGGGGS	13,215	KORV_Q9TTC1_3mut
GSSEAAAKGGS	13,216	MLVAV_P03356_3mutA
GSSGSSGSSGSSGSS	13,217	MLVMS_P03355_3mut
EAAAKGGGGGS	13,218	PERV_Q4VFZ2_3mutA_WS
GSSGGGGGS	13,219	PERV_Q4VFZ2_3mut
GGGEAAAKPAP	13,220	MLVMS_P03355_3mut

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
GSSGGSPAP	13,221	PERV_Q4VFZ2_3mutA_WS
GSSGGGPAP	13,222	BAEVM_P10272_3mutA
GGGGGSGSS	13,223	MLVMS_P03355_PLV919
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	13,224	BAEVM_P10272_3mut
PAPEAAAK	13,225	MLVMS_P03355_3mut
GGGGSGGGGSGGGGS	13,226	FLV_P10273_3mutA
GGSGSSGGG	13,227	WMSV_P03359_3mutA
EAAAKGGS	13,228	PERV_Q4VFZ2_3mut
EAAAKGSSPAP	13,229	MLVCB_P08361_3mut
EAAAKGGSGSS	13,230	WMSV_P03359_3mutA
GSSGSS	13,231	PERV_Q4VFZ2_3mutA_WS
PAPAPAPAP	13,232	MLVMS_P03355_PLV919
GGSGGG	13,233	PERV_Q4VFZ2_3mutA_WS
GSS	13,234	MLVBM_Q7SVK7_3mutA_WS
PAP	13,235	KORV_Q9TTC1-Pro_3mutA
GGSGSSEAAAK	13,236	MLVFF_P26809_3mut
PAPEAAAKGSS	13,237	KORV_Q9TTC1-Pro_3mutA
GGSGGS	13,238	MLVCB_P08361_3mutA
GGGGGGG	13,239	PERV_Q4VFZ2_3mutA_WS
GGSPAPEAAAK	13,240	MLVBM_Q7SVK7_3mut
EAAAKEAAAKEAAAKEAAAKEAAAKEAAAK	13,241	KORV_Q9TTC1_3mutA
GGSPAP	13,242	MLVMS_P03355_3mut
GGSEAAAKGGG	13,243	PERV_Q4VFZ2_3mut
GGGGSGGGGS	13,244	FLV_P10273_3mutA
GGGEAAAK	13,245	BAEVM_P10272_3mutA
GGGGSGGGGSGGGGSGGGGSGGGGSGGGGS	13,246	SFV3L_P27401_2mut
GGSEAAAKPAP	13,247	KORV_Q9TTC1-Pro_3mutA
GSSGGGEAAAK	13,248	MLVMS_P03355_PLV919
GGGGGSEAAAK	13,249	MLVMS_P03355_PLV919
EAAAKGGSGGG	13,250	MLVMS_P03355_3mutA_WS
GGGGSSPAP	13,251	MLVAV_P03356_3mutA
EAAAKEAAAK	13,252	MLVMS_P03355_3mutA_WS
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	13,253	SFV3L_P27401_2mut
GSSGSSGSSGSSGSS	13,254	MLVMS_P03355_PLV919
GSSGGG	13,255	KORV_Q9TTC1-Pro_3mutA
GSSGGS	13,256	MLVFF_P26809_3mutA
GGGGSGGGGS	13,257	XMRV6_A1Z651_3mutA
PAPGSS	13,258	MLVBM_Q7SVK7_3mutA_WS
GGGPAPEAAAK	13,259	XMRV6_A1Z651_3mutA

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
EAAAKGGS	13,260	MLVFF_P26809_3mut
GSS	13,261	KORV_Q9TTC1_3mutA
GGGG	13,262	PERV_Q4VFZ2_3mut
GGGGGSEAAAK	13,263	AVIRE_P03360_3mutA
GSSGSSGSSGSSGSS	13,264	MLVMS_P03355_PLV919
PAPGGSGGG	13,265	PERV_Q4VFZ2_3mut
GGGPAP	13,266	PERV_Q4VFZ2_3mut
GGGPAPEAAAK	13,267	AVIRE_P03360_3mutA
GGGEAAAK	13,268	MLVCB_P08361_3mut
GGG	13,269	MLVFF_P26809_3mutA
EAAAKPAPGSS	13,270	XMRV6_A1Z651_3mutA
GGSGSSEAAAK	13,271	PERV_Q4VFZ2_3mutA_WS
EAAAKGSS	13,272	MLVMS_P03355_3mut
GGSGSSEAAAK	13,273	BAEVM_P10272_3mut
GGSGGG	13,274	MLVBM_Q7SVK7_3mutA_WS
GGGPAP	13,275	MLVMS_P03355_PLV919
GGSPAPGGG	13,276	PERV_Q4VFZ2_3mutA_WS
GGGGGSEAAAK	13,277	MLVFF_P26809_3mutA
EAAAKGSSGGS	13,278	MLVBM_Q7SVK7_3mut
PAPAP	13,279	XMRV6_A1Z651_3mut
GSSPAPGGS	13,280	MLVBM_Q7SVK7_3mutA_WS
GSSEAAAKGGG	13,281	WMSV_P03359_3mutA
EAAAKGGGGGS	13,282	PERV_Q4VFZ2_3mut
GSSGSSGSSGSSGSS	13,283	MLVCB_P08361_3mutA
EAAAKGGGGSS	13,284	PERV_Q4VFZ2_3mut
EAAAKGSS	13,285	PERV_Q4VFZ2_3mut
EAAAKEAAAKEAAAKEAAAKEAAAKEAAAK	13,286	AVIRE_P03360_3mutA
EAAAKGGS	13,287	MLVCB_P08361_3mut
GSSGGSEAAAK	13,288	MLVAV_P03356_3mutA
EAAAKPAPGGS	13,289	PERV_Q4VFZ2_3mut
GGSGGS	13,290	MLVAV_P03356_3mutA
EAAAKGSSGGG	13,291	AVIRE_P03360_3mutA
GGSGGSGGSGGS	13,292	PERV_Q4VFZ2_3mut
GGGGGGGG	13,293	KORV_Q9TTC1_3mutA
GGSGSSEAAAK	13,294	MLVCB_P08361_3mutA
EAAAKGGG	13,295	MLVBM_Q7SVK7_3mutA_WS
GGGGSGGGGSGGGGS	13,296	MLVCB_P08361_3mut
GGSGGSGGSGGS	13,297	PERV_Q4VFZ2_3mutA_WS
PAPAPAPAPAP	13,298	WMSV_P03359_3mut

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
EAAAKEAAAKEAAAKEAAAK	13,299	PERV_Q4VFZ2_3mut
GGSGGSGGS	13,300	XMRV6_A1Z651_3mutA
PAPGGGGSS	13,301	BAEVM_P10272_3mutA
GSSEAAAKGGS	13,302	MLVCB_P08361_3mut
GSSGGGPAP	13,303	MLVCB_P08361_3mutA
GGSGSS	13,304	MLVBM_Q7SVK7_3mutA_WS
GGGGGSEAAAK	13,305	MLVAV_P03356_3mutA
GSSEAAAK	13,306	PERV_Q4VFZ2_3mutA_WS
GGGGGSGSS	13,307	MLVBM_Q7SVK7_3mutA_WS
EAAAKGGSGSS	13,308	MLVFF_P26809_3mut
PAP	13,309	FLV_P10273_3mutA
GGGGG	13,310	MLVMS_P03355_3mutA_WS
EAAAK	13,311	PERV_Q4VFZ2_3mut
GSS	13,312	FLV_P10273_3mutA
PAPAPAPAPAPAP	13,313	KORV_Q9TTC1-Pro_3mutA
EAAAKEAAAKEAAAKEAAAK	13,314	MLVCB_P08361_3mut
EAAAKGGGGSEAAAK	13,315	XMRV6_A1Z651_3mut
PAPGGSGGG	13,316	MLVBM_Q7SVK7_3mutA_WS
GGSGGGPAP	13,317	WMSV_P03359_3mutA
GGGGSSEAAAK	13,318	MLVBM_Q7SVK7_3mutA_WS
PAPGGGGSS	13,319	MLVCB_P08361_3mut
GGSGGSGGSGGS	13,320	PERV_Q4VFZ2_3mutA_WS
PAPGGSGGG	13,321	MLVMS_P03355_3mutA_WS
GSSPAPGGS	13,322	MLVCB_P08361_3mutA
GSSGSSGSS	13,323	MLVFF_P26809_3mut
PAPGGGGGS	13,324	MLVBM_Q7SVK7_3mutA_WS
GSSPAP	13,325	PERV_Q4VFZ2_3mut
GGSGGG	13,326	KORV_Q9TTC1-Pro_3mut
EAAAKGGGGSEAAAK	13,327	PERV_Q4VFZ2_3mutA_WS
GGSPAPEAAAK	13,328	PERV_Q4VFZ2_3mutA_WS
EAAAKPAP	13,329	BAEVM_P10272_3mut
GGGGSGGGGSGGGGSGGGGSGGGGSGGGGS	13,330	MLVMS_P03355_3mut
EAAAKGGGGSS	13,331	MLVFF_P26809_3mut
EAAAKEAAAK	13,332	MLVCB_P08361_3mut
GSSEAAAKGGS	13,333	PERV_Q4VFZ2_3mut
GGSPAP	13,334	KORV_Q9TTC1-Pro_3mutA
EAAAKEAAAKEAAAKEAAAK	13,335	MLVMS_P03355_3mutA_WS
GSSGSSGSSGSSGSS	13,336	BAEVM_P10272_3mut
PAPEAAAK	13,337	MLVMS_P03355_3mut

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
GSSGGSPAP	13,338	PERV_Q4VFZ2
GGGPAPGGS	13,339	BAEVM_P10272_3mutA
EAAAKPAPGGS	13,340	MLVMS_P03355_PLV919
GGGGSGGGGS	13,341	PERV_Q4VFZ2
GGGEAAAK	13,342	KORV_Q9TTC1-Pro_3mut
EAAAKGGGGGS	13,343	FLV_P10273_3mutA
GGSPAPGSS	13,344	MLVMS_P03355_3mut
GSSPAPEAAAK	13,345	MLVMS_P03355_3mutA_WS
GSAGSAAGSGEF	13,346	MLVBM_Q7SVK7_3mutA_WS
EAAAK	13,347	BAEVM_P10272_3mutA
EAAAKGGGGSS	13,348	BAEVM_P10272_3mutA
GGG	13,349	WMSV_P03359_3mut
GGSGSSPAP	13,350	BAEVM_P10272_3mut
GGSEAAAKPAP	13,351	MLVBM_Q7SVK7_3mutA_WS
EAAAKGGSGSS	13,352	MLVCB_P08361_3mut
PAPGSS	13,353	MLVAV_P03356_3mutA
PAPEAAAKGGG	13,354	MLVCB_P08361_3mutA
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	13,355	FOAMV_P14350-Pro_2mut
GSSGSSGSS	13,356	PERV_Q4VFZ2_3mut
PAPGGG	13,357	MLVMS_P03355_3mut
PAPGGS	13,358	PERV_Q4VFZ2_3mut
GSSGGG	13,359	MLVMS_P03355_PLV919
GSSGSSGSSGSSGSSGSS	13,360	WMSV_P03359_3mut
PAP	13,361	AVIRE_P03360_3mutA
EAAAKGSSPAP	13,362	MLVBM_Q7SVK7_3mutA_WS
GSSGSSGSSGSS	13,363	MLVMS_P03355_PLV919
GGGGSGGGGSGGGGSGGGGSGGGGS	13,364	AVIRE_P03360
GGGGS	13,365	PERV_Q4VFZ2_3mut
EAAAKGSSGGG	13,366	MLVBM_Q7SVK7_3mutA_WS
GGGGGG	13,367	KORV_Q9TTC1-Pro_3mut
GGSGSSEAAAK	13,368	PERV_Q4VFZ2_3mut
GSSPAPEAAAK	13,369	MLVBM_Q7SVK7_3mutA_WS
GGGGSGGGGS	13,370	MLVBM_Q7SVK7_3mutA_WS
GSSGGGGGS	13,371	MLVAV_P03356_3mutA
GSAGSAAGSGEF	13,372	WMSV_P03359_3mutA
GGGEAAAKGSS	13,373	BAEVM_P10272_3mutA
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	13,374	FFV_O93209-Pro_2mut
PAPGGSGGG	13,375	MLVCB_P08361_3mutA
EAAAKEAAAKEAAAKEAAAKEAAAK	13,376	SFV3L_P27401_2mut

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
GGSGSSPAP	13,377	MLVMS_P03355_PLV919
GGGGGG	13,378	PERV_Q4VFZ2_3mut
EAAAKEAAAKEAAAKEAAAKEAAAK	13,379	PERV_Q4VFZ2_3mut
EAAAKGSSPAP	13,380	MLVFF_P26809_3mut
GGGPAPGGS	13,381	MLVBM_Q7SVK7_3mutA_WS
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	13,382	SFV3L_P27401
PAP	13,383	PERV_Q4VFZ2_3mut
EAAAKGGS	13,384	MLVMS_P03355_PLV919
GSSGGSEAAAK	13,385	WMSV_P03359_3mutA
GGSGSSEAAAK	13,386	KORV_Q9TTC1-Pro_3mutA
EAAAKEAAAKEAAAK	13,387	PERV_Q4VFZ2
GGSGGGEAAAK	13,388	MLVMS_P03355_3mutA_WS
GGGGSGGGGSGGGGSGGGGS	13,389	BAEVM_P10272_3mut
EAAAKGSS	13,390	XMRV6_A1Z651_3mutA
GSSGGGGGS	13,391	WMSV_P03359_3mutA
GSSGSSGSSGSSGSSGSS	13,392	MLVFF_P26809_3mutA
GGSGSS	13,393	MLVAV_P03356_3mutA
EAAAKGGGGSEAAAK	13,394	MLVMS_P03355_PLV919
EAAAKGGGPAP	13,395	PERV_Q4VFZ2
GGSEAAAKGGG	13,396	MLVAV_P03356_3mutA
EAAAKEAAAKEAAAKEAAAKEAAAKEAAAK	13,397	MLVBM_Q7SVK7_3mut
EAAAKEAAAKEAAAKEAAAKEAAAKEAAAK	13,398	KORV_Q9TTC1-Pro_3mutA
GSSPAPEAAAK	13,399	MLVFF_P26809_3mutA
GGGGSEAAAKGGGGS	13,400	PERV_Q4VFZ2_3mut
GSSGSSGSSGSS	13,401	PERV_Q4VFZ2_3mut
GGSEAAAK	13,402	MLVFF_P26809_3mutA
GGGGGGGG	13,403	MLVMS_P03355_3mut
GSSGGG	13,404	XMRV6_A1Z651_3mutA
EAAAKGGS	13,405	BAEVM_P10272_3mutA
GGGGS	13,406	BAEVM_P10272_3mutA
GGSEAAAKGGG	13,407	KORV_Q9TTC1-Pro_3mutA
GGSGSSGGG	13,408	KORV_Q9TTC1_3mutA
GGSGSSEAAAK	13,409	WMSV_P03359_3mut
EAAAKGGSGSS	13,410	MLVBM_Q7SVK7_3mutA_WS
GGS	13,411	BAEVM_P10272_3mutA
GGGPAPGSS	13,412	WMSV_P03359_3mutA
GSSGSSGSSGSSGSS	13,413	AVIRE_P03360_3mut
GGGEAAAKPAP	13,414	XMRV6_A1Z651_3mut
GSSGGG	13,415	MLVFF_P26809_3mutA

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
GGSPAPGSS	13,416	PERV_Q4VFZ2_3mut
PAPGGS	13,417	MLVCB_P08361_3mut
PAPAPAPAPAP	13,418	KORV_Q9TTC1_3mutA
GSSGGS	13,419	MLVCB_P08361_3mutA
GSSGGSEAAAK	13,420	PERV_Q4VFZ2_3mut
EAAAKGSSGGS	13,421	MLVMS_P03355_PLV919
EAAAKGGG	13,422	WMSV_P03359_3mut
PAPGGGGGS	13,423	BAEVM_P10272_3mutA
GGGGSEAAAKGGGGS	13,424	WMSV_P03359_3mutA
EAAAKEAAAKEAAAKEAAAKEAAAKEAAAK	13,425	MLVMS_P03355_3mutA_WS
GGS	13,426	KORV_Q9TTC1-Pro_3mutA
GSSGGSPAP	13,427	BAEVM_P10272_3mutA
GGG	13,428	MLVMS_P03355_PLV919
PAPGSS	13,429	KORV_Q9TTC1-Pro_3mut
GGSEAAAKGGG	13,430	FLV_P10273_3mutA
GGSEAAAKPAP	13,431	PERV_Q4VFZ2_3mutA_WS
GGGGSSPAP	13,432	XMRV6_A1Z651_3mutA
EAAAKEAAAKEAAAKEAAAKEAAAK	13,433	PERV_Q4VFZ2_3mutA_WS
GGGG	13,434	PERV_Q4VFZ2_3mutA_WS
GGSEAAAKPAP	13,435	MLVMS_P03355_3mut
PAPGSSGGG	13,436	MLVMS_P03355_3mutA_WS
PAPEAAAKGGS	13,437	AVIRE_P03360_3mut
GGGGSSPAP	13,438	MLVMS_P03355_3mutA_WS
GGGGSGGGGSGGGGSGGGGS	13,439	PERV_Q4VFZ2_3mut
GGGEAAAK	13,440	MLVMS_P03355_3mut
GGGGSS	13,441	MLVFF_P26809_3mut
GGSPAPGSS	13,442	XMRV6_A1Z651_3mut
GGGGS	13,443	KORV_Q9TTC1-Pro_3mutA
EAAAKGSSGGS	13,444	FLV_P10273_3mutA
GSS	13,445	MLVMS_P03355_PLV919
GGGG	13,446	MLVMS_P03355_PLV919
GSSGGS	13,447	MLVMS_P03355_PLV919
GGSGGSGGSGGS	13,448	MLVMS_P03355_3mut
PAPEAAAKGGS	13,449	MLVMS_P03355_3mut
EAAAKGSSGGG	13,450	BAEVM_P10272_3mutA
GSSEAAAK	13,451	KORV_Q9TTC1-Pro_3mutA
GSAGSAAGSGEF	13,452	KORV_Q9TTC1_3mutA
GGGGGSEAAAK	13,453	MLVCB_P08361_3mut
GGGG	13,454	WMSV_P03359_3mut

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
GGGGSSEAAAK	13,455	MLVMS_P03355_PLV919
PAPGGG	13,456	WMSV_P03359_3mutA
EAAAKGGSGGG	13,457	MLVAV_P03356_3mutA
GGGPAPGGS	13,458	MLVMS_P03355_3mut
EAAAKPAP	13,459	PERV_Q4VFZ2_3mutA_WS
GSSGSSGSS	13,460	KORV_Q9TTC1-Pro_3mutA
GSSPAPGGS	13,461	XMRV6_A1Z651_3mut
GGGGGSPAP	13,462	BAEVM_P10272_3mutA
GGSGSSGGG	13,463	PERV_Q4VFZ2_3mutA_WS
GGGEAAAKGSS	13,464	AVIRE_P03360_3mut
GSSEAAAK	13,465	FLV_P10273_3mutA
EAAAK	13,466	MLVMS_P03355_3mut
EAAAKGGSGSS	13,467	WMSV_P03359_3mut
GSSEAAAKGGG	13,468	PERV_Q4VFZ2_3mut
PAPGSSGGG	13,469	BAEVM_P10272_3mutA
EAAAKGGGGGS	13,470	MLVMS_P03355_3mut
GGSEAAAKPAP	13,471	AVIRE_P03360_3mut
GGGPAPGGS	13,472	XMRV6_A1Z651_3mut
GGGGS	13,473	KORV_Q9TTC1_3mutA
GGSGGSGGSGGSGGS	13,474	XMRV6_A1Z651_3mut
GGGPAP	13,475	KORV_Q9TTC1-Pro_3mut
EAAAKPAP	13,476	MLVBM_Q7SVK7_3mutA_WS
GGSEAAAK	13,477	MLVMS_P03355_PLV919
GSSEAAAKPAP	13,478	KORV_Q9TTC1-Pro_3mutA
GGSGSS	13,479	MLVMS_P03355_3mut
EAAAKPAPGGG	13,480	PERV_Q4VFZ2_3mut
GGSPAPEAAAK	13,481	KORV_Q9TTC1_3mutA
GGSEAAAKGGG	13,482	AVIRE_P03360_3mutA
GGGGSEAAAKGGGGS	13,483	MLVMS_P03355_PLV919
GSSGGGEAAAK	13,484	KORV_Q9TTC1-Pro_3mutA
EAAAKGGGPAP	13,485	WMSV_P03359_3mut
GSSPAP	13,486	XMRV6_A1Z651_3mutA
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	13,487	SFV3L_P27401-Pro
GGSEAAAKGSS	13,488	MLVMS_P03355_PLV919
GSSGGSEAAAK	13,489	KORV_Q9TTC1-Pro_3mutA
GGSEAAAKGSS	13,490	KORV_Q9TTC1-Pro_3mutA
EAAAKGGG	13,491	AVIRE_P03360_3mutA
GSSGGSEAAAK	13,492	BAEVM_P10272_3mutA
GGGGSEAAAKGGGGS	13,493	KORV_Q9TTC1-Pro_3mut

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
PAPGSSEAAAK	13,494	MLVMS_P03355_3mut
PAPEAAAK	13,495	WMSV_P03359_3mut
PAPGGSGSS	13,496	PERV_Q4VFZ2_3mutA_WS
PAPGSS	13,497	BAEVM_P10272_3mut
PAPGGGGGS	13,498	MLVMS_P03355_3mut
EAAAKPAPGSS	13,499	MLVBM_Q7SVK7_3mutA_WS
GSSPAPGGS	13,500	MLVMS_P03355_PLV919
GGSGSSEAAAK	13,501	MLVMS_P03355_3mut
GGGGGG	13,502	KORV_Q9TTC1-Pro_3mutA
EAAAKEAAAKEAAAKEAAAK	13,503	MLVBM_Q7SVK7_3mut
GGSPAPGSS	13,504	MLVMS_P03355_PLV919
PAPAPAPAPAP	13,505	MLVCB_P08361_3mut
GGSGSSPAP	13,506	WMSV_P03359_3mutA
EAAAKGGSGGG	13,507	PERV_Q4VFZ2_3mutA_WS
GSSGSSGSSGSSGSS	13,508	PERV_Q4VFZ2_3mut
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	13,509	KORV_Q9TTC1_3mutA
GSSGGGEAAAK	13,510	WMSV_P03359_3mutA
GSSGGSEAAAK	13,511	FLV_P10273_3mutA
GGGGGGGG	13,512	PERV_Q4VFZ2_3mut
PAPGGSEAAAK	13,513	FLV_P10273_3mutA
GGGGSSPAP	13,514	BAEVM_P10272_3mutA
PAPAPAPAP	13,515	WMSV_P03359_3mut
GGSEAAAKPAP	13,516	PERV_Q4VFZ2_3mut
PAPGGSGGG	13,517	BAEVM_P10272_3mutA
EAAAKEAAAKEAAAKEAAAKEAAAKEAAAK	13,518	MLVMS_P03355_3mut
GGGGSGGGGSGGGGS	13,519	PERV_Q4VFZ2_3mut
GGSGGGPAP	13,520	PERV_Q4VFZ2_3mut
GGGPAPEAAAK	13,521	MLVFF_P26809_3mut
GGGGGSGSS	13,522	MLVMS_P03355_3mutA_WS
GSS	13,523	MLVCB_P08361_3mut
GGGGGSPAP	13,524	MLVMS_P03355_PLV919
GGSPAP	13,525	MLVAV_P03356_3mutA
GGGPAPGGS	13,526	KORV_Q9TTC1-Pro_3mutA
PAPGSSGGG	13,527	FLV_P10273_3mutA
PAPGSSGGG	13,528	WMSV_P03359_3mutA
PAPGGS	13,529	MLVBM_Q7SVK7_3mutA_WS
GGGEAAAKGSS	13,530	PERV_Q4VFZ2_3mutA_WS
GGSEAAAKGSS	13,531	MLVBM_Q7SVK7_3mutA_WS
PAPGGSEAAAK	13,532	MLVCB_P08361_3mut

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
GGSEAAAKGGG	13,533	XMRV6_A1Z651_3mutA
GGSGGGGSS	13,534	WMSV_P03359_3mut
GGGEAAAKPAP	13,535	KORV_Q9TTC1_3mutA
EAAAKGSS	13,536	KORV_Q9TTC1-Pro_3mut
PAPEAAAKGSS	13,537	MLVFF_P26809_3mut
GSAGSAAGSGEF	13,538	PERV_Q4VFZ2_3mut
EAAAKGGGGGS	13,539	WMSV_P03359_3mut
EAAAKGSSPAP	13,540	WMSV_P03359_3mutA
GGGGSEAAAKGGGGS	13,541	XMRV6_A1Z651_3mutA
GSSEAAAKPAP	13,542	SFV3L_P27401-Pro_2mutA
GGGGGG	13,543	PERV_Q4VFZ2_3mutA_WS
PAPGGS	13,544	BAEVM_P10272_3mut
PAP	13,545	AVIRE_P03360_3mut
PAPAPAP	13,546	MLVBM_Q7SVK7_3mutA_WS
GGGG	13,547	PERV_Q4VFZ2_3mutA_WS
GSSGGSEAAAK	13,548	MLVBM_Q7SVK7_3mut
GGSGGGGSS	13,549	MLVFF_P26809_3mut
GGGGSSGGS	13,550	AVIRE_P03360_3mutA
GSSPAPGGG	13,551	PERV_Q4VFZ2_3mutA_WS
GGSEAAAKPAP	13,552	MLVMS_P03355_PLV919
PAP	13,553	KORV_Q9TTC1-Pro_3mut
GSSGGS	13,554	PERV_Q4VFZ2_3mut
GGGGG	13,555	PERV_Q4VFZ2_3mut
GSSGGGPAP	13,556	FLV_P10273_3mutA
GSSEAAAKGGG	13,557	KORV_Q9TTC1-Pro_3mut
EAAAKEAAAKEAAAKEAAAKEAAAKEAAAK	13,558	MLVCB_P08361_3mut
GGSEAAAKPAP	13,559	MLVCB_P08361_3mut
PAPAPAPAPAPAP	13,560	BAEVM_P10272_3mutA
GGGGSEAAAKGGGGS	13,561	MLVMS_P03355_3mut
EAAAKPAPGSS	13,562	MLVMS_P03355_3mut
GSSGSSGSSGSSGSS	13,563	MLVBM_Q7SVK7_3mutA_WS
PAPEAAAKGSS	13,564	MLVAV_P03356_3mut
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	13,565	AVIRE_P03360_3mut
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	13,566	PERV_Q4VFZ2_3mut
GGSEAAAKGGG	13,567	PERV_Q4VFZ2_3mutA_WS
GGSGGGGSS	13,568	MLVFF_P26809_3mutA
PAPEAAAKGSS	13,569	MLVCB_P08361_3mut
GGG	13,570	PERV_Q4VFZ2_3mutA_WS
GGSGGGEAAAK	13,571	MLVMS_P03355_3mut

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
EAAAKGGGGSS	13,572	WMSV_P03359_3mut
GSSPAPGGG	13,573	WMSV_P03359_3mutA
EAAAKGSSGGG	13,574	PERV_Q4VFZ2_3mut
GGSGGGEAAAK	13,575	PERV_Q4VFZ2_3mutA_WS
GGSGGSGGSGGSGGS	13,576	PERV_Q4VFZ2_3mutA_WS
EAAAKPAPGGS	13,577	PERV_Q4VFZ2_3mutA_WS
GGGGGSEAAAK	13,578	PERV_Q4VFZ2_3mutA_WS
GSSPAP	13,579	MLVFF_P26809_3mut
GGGEAAAKPAP	13,580	AVIRE_P03360_3mut
GSSGGSEAAAK	13,581	MLVMS_P03355_PLV919
EAAAKPAPGGS	13,582	WMSV_P03359_3mutA
PAPGGG	13,583	KORV_Q9TTC1_3mutA
EAAAKGSSPAP	13,584	KORV_Q9TTC1-Pro_3mut
GSSPAPEAAAK	13,585	MLVFF_P26809_3mut
GGSGGGEAAAK	13,586	MLVFF_P26809_3mutA
GSSGSSGSS	13,587	WMSV_P03359_3mutA
EAAAKGGS	13,588	BAEVM_P10272_3mut
EAAAKPAPGGS	13,589	KORV_Q9TTC1_3mutA
EAAAKPAPGGS	13,590	BAEVM_P10272_3mutA
GSSGGGGGS	13,591	PERV_Q4VFZ2_3mut
PAPGGGGSS	13,592	PERV_Q4VFZ2_3mut
GSSGSSGSS	13,593	WMSV_P03359_3mut
EAAAKEAAAKEAAAKEAAAK	13,594	WMSV_P03359_3mut
GGS	13,595	AVIRE_P03360_3mut
EAAAKPAPGSS	13,596	MLVFF_P26809_3mut
EAAAKGGG	13,597	KORV_Q9TTC1_3mut
PAPGSSEAAAK	13,598	MLVMS_P03355_3mut
PAPGSSGGS	13,599	MLVMS_P03355_PLV919
GSSPAPEAAAK	13,600	MLVMS_P03355_3mut
GSSGSSGSSGSSGSSGSS	13,601	WMSV_P03359_3mutA
GGGGS	13,602	BAEVM_P10272_3mut
GSSPAP	13,603	MLVMS_P03355_3mut
EAAAKGGGGSEAAAK	13,604	KORV_Q9TTC1-Pro_3mutA
EAAAKEAAAK	13,605	WMSV_P03359_3mutA
GGGGSSGGS	13,606	MLVCB_P08361_3mutA
PAPGGSEAAAK	13,607	BAEVM_P10272_3mut
EAAAKGGSPAP	13,608	MLVFF_P26809_3mut
GSSGGSGGG	13,609	MLVBM_Q7SVK7_3mutA_WS
GSSGGS	13,610	PERV_Q4VFZ2_3mut

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
PAPGGSGSS	13,611	PERV_Q4VFZ2_3mutA_WS
EAAAKGGSGSS	13,612	KORV_Q9TTC1-Pro_3mutA
PAPAP	13,613	MLVCB_P08361_3mut
EAAAKGSSPAP	13,614	PERV_Q4VFZ2_3mutA_WS
EAAAKPAPGGG	13,615	MLVMS_P03355_PLV919
GGGGSGGGGSGGGGSGGGGSGGGGSGGGGS	13,616	MLVBM_Q7SVK7_3mut
EAAAKGGGGSS	13,617	MLVMS_P03355_PLV919
PAPEAAAK	13,618	PERV_Q4VFZ2_3mut
EAAAKPAPGSS	13,619	BAEVM_P10272_3mutA
GGSPAP	13,620	PERV_Q4VFZ2_3mutA_WS
GGSGGS	13,621	BAEVM_P10272_3mutA
PAPEAAAKGSS	13,622	KORV_Q9TTC1_3mut
PAPGSS	13,623	MLVMS_P03355_PLV919
PAPAPAPAPAP	13,624	MLVAV_P03356_3mutA
GGG	13,625	XMRV6_A1Z651_3mutA
GGGPAP	13,626	PERV_Q4VFZ2_3mutA_WS
GSSPAPEAAAK	13,627	KORV_Q9TTC1_3mutA
PAP	13,628	BAEVM_P10272_3mutA
GGSPAP	13,629	BAEVM_P10272_3mutA
PAPEAAAKGGS	13,630	MLVMS_P03355_PLV919
PAPGSSGGS	13,631	PERV_Q4VFZ2_3mutA_WS
PAPAPAPAPAPAP	13,632	PERV_Q4VFZ2_3mut
EAAAKEAAAKEAAAK	13,633	MLVCB_P08361_3mut
GGSGGSGGSGGSGGS	13,634	MLVMS_P03355_PLV919
EAAAKPAPGGS	13,635	MLVMS_P03355_3mut
GGSGGS	13,636	MLVMS_P03355_PLV919
EAAAKPAP	13,637	MLVMS_P03355_3mutA_WS
GGSEAAAK	13,638	XMRV6_A1Z651_3mutA
GGSGGG	13,639	KORV_Q9TTC1_3mut
GGSGGGEAAAK	13,640	PERV_Q4VFZ2_3mut
PAPEAAAKGGG	13,641	AVIRE_P03360
PAPAP	13,642	PERV_Q4VFZ2_3mut
GSS	13,643	KORV_Q9TTC1-Pro_3mutA
EAAAKGSSGGG	13,644	MLVAV_P03356_3mutA
GGSPAPGSS	13,645	MLVBM_Q7SVK7_3mutA_WS
PAPEAAAK	13,646	MLVAV_P03356_3mut
EAAAKGGSPAP	13,647	BAEVM_P10272_3mutA
PAPAPAPAP	13,648	WMSV_P03359_3mutA
PAPGGSEAAAK	13,649	MLVMS_P03355_3mut

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
GGSGGSGGSGGS	13,650	WMSV_P03359_3mut
GGGGGSGSS	13,651	XMRV6_A1Z651_3mut
PAPGGSGGG	13,652	KORV_Q9TTC1_3mutA
GGS	13,653	MLVMS_P03355_3mut
EAAAK	13,654	WMSV_P03359_3mut
GGGEAAAKGSS	13,655	MLVBM_Q7SVK7_3mutA_WS
GGSPAPGSS	13,656	MLVCB_P08361_3mut
GGSEAAAKPAP	13,657	PERV_Q4VFZ2_3mut
GGGGSGGGGSGGGGSGGGGSGGGGS	13,658	MLVCB_P08361_3mutA
GGSGSS	13,659	BAEVM_P10272_3mutA
GGGEAAAKGSS	13,660	WMSV_P03359_3mutA
EAAAKGGSPAP	13,661	WMSV_P03359_3mut
GSSPAPEAAAK	13,662	MLVMS_P03355_3mut
GGSGGSGGSGGS	13,663	MLVMS_P03355_PLV919
GSSPAPEAAAK	13,664	WMSV_P03359_3mut
GSSGSSGSSGSS	13,665	PERV_Q4VFZ2
GGSGSSEAAAK	13,666	WMSV_P03359_3mutA
GGSGGG	13,667	MLVFF_P26809_3mut
GGSPAPGGG	13,668	MLVFF_P26809_3mut
GGSGGSGGS	13,669	BAEVM_P10272_3mutA
GGGGSSEAAAK	13,670	MLVBM_Q7SVK7_3mut
GGSPAPGSS	13,671	MLVMS_P03355_3mut
EAAAKPAPGSS	13,672	AVIRE_P03360_3mut
GGGGSSGGS	13,673	FLV_P10273_3mutA
GGSPAPEAAAK	13,674	PERV_Q4VFZ2_3mut
GGSEAAAK	13,675	MLVMS_P03355_3mutA_WS
GSSGSSGSSGSS	13,676	MLVCB_P08361_3mutA
EAAAKEAAAKEAAAKEAAAKEAAAK	13,677	MLVMS_P03355_PLV919
GGGGG	13,678	PERV_Q4VFZ2_3mut
GGSEAAAKGSS	13,679	MLVCB_P08361_3mutA
GSSGGG	13,680	MLVBM_Q7SVK7_3mutA_WS
PAPGSSGGG	13,681	KORV_Q9TTC1-Pro_3mutA
GGSGGS	13,682	BAEVM_P10272_3mut
EAAAKGGGGGS	13,683	MLVBM_Q7SVK7_3mutA_WS
GGSGSSPAP	13,684	MLVCB_P08361_3mut
PAPGSSGGG	13,685	KORV_Q9TTC1
PAPGGSGGG	13,686	MLVMS_P03355_3mut
GGGG	13,687	WMSV_P03359_3mutA
EAAAKGGSPAP	13,688	MLVCB_P08361_3mut

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
GSSGSS	13,689	FLV_P10273_3mutA
GGSEAAAKPAP	13,690	SFV3L_P27401_2mut
EAAAKGSSGGS	13,691	MLVAV_P03356_3mutA
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	13,692	MLVAV_P03356_3mutA
EAAAKGGSGSS	13,693	PERV_Q4VFZ2_3mutA_WS
GGGGG	13,694	MLVCB_P08361_3mut
GGGEAAAK	13,695	BAEVM_P10272_3mut
GGSGGSGGSGGS	13,696	MLVCB_P08361_3mut
EAAAKEAAAKEAAAKEAAAKEAAAKEAAAK	13,697	PERV_Q4VFZ2
PAPAPAPAPAP	13,698	MLVMS_P03355_3mutA_WS
EAAAKEAAAK	13,699	XMRV6_A1Z651_3mut
GSSGGSEAAAK	13,700	PERV_Q4VFZ2_3mutA_WS
PAPGGSEAAAK	13,701	KORV_Q9TTC1-Pro_3mutA
EAAAKGGGPAP	13,702	MLVBM_Q7SVK7_3mutA_WS
PAPGGSGSS	13,703	PERV_Q4VFZ2
SGSETPGTSESATPES	13,704	MLVMS_P03355_3mut
GGSGGS	13,705	MLVMS_P03355_PLV919
EAAAKGGS	13,706	FLV_P10273_3mut
GGSPAPGSS	13,707	MLVMS_P03355_3mutA_WS
EAAAKEAAAKEAAAKEAAAK	13,708	FFV_O93209_2mut
GSSGGSGGG	13,709	MLVMS_P03355_3mutA_WS
PAPGSSEAAAK	13,710	WMSV_P03359_3mut
PAPAPAPAPAPAP	13,711	KORV_Q9TTC1_3mutA
GGGGSS	13,712	BAEVM_P10272_3mut
GGGGSEAAAKGGGGS	13,713	AVIRE_P03360_3mut
GSSPAPEAAAK	13,714	KORV_Q9TTC1-Pro_3mutA
PAPEAAAKGGG	13,715	MLVBM_Q7SVK7_3mut
EAAAKEAAAK	13,716	WMSV_P03359_3mut
EAAAK	13,717	SFV3L_P27401-Pro_2mutA
GSSGGSGGG	13,718	XMRV6_A1Z651_3mutA
GGGEAAAKPAP	13,719	WMSV_P03359_3mutA
GGSGGS	13,720	MLVFF_P26809_3mutA
EAAAKEAAAKEAAAKEAAAKEAAAKEAAAK	13,721	FOAMV_P14350_2mutA
GGGGG	13,722	MLVAV_P03356_3mutA
GSSGGSEAAAK	13,723	BAEVM_P10272_3mut
SGGSSGGSSGSETPGTSESATPESSGGSSGGSS	13,724	SFV1_P23074
GGSGGGPAP	13,725	MLVCB_P08361_3mut
GGSGSS	13,726	PERV_Q4VFZ2_3mut
SGSETPGTSESATPES	13,727	MLVFF_P26809_3mut

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
EAAAKGGSPAP	13,728	MLVMS_P03355_3mut
PAPAP	13,729	PERV_Q4VFZ2_3mut
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	13,730	MLVBM_Q7SVK7_3mut
GGGGGS	13,731	BAEVM_P10272_3mutA
EAAAKEAAAK	13,732	AVIRE_P03360_3mut
GSSGGSEAAAK	13,733	PERV_Q4VFZ2_3mut
GGGEAAAK	13,734	WMSV_P03359_3mut
GSSGGGEAAAK	13,735	AVIRE_P03360_3mutA
GGG	13,736	XMRV6_A1Z651_3mut
GGGGSEAAAKGGGGS	13,737	BAEVM_P10272_3mut
GGGG	13,738	MLVMS_P03355_3mut
GGSGGS	13,739	MLVMS_P03355_3mutA_WS
GGSGGGGSS	13,740	MLVBM_Q7SVK7_3mutA_WS
GSSPAPGGS	13,741	PERV_Q4VFZ2_3mut
GSSPAPEAAAK	13,742	PERV_Q4VFZ2_3mutA_WS
EAAAKGGS	13,743	WMSV_P03359_3mut
GGSGGSGGSGGS	13,744	PERV_Q4VFZ2_3mut
GGGGSSEAAAK	13,745	KORV_Q9TTC1-Pro_3mut
PAPAPAPAPAPAP	13,746	MLVAV_P03356_3mut
EAAAKGSSGGG	13,747	MLVMS_P03355_PLV919
GGGGG	13,748	MLVBM_Q7SVK7_3mutA_WS
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	13,749	FFV_O93209_2mutA
SGGSSGGSSGSETPGTSESATPESSGGSSGGSS	13,750	KORV_Q9TTC1-Pro_3mut
GGSPAPGGG	13,751	MLVMS_P03355_3mutA_WS
GGGEAAAKGGS	13,752	MLVMS_P03355_3mut
GGGEAAAK	13,753	PERV_Q4VFZ2_3mut
PAPEAAAKGGG	13,754	MLVMS_P03355_3mut
GSSGSSGSSGSSGSSGSS	13,755	BAEVM_P10272_3mutA
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	13,756	GALV_P21414_3mutA
EAAAKGGSPAP	13,757	FFV_O93209-Pro
EAAAKEAAAK	13,758	MLVFF_P26809_3mut
GGGGSGGGGSGGGGSGGGGSGGGGSGGGGS	13,759	PERV_Q4VFZ2_3mutA_WS
GGSGGSGGSGGS	13,760	MLVAV_P03356_3mutA
EAAAKEAAAKEAAAKEAAAKEAAAK	13,761	SFV3L_P27401_2mutA
GSSGSSGSSGSSGSSGSS	13,762	BAEVM_P10272_3mut
GGGGS	13,763	MLVMS_P03355_PLV919
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	13,764	SFV1_P23074
GGGGSGGGGS	13,765	KORV_Q9TTC1-Pro_3mutA
GGGGSGGGGS	13,766	MLVMS_P03355_3mut

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
GGSGSS	13,767	KORV_Q9TTC1_3mutA
GSSPAPGGG	13,768	PERV_Q4VFZ2_3mut
GSSGGSPAP	13,769	PERV_Q4VFZ2_3mutA_WS
PAPGGS	13,770	PERV_Q4VFZ2_3mutA_WS
GGSPAPEAAAK	13,771	FOAMV_P14350_2mutA
GGGPAPGGS	13,772	SFV3L_P27401_2mut
PAPGSSGGG	13,773	MLVCB_P08361_3mut
GSSGGGEAAAK	13,774	AVIRE_P03360_3mut
GSSGGG	13,775	XMRV6_A1Z651_3mut
GSSGSS	13,776	PERV_Q4VFZ2_3mut
GSSGGG	13,777	MLVAV_P03356_3mutA
PAPGGGGGS	13,778	PERV_Q4VFZ2_3mut
GSSEAAAK	13,779	MLVMS_P03355_3mut
PAPGGG	13,780	FLV_P10273_3mutA
GGGGSGGGGS	13,781	PERV_Q4VFZ2_3mut
GSSGGS	13,782	MLVMS_P03355_PLV919
GGGGSGGGGS	13,783	SFV3L_P27401_2mut
EAAAKGGSGSS	13,784	FLV_P10273_3mutA
GSSEAAAKGGS	13,785	MLVMS_P03355_3mutA_WS
PAPGSSEAAAK	13,786	SFV3L_P27401_2mutA
GGGGSGGGGS	13,787	SFV3L_P27401-Pro_2mutA
PAPGSSEAAAK	13,788	PERV_Q4VFZ2_3mut
PAPGSSEAAAK	13,789	PERV_Q4VFZ2
GGSPAPGGG	13,790	AVIRE_P03360_3mut
GGGGGS	13,791	PERV_Q4VFZ2_3mutA_WS
GGGGSSGGS	13,792	PERV_Q4VFZ2_3mut
PAPAPAPAP	13,793	AVIRE_P03360_3mutA
GGSGGS	13,794	WMSV_P03359_3mutA
GGGPAPGGS	13,795	PERV_Q4VFZ2_3mut
GGSGGSGGSGGSGGS	13,796	MLVMS_P03355_PLV919
GGSGGG	13,797	PERV_Q4VFZ2_3mut
EAAAKEAAAK	13,798	SFV3L_P27401_2mut
PAPGSS	13,799	XMRV6_A1Z651_3mut
GSSEAAAK	13,800	MLVFF_P26809_3mut
GGSPAPGGG	13,801	MLVMS_P03355_3mut
EAAAKGGG	13,802	WMSV_P03359_3mutA
GSSEAAAKGGS	13,803	PERV_Q4VFZ2_3mutA_WS
GSSGGSPAP	13,804	FFV_O93209
GGGGGS	13,805	KORV_Q9TTC1-Pro_3mut

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
GSSGGG	13,806	MLVCB_P08361_3mut
GSSGSS	13,807	MLVCB_P08361_3mutA
GGSEAAAKPAP	13,808	BAEVM_P10272_3mut
EAAAKGGGGSS	13,809	MLVCB_P08361_3mut
EAAAKPAPGGS	13,810	KORV_Q9TTC1-Pro_3mutA
GSSGSSGSSGSSGSS	13,811	MLVAV_P03356_3mutA
GGGGSEAAAKGGGGS	13,812	PERV_Q4VFZ2_3mutA_WS
GGSGSS	13,813	KORV_Q9TTC1-Pro_3mut
GSS	13,814	SFV3L_P27401-Pro_2mutA
PAPAP	13,815	BAEVM_P10272_3mut
EAAAKPAP	13,816	BAEVM_P10272
EAAAKEAAAKEAAAKEAAAKEAAAK	13,817	KORV_Q9TTC1-Pro_3mut
GGGGGGG	13,818	PERV_Q4VFZ2_3mutA_WS
GGGGS	13,819	MLVMS_P03355_3mut
GSSGGG	13,820	FLV_P10273_3mutA
PAPAPAPAPAP	13,821	FLV_P10273_3mut
EAAAKEAAAKEAAAK	13,822	WMSV_P03359_3mutA
GSSGGS	13,823	MLVBM_Q7SVK7_3mutA_WS
EAAAKPAPGGG	13,824	MLVMS_P03355_3mut
GSSPAPGGS	13,825	WMSV_P03359_3mut
PAPGSSGGG	13,826	PERV_Q4VFZ2_3mutA_WS
GSSGGG	13,827	AVIRE_P03360_3mutA
PAPGGSGSS	13,828	MLVFF_P26809_3mut
PAPGSS	13,829	PERV_Q4VFZ2_3mut
GGGGGSGSS	13,830	WMSV_P03359_3mutA
EAAAKGGGGSS	13,831	MLVBM_Q7SVK7_3mutA_WS
GGGGGGG	13,832	BAEVM_P10272_3mut
PAPEAAAKGSS	13,833	MLVMS_P03355_3mut
GGSGGGEAAAK	13,834	MLVMS_P03355_PLV919
EAAAKGGGGGS	13,835	MLVCB_P08361_3mut
PAPGGS	13,836	KORV_Q9TTC1-Pro_3mut
GGGG	13,837	FLV_P10273_3mutA
EAAAKGGSGSS	13,838	MLVBM_Q7SVK7_3mutA_WS
GGGGSSGGS	13,839	MLVMS_P03355_3mutA_WS
GGGGGGGG	13,840	WMSV_P03359_3mut
GGSGSSGGG	13,841	MLVMS_P03355_PLV919
GSSEAAAKGGS	13,842	KORV_Q9TTC1-Pro_3mutA
EAAAKPAPGSS	13,843	MLVCB_P08361_3mut
GGSPAPGSS	13,844	KORV_Q9TTC1_3mutA

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
PAPGSSGGG	13,845	BAEVM_P10272_3mut
EAAAKPAPGSS	13,846	WMSV_P03359_3mut
GGSPAPEAAAK	13,847	XMRV6_A1Z651_3mutA
GSSPAP	13,848	FLV_P10273_3mutA
GSS	13,849	BAEVM_P10272_3mutA
EAAAKPAPGGS	13,850	FLV_P10273_3mutA
GGSGSSPAP	13,851	FLV_P10273_3mutA
PAPGSSGGS	13,852	MLVMS_P03355_3mut
GSAGSAAGSGEF	13,853	PERV_Q4VFZ2_3mutA_WS
GSSGGSEAAAK	13,854	KORV_Q9TTC1_3mutA
GSSGGS	13,855	MLVMS_P03355_3mutA_WS
EAAAKGGGGSEAAAK	13,856	SFV3L_P27401_2mut
GSSGGS	13,857	PERV_Q4VFZ2_3mutA_WS
GGSPAPEAAAK	13,858	FLV_P10273_3mut
GGSEAAAKGSS	13,859	PERV_Q4VFZ2_3mutA_WS
GSSPAPEAAAK	13,860	PERV_Q4VFZ2_3mutA_WS
GGSGSSGGG	13,861	PERV_Q4VFZ2_3mut
GGGG	13,862	AVIRE_P03360_3mutA
GGSEAAAKPAP	13,863	WMSV_P03359_3mut
GSSGGSPAP	13,864	MLVAV_P03356_3mutA
GSSGGSEAAAK	13,865	MLVMS_P03355_3mut
PAPEAAAKGGS	13,866	KORV_Q9TTC1-Pro_3mut
GGSPAP	13,867	PERV_Q4VFZ2_3mutA_WS
GGSEAAAK	13,868	MLVAV_P03356_3mutA
EAAAKGGGGSEAAAK	13,869	KORV_Q9TTC1-Pro_3mut
SGGSSGGSSGSETPGTSESATPESSGGSSGGSS	13,870	MLVMS_P03355_PLV919
GSSEAAAK	13,871	KORV_Q9TTC1_3mutA
GGG	13,872	AVIRE_P03360
GGSEAAAKGSS	13,873	MLVBM_Q7SVK7_3mut
GGSEAAAKGSS	13,874	MLVMS_P03355_3mut
GGSPAPEAAAK	13,875	MLVCB_P08361_3mut
GGSGGGEAAAK	13,876	MLVCB_P08361_3mut
GGSEAAAKPAP	13,877	MLVMS_P03355_3mutA_WS
EAAAKGGSGSS	13,878	KORV_Q9TTC1-Pro_3mut
GGGEAAAKGGS	13,879	MLVCB_P08361_3mut
EAAAKGGGGSEAAAK	13,880	FLV_P10273_3mutA
GGSPAP	13,881	MLVFF_P26809_3mut
GGGGSSGGS	13,882	XMRV6_A1Z651_3mutA
PAP	13,883	MLVCB_P08361_3mut

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
GGS	13,884	SFV3L_P27401-Pro_2mutA
GGGGSGGGGS	13,885	MLVMS_P03355_3mut
GGGEAAAKGGS	13,886	MLVAV_P03356_3mutA
GSSGSSGSSGSSGSSGSS	13,887	MLVMS_P03355_PLV919
PAPGSS	13,888	MLVCB_P08361_3mut
GGSGGSGGS	13,889	MLVMS_P03355_PLV919
PAPGGSGGG	13,890	FLV_P10273_3mutA
GGGGSGGGGSGGGGS	13,891	FLV_P10273_3mut
GGSGSSGGG	13,892	KORV_Q9TTC1-Pro_3mutA
GGSGGSGGS	13,893	GALV_P21414_3mutA
GGGEAAAKGGS	13,894	WMSV_P03359_3mut
SGSETPGTSESATPES	13,895	KORV_Q9TTC1_3mutA
EAAAKGGGGGS	13,896	KORV_Q9TTC1-Pro_3mut
EAAAKGSSPAP	13,897	BAEVM_P10272_3mut
GGGG	13,898	MLVCB_P08361_3mut
GGGGSGGGGSGGGGSGGGGSGGGGS	13,899	MLVBM_Q7SVK7_3mut
GSSGGSGGG	13,900	MLVMS_P03355_PLV919
GGSGSS	13,901	MLVFF_P26809_3mut
EAAAKGGS	13,902	AVIRE_P03360_3mutA
GSSEAAAKGGS	13,903	MLVBM_Q7SVK7_3mutA_WS
EAAAKPAPGGG	13,904	WMSV_P03359_3mut
PAPGSSGGG	13,905	MLVCB_P08361_3mutA
GGGGSSEAAAK	13,906	KORV_Q9TTC1-Pro_3mutA
GSSEAAAKPAP	13,907	BAEVM_P10272_3mutA
PAPGGGEAAAK	13,908	MLVBM_Q7SVK7_3mutA_WS
GGSGGGEAAAK	13,909	MLVCB_P08361_3mutA
GGGGSGGGGSGGGGSGGGGSGGGGSGGGGS	13,910	FFV_O93209
EAAAKGGGGGS	13,911	GALV_P21414_3mutA
GGSPAPGGG	13,912	MLVMS_P03355_3mut
GSSGSSGSS	13,913	FLV_P10273_3mutA
EAAAK	13,914	MLVBM_Q7SVK7_3mut
GGGGSSGGS	13,915	MLVMS_P03355_3mut
GGSGSSPAP	13,916	PERV_Q4VFZ2_3mut
EAAAKEAAAKEAAAKEAAAK	13,917	BAEVM_P10272_3mut
GGGPAPGSS	13,918	MLVMS_P03355_3mut
GSSPAPGGS	13,919	PERV_Q4VFZ2_3mutA_WS
PAPAP	13,920	FLV_P10273_3mutA
PAPAPAPAP	13,921	PERV_Q4VFZ2_3mut
GGGGGSEAAAK	13,922	GALV_P21414_3mutA

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
GGGGGSGSS	13,923	BAEVM_P10272_3mutA
GGGEAAAKGSS	13,924	KORV_Q9TTC1_3mutA
GGGGGSPAP	13,925	AVIRE_P03360_3mut
GGGGGSEAAAK	13,926	SFV3L_P27401_2mutA
GGS	13,927	KORV_Q9TTC1_3mutA
GGGGGGG	13,928	PERV_Q4VFZ2_3mut
SGSETPGTSESATPES	13,929	SFV3L_P27401_2mutA
EAAAKGGSGGG	13,930	MLVMS_P03355_3mut
GGGGS	13,931	MLVFF_P26809_3mut
EAAAKGSSGGG	13,932	BAEVM_P10272_3mut
EAAAKPAPGGS	13,933	MLVF5_P26810_3mutA
SGGSSGGSSGSETPGTSESATPESSGGSSGGSS	13,934	SFV3L_P27401_2mutA
GGSPAPGGG	13,935	WMSV_P03359_3mutA
GSAGSAAGSGEF	13,936	MLVFF_P26809_3mut
GGGGSSGGS	13,937	MLVMS_P03355_3mutA_WS
GGGGGGG	13,938	MLVCB_P08361_3mut
GSSEAAAK	13,939	WMSV_P03359_3mut
PAPGSS	13,940	FLV_P10273_3mutA
GSSGGG	13,941	PERV_Q4VFZ2_3mutA_WS
PAPGGG	13,942	MLVFF_P26809_3mut
GGGGGSPAP	13,943	MLVMS_P03355_3mut
GGSEAAAK	13,944	XMRV6_A1Z651_3mut
GSSGGG	13,945	PERV_Q4VFZ2_3mut
GGSGGSGGSGGS	13,946	MLVMS_P03355_3mut
PAPAP	13,947	AVIRE_P03360_3mut
GGSEAAAK	13,948	PERV_Q4VFZ2_3mut
GGGGS	13,949	MLVMS_P03355_PLV919
GGGG	13,950	BAEVM_P10272_3mutA
EAAAKGGGGSS	13,951	MLVCB_P08361_3mutA
EAAAKEAAAKEAAAK	13,952	GALV_P21414_3mutA
PAPGGGEAAAK	13,953	KORV_Q9TTC1
EAAAKGGSPAP	13,954	MLVMS_P03355_3mut
GGSGSSEAAAK	13,955	MLVMS_P03355_3mut
GGSPAPEAAAK	13,956	FLV_P10273_3mutA
GGGGGGG	13,957	PERV_Q4VFZ2_3mut
EAAAKEAAAKEAAAKEAAAKEAAAKEAAAK	13,958	SFV1_P23074_2mutA
EAAAKGSSGGS	13,959	MLVMS_P03355_3mut
GSSEAAAKPAP	13,960	MLVFF_P26809_3mut
GGGGSS	13,961	FLV_P10273_3mutA

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
EAAAKGGSGGG	13,962	AVIRE_P03360_3mutA
GGSGGS	13,963	PERV_Q4VFZ2_3mutA_WS
GGGGGSPAP	13,964	AVIRE_P03360_3mutA
EAAAKEAAAKEAAAK	13,965	XMRV6_A1Z651_3mut
PAPEAAAKGGS	13,966	FLV_P10273_3mutA
GSSGGSEAAAK	13,967	MLVCB_P08361_3mut
EAAAKGGSGGG	13,968	MLVMS_P03355
GGSGGGPAP	13,969	MLVMS_P03355_3mut
GGS	13,970	XMRV6_A1Z651_3mut
GGSEAAAKPAP	13,971	MLVFF_P26809_3mut
EAAAKGGG	13,972	MLVMS_P03355_PLV919
GSSGSSGSSGSS	13,973	WMSV_P03359_3mut
GGSGSSPAP	13,974	PERV_Q4VFZ2_3mut
GGGEAAAK	13,975	MLVMS_P03355_3mutA_WS
GSSPAPGGS	13,976	KORV_Q9TTC1-Pro_3mutA
GSSEAAAKGGG	13,977	SFV3L_P27401_2mut
EAAAKPAPGGS	13,978	MLVCB_P08361_3mut
GGSGGGEAAAK	13,979	PERV_Q4VFZ2
GGSGSS	13,980	MLVCB_P08361_3mut
GGSGGGEAAAK	13,981	MLVBM_Q7SVK7_3mutA_WS
GGSGGSGGSGGSGGSGGS	13,982	FLV_P10273_3mut
PAPEAAAKGSS	13,983	MLVMS_P03355_3mut
EAAAKGSSGGS	13,984	WMSV_P03359_3mutA
GGSGSSEAAAK	13,985	MLVCB_P08361_3mut
GGSGSSEAAAK	13,986	KORV_Q9TTC1_3mutA
GSSGGSGGG	13,987	MLVMS_P03355_PLV919
EAAAKGGSGGG	13,988	SFV3L_P27401-Pro_2mutA
GGSGGS	13,989	AVIRE_P03360_3mutA
GSAGSAAGSGEF	13,990	MLVMS_P03355_PLV919
GGSGSS	13,991	GALV_P21414_3mutA
GGGG	13,992	MLVFF_P26809_3mutA
GGGGSGGGGSGGGGSGGGGS	13,993	WMSV_P03359_3mut
SGSETPGTSESATPES	13,994	BAEVM_P10272_3mut
EAAAKEAAAKEAAAKEAAAK	13,995	FOAMV_P14350_2mutA
GGGEAAAKGGS	13,996	FLV_P10273_3mutA
GSSGGSEAAAK	13,997	MLVFF_P26809_3mut
EAAAKGGGGSS	13,998	MLVAV_P03356_3mut
PAPGGSEAAAK	13,999	KORV_Q9TTC1-Pro_3mut
EAAAK	14,000	XMRV6_A1Z651_3mut

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
GSSGSSGSSGSSGSSGSS	14,001	PERV_Q4VFZ2_3mut
GGGG	14,002	MLVCB_P08361_3mutA
GSSGSS	14,003	WMSV_P03359_3mutA
GSSGGSPAP	14,004	AVIRE_P03360_3mut
GGSGGSGGS	14,005	MLVCB_P08361_3mut
EAAAKGGGPAP	14,006	FLV_P10273_3mutA
GGGGSGGGGS	14,007	MLVCB_P08361_3mut
GGSEAAAKGSS	14,008	PERV_Q4VFZ2_3mutA_WS
EAAAKEAAAKEAAAKEAAAKEAAAKEAAAK	14,009	SFV3L_P27401_2mutA
GGSGSSEAAAK	14,010	PERV_Q4VFZ2_3mutA_WS
EAAAKEAAAKEAAAKEAAAK	14,011	SFV3L_P27401-Pro_2mutA
GSSEAAAKGGS	14,012	FLV_P10273_3mutA
GGSGSS	14,013	PERV_Q4VFZ2
GGSGSSEAAAK	14,014	SFV3L_P27401-Pro_2mutA
GSSGSSGSS	14,015	XMRV6_A1Z651_3mutA
EAAAKGSSPAP	14,016	KORV_Q9TTC1_3mutA
EAAAKPAP	14,017	FLV_P10273_3mutA
GGSGSSEAAAK	14,018	KORV_Q9TTC1-Pro_3mut
GGGGSGGGGSGGGGSGGGGSGGGGSGGGGS	14,019	KORV_Q9TTC1_3mutA
GGGGSGGGGSGGGGS	14,020	KORV_Q9TTC1-Pro_3mutA
GGGGGGG	14,021	FLV_P10273_3mut
EAAAKGSS	14,022	WMSV_P03359_3mut
EAAAKGGGPAP	14,023	MLVCB_P08361_3mut
GSSGSS	14,024	MLVBM_Q7SVK7_3mutA_WS
EAAAKGGGGGS	14,025	MLVFF_P26809_3mut
GGSGGGEAAAK	14,026	FLV_P10273_3mutA
PAPGSS	14,027	MLVFF_P26809_3mutA
PAPGSS	14,028	BAEVM_P10272_3mutA
GGSPAPGSS	14,029	AVIRE_P03360_3mut
GGGGSSEAAAK	14,030	MLVMS_P03355_3mut
GSSGGGGGS	14,031	FFV_O93209-Pro
EAAAKGSSPAP	14,032	PERV_Q4VFZ2_3mut
GSSPAPGGS	14,033	PERV_Q4VFZ2_3mut
GGGGGG	14,034	BAEVM_P10272_3mut
EAAAKGGGGSS	14,035	PERV_Q4VFZ2_3mutA_WS
PAPGGSEAAAK	14,036	KORV_Q9TTC1_3mutA
SGGSSGGSSGSETPGTSESATPESSGGSSGGSS	14,037	MLVMS_P03355_3mutA_WS
GSSGSSGSSGSS	14,038	MLVMS_P03355_3mut
EAAAKGSSGGG	14,039	MLVMS_P03355_PLV919

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
GGSEAAAKPAP	14,040	AVIRE_P03360_3mutA
GSSGSSGSSGSSGSS	14,041	WMSV_P03359_3mutA
GGGEAAAKPAP	14,042	FLV_P10273_3mutA
PAPGSSGGG	14,043	KORV_Q9TTC1_3mutA
GSSGSS	14,044	MLVMS_P03355_3mutA_WS
PAPEAAAK	14,045	BAEVM_P10272_3mut
GGGPAPGSS	14,046	PERV_Q4VFZ2
GSSGGSPAP	14,047	MLVFF_P26809_3mut
GGGGSS	14,048	SFV3L_P27401_2mut
PAPEAAAKGSS	14,049	SFV3L_P27401_2mut
GGSGGGPAP	14,050	XMRV6_A1Z651_3mutA
PAPGGS	14,051	BAEVM_P10272_3mutA
EAAAKGGGGGS	14,052	AVIRE_P03360_3mut
GSSGGSPAP	14,053	KORV_Q9TTC1-Pro_3mutA
GSSGGGGGS	14,054	WMSV_P03359_3mut
GGGEAAAKGGS	14,055	AVIRE_P03360_3mut
GGGEAAAKGSS	14,056	BAEVM_P10272_3mut
PAPEAAAKGSS	14,057	MLVAV_P03356_3mutA
GSSGSSGSSGSSGSS	14,058	MLVCB_P08361_3mut
GGSPAPGSS	14,059	FLV_P10273_3mutA
EAAAKGSSPAP	14,060	BAEVM_P10272_3mutA
GGSGGSGGSGGSGGSGGS	14,061	PERV_Q4VFZ2
GGGGSSEAAAK	14,062	FLV_P10273_3mutA
GGGGSSPAP	14,063	FFV_O93209
GSSGGSPAP	14,064	MLVMS_P03355_3mut
GGGPAPGSS	14,065	MLVMS_P03355_PLV919
PAPGSSGGS	14,066	PERV_Q4VFZ2_3mut
GGGGGSPAP	14,067	MLVFF_P26809_3mut
SGSETPGTSESATPES	14,068	MLVMS_P03355_3mutA_WS
GSSGSSGSSGSSGSS	14,069	KORV_Q9TTC1_3mutA
GSSPAPGGG	14,070	WMSV_P03359_3mut
PAPAPAPAPAPAP	14,071	SFV3L_P27401_2mutA
GGGPAPGGS	14,072	MLVMS_P03355_3mut
PAPGGSEAAAK	14,073	WMSV_P03359_3mut
GGGGSSEAAAK	14,074	FFV_O93209-Pro
GGSPAPGGG	14,075	FLV_P10273_3mutA
GSSPAPEAAAK	14,076	AVIRE_P03360_3mut
GGGEAAAK	14,077	FLV_P10273_3mutA
PAPEAAAKGGG	14,078	MLVCB_P08361_3mut

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
GGSPAPGGG	14,079	MLVCB_P08361_3mut
GGSGGGGSS	14,080	BAEVM_P10272_3mutA
GSSPAPEAAAK	14,081	MLVCB_P08361_3mut
GGSPAPGGG	14,082	KORV_Q9TTC1-Pro_3mutA
PAPGGSGSS	14,083	KORV_Q9TTC1_3mutA
GSSPAP	14,084	KORV_Q9TTC1-Pro_3mutA
SGSETPGTSESATPES	14,085	MLVMS_P03355
GSSGSSGSS	14,086	MLVAV_P03356_3mutA
PAPGSSGGS	14,087	PERV_Q4VFZ2_3mutA_WS
PAPGGS	14,088	KORV_Q9TTC1-Pro_3mutA
PAPEAAAKGGG	14,089	SFV3L_P27401-Pro_2mutA
GGSGGSGGS	14,090	BAEVM_P10272_3mut
PAPGGS	14,091	MLVFF_P26809_3mut
GSSGGSPAP	14,092	MLVMS_P03355_PLV919
GSSGGGGGS	14,093	FLV_P10273_3mutA
GGGGGSPAP	14,094	KORV_Q9TTC1-Pro_3mut
EAAAKPAPGSS	14,095	SFV3L_P27401-Pro_2mutA
EAAAKGGSPAP	14,096	KORV_Q9TTC1-Pro
GGGPAPEAAAK	14,097	MLVMS_P03355_PLV919
GGSEAAAKGSS	14,098	MLVMS_P03355
PAPEAAAKGSS	14,099	KORV_Q9TTC1_3mutA
PAPEAAAKGGS	14,100	WMSV_P03359_3mutA
GSSGGG	14,101	PERV_Q4VFZ2_3mutA_WS
EAAAKGGGGSS	14,102	MLVMS_P03355_PLV919
EAAAKGGSPAP	14,103	AVIRE_P03360_3mutA
GGGGSSGGS	14,104	MLVMS_P03355_PLV919
PAPEAAAKGSS	14,105	PERV_Q4VFZ2_3mutA_WS
EAAAKGGGGGS	14,106	BAEVM_P10272_3mut
GSSGGGGGS	14,107	MLVMS_P03355_3mut
PAPAPAPAP	14,108	KORV_Q9TTC1_3mutA
GGSGGSGGSGGS	14,109	MLVAV_P03356_3mut
PAPAPAPAP	14,110	SFV3L_P27401_2mut
GSSEAAAKPAP	14,111	MLVMS_P03355_3mut
GGSGGGEAAAK	14,112	SFV3L_P27401_2mutA
GSSGGSGGG	14,113	MLVMS_P03355_3mutA_WS
GGGGGSPAP	14,114	MLVCB_P08361_3mutA
GGGEAAAKGSS	14,115	XMRV6_A1Z651_3mutA
GGGGSSPAP	14,116	BAEVM_P10272_3mut
GGSGGG	14,117	PERV_Q4VFZ2_3mut

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
GGGGSS	14,118	MLVBM_Q7SVK7_3mutA_WS
EAAAKGSSGGS	14,119	PERV_Q4VFZ2_3mutA_WS
GSSGGGGGS	14,120	PERV_Q4VFZ2
EAAAKGSSGGS	14,121	PERV_Q4VFZ2_3mut
EAAAKEAAAK	14,122	MLVAV_P03356_3mut
GSSGGGEAAAK	14,123	MLVAV_P03356_3mut
GSSPAPGGG	14,124	XMRV6_A1Z651_3mut
GGGGSGGGGSGGGGS	14,125	PERV_Q4VFZ2_3mut
EAAAKEAAAKEAAAKEAAAK	14,126	KORV_Q9TTC1_3mutA
EAAAKGGSGSS	14,127	MLVBM_Q7SVK7_3mut
PAPEAAAK	14,128	BLVJ_P03361
GSSGGG	14,129	FFV_O93209-Pro
GGSGGGEAAAK	14,130	KORV_Q9TTC1-Pro_3mutA
EAAAK	14,131	FLV_P10273_3mutA
GGGGSSPAP	14,132	MLVMS_P03355_3mut
GSS	14,133	SFV3L_P27401-Pro_2mut
PAPEAAAKGSS	14,134	BAEVM_P10272_3mut
GGGGGSPAP	14,135	PERV_Q4VFZ2_3mut
GSSGSSGSS	14,136	BAEVM_P10272_3mutA
GGGGSGGGGSGGGGSGGGGS	14,137	SFV1_P23074_2mut
GGGGSSEAAAK	14,138	SFV3L_P27401_2mutA
GGGGSGGGGSGGGGSGGGGS	14,139	FOAMV_P14350-Pro_2mut
PAPGSSEAAAK	14,140	MLVBM_Q7SVK7_3mutA_WS
GGGGGSGSS	14,141	MLVFF_P26809_3mutA
GGSEAAAKGGG	14,142	MLVBM_Q7SVK7_3mut
PAPGSSGGG	14,143	PERV_Q4VFZ2
GGS	14,144	PERV_Q4VFZ2_3mutA_WS
EAAAKGGSGSS	14,145	FLV_P10273_3mut
GGGEAAAK	14,146	WMSV_P03359_3mutA
GGSEAAAKPAP	14,147	MLVBM_Q7SVK7_3mut
SGSETPGTSESATPES	14,148	FOAMV_P14350-Pro_2mutA
EAAAKPAPGGS	14,149	AVIRE_P03360_3mut
EAAAKGGGGGS	14,150	KORV_Q9TTC1-Pro_3mutA
GGGGS	14,151	PERV_Q4VFZ2_3mut
GGSEAAAKGSS	14,152	MLVFF_P26809_3mutA
GGSEAAAKGGG	14,153	AVIRE_P03360
GGSGGSGGSGGSGGSGGS	14,154	SFV3L_P27401_2mut
GGSEAAAKGSS	14,155	SFV3L_P27401-Pro_2mutA
GGGEAAAKPAP	14,156	MLVCB_P08361_3mut

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
GGSEAAAK	14,157	MLVMS_P03355_PLV919
GGSPAPGSS	14,158	KORV_Q9TTC1-Pro_3mutA
GSSPAPEAAAK	14,159	WMSV_P03359_3mutA
GGSGSS	14,160	KORV_Q9TTC1-Pro_3mutA
PAPGGGGGS	14,161	AVIRE_P03360_3mut
PAPEAAAKGSS	14,162	FFV_O93209-Pro
GGSGGGEAAAK	14,163	WMSV_P03359_3mut
PAPGGG	14,164	MLVMS_P03355_3mut
EAAAKGGG	14,165	FLV_P10273_3mutA
GSSGSSGSSGSS	14,166	MLVCB_P08361_3mut
EAAAKGGSGGG	14,167	FFV_O93209
GSSPAPGGS	14,168	PERV_Q4VFZ2_3mutA_WS
GSSPAPGGS	14,169	MLVCB_P08361_3mut
GGGPAP	14,170	WMSV_P03359_3mutA
GGGPAP	14,171	KORV_Q9TTC1_3mutA
GGSPAPGSS	14,172	KORV_Q9TTC1-Pro_3mut
PAPAP	14,173	MLVMS_P03355_3mut
GGGGGGG	14,174	MLVMS_P03355_3mut
GGGGG	14,175	KORV_Q9TTC1-Pro_3mut
GSAGSAAGSGEF	14,176	FOAMV_P14350_2mutA
PAPAP	14,177	KORV_Q9TTC1-Pro_3mutA
GGSEAAAKGGG	14,178	SFV3L_P27401-Pro_2mutA
PAPAP	14,179	WMSV_P03359_3mut
GGGGSGGGGSGGGGS	14,180	SFV3L_P27401_2mut
PAPGGS	14,181	KORV_Q9TTC1_3mutA
GGGEAAAKPAP	14,182	FLV_P10273_3mut
GGGGGS	14,183	MLVAV_P03356_3mutA
GSSEAAAKGGG	14,184	WMSV_P03359_3mut
EAAAKGGGGSS	14,185	GALV_P21414_3mutA
GSSGGS	14,186	MLVAV_P03356_3mutA
GSSGGG	14,187	MLVBM_Q7SVK7_3mut
PAPAPAP	14,188	SFV3L_P27401-Pro_2mutA
GGGG	14,189	KORV_Q9TTC1_3mutA
EAAAKPAPGGS	14,190	MLVFF_P26809_3mut
GGGGSGGGGS	14,191	XMRV6_A1Z651_3mut
EAAAKGGG	14,192	MLVCB_P08361_3mut
GGGGSSPAP	14,193	KORV_Q9TTC1_3mutA
GSSEAAAKGGG	14,194	KORV_Q9TTC1-Pro_3mutA
GGGGG	14,195	BLVJ_P03361_2mutB

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
GGGEAAAKGSS	14,196	FFV_O93209-Pro
GSSGSSGSS	14,197	BAEVM_P10272_3mut
GSSGGSPAP	14,198	PERV_Q4VFZ2_3mut
EAAAKGGS	14,199	KORV_Q9TTC1_3mut
GGSPAPEAAAK	14,200	AVIRE_P03360_3mut
GGSEAAAK	14,201	WMSV_P03359_3mut
GSSGGS	14,202	KORV_Q9TTC1-Pro_3mutA
GGGPAPEAAAK	14,203	KORV_Q9TTC1_3mutA
PAPGSS	14,204	WMSV_P03359_3mutA
GGSEAAAKGSS	14,205	FLV_P10273_3mutA
EAAAKEAAAKEAAAKEAAAKEAAAK	14,206	SFV3L_P27401
GSSEAAAKGGG	14,207	SFV3L_P27401-Pro_2mutA
GGGGSEAAAKGGGGS	14,208	KORV_Q9TTC1-Pro_3mutA
GGSGGSGGS	14,209	WMSV_P03359_3mut
GGGGGSGSS	14,210	KORV_Q9TTC1-Pro
GGGGSGGGGSGGGGSGGGGS	14,211	MLVMS_P03355_3mut
EAAAKGGG	14,212	PERV_Q4VFZ2
GGSEAAAKGGG	14,213	KORV_Q9TTC1-Pro_3mut
GSSGGSGGG	14,214	PERV_Q4VFZ2_3mutA_WS
GGGGGS	14,215	PERV_Q4VFZ2_3mut
GSAGSAAGSGEF	14,216	PERV_Q4VFZ2
PAPEAAAKGSS	14,217	BAEVM_P10272_3mutA
GSSPAPGGG	14,218	MLVCB_P08361_3mut
GGGGSSPAP	14,219	KORV_Q9TTC1-Pro_3mutA
PAPGGSGGG	14,220	MLVFF_P26809_3mut
GSSPAP	14,221	KORV_Q9TTC1_3mutA
PAPGSS	14,222	SFV3L_P27401-Pro_2mut
GGSGGGGSS	14,223	MLVMS_P03355_PLV919
GSSGGS	14,224	WMSV_P03359_3mutA
EAAAKGGGGGS	14,225	PERV_Q4VFZ2
GGGGG	14,226	KORV_Q9TTC1_3mutA
EAAAKGSS	14,227	MLVMS_P03355_PLV919
EAAAKEAAAKEAAAKEAAAKEAAAK	14,228	FLV_P10273_3mut
EAAAKEAAAKEAAAKEAAAK	14,229	SFV3L_P27401-Pro_2mut
GSAGSAAGSGEF	14,230	SFV3L_P27401_2mutA
GGGPAPGGS	14,231	FLV_P10273_3mutA
GGSEAAAKGGG	14,232	MLVCB_P08361_3mut
PAPGGGEAAAK	14,233	BAEVM_P10272_3mut
EAAAKPAPGSS	14,234	FOAMV_P14350_2mut

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
GGSEAAAK	14,235	KORV_Q9TTC1_3mutA
GGSGSS	14,236	AVIRE_P03360
GGSPAPEAAAK	14,237	MLVMS_P03355_PLV919
GGGGS	14,238	XMRV6_A1Z651_3mut
GGSPAPGGG	14,239	XMRV6_A1Z651_3mut
EAAAKPAPGGS	14,240	PERV_Q4VFZ2
GSSPAP	14,241	BAEVM_P10272_3mut
GGSGSSGGG	14,242	FLV_P10273_3mutA
PAPGGG	14,243	PERV_Q4VFZ2_3mutA_WS
GSSGGSEAAAK	14,244	MLVBM_Q7SVK7_3mut
GGSEAAAK	14,245	MLVMS_P03355_3mut
GGGPAPGGS	14,246	MLVFF_P26809_3mut
GSAGSAAGSGEF	14,247	MLVBM_Q7SVK7_3mutA_WS
EAAAKPAPGGS	14,248	SFVCP_Q87040
PAPGGG	14,249	PERV_Q4VFZ2_3mutA_WS
GSSPAPEAAAK	14,250	MLVBM_Q7SVK7
PAPEAAAK	14,251	MLVBM_Q7SVK7_3mut
PAPGGGGGS	14,252	AVIRE_P03360_3mutA
GGSEAAAKPAP	14,253	MLVBM_Q7SVK7_3mut
EAAAKGSS	14,254	WMSV_P03359_3mutA
GGGEAAAK	14,255	MLVFF_P26809_3mutA
EAAAKEAAAKEAAAK	14,256	MLVMS_P03355_3mut
PAPEAAAKGGG	14,257	BAEVM_P10272_3mut
PAPAPAP	14,258	MLVCB_P08361_3mut
EAAAKPAPGGS	14,259	BAEVM_P10272_3mut
GGGGSGGGGS	14,260	FLV_P10273_3mut
GGGGSEAAAKGGGGS	14,261	KORV_Q9TTC1_3mut
EAAAK	14,262	FLV_P10273_3mut
PAPAPAP	14,263	WMSV_P03359_3mut
GGGGSEAAAKGGGGS	14,264	FFV_O93209-Pro
GGSPAPEAAAK	14,265	MLVMS_P03355_3mut
GGSGSSGGG	14,266	XMRV6_A1Z651_3mut
GGSPAPGSS	14,267	PERV_Q4VFZ2_3mut
SGGSSGGSSGSETPGTSESATPESSGGSSGGSS	14,268	SFV3L_P27401-Pro_2mutA
EAAAKGGGPAP	14,269	BAEVM_P10272_3mutA
GSSGGSEAAAK	14,270	MLVMS_P03355_3mutA_WS
SGSETPGTSESATPES	14,271	PERV_Q4VFZ2_3mutA_WS
EAAAKEAAAKEAAAKEAAAKEAAAK	14,272	KORV_Q9TTC1-Pro_3mutA
GSSGSSGSS	14,273	KORV_Q9TTC1_3mutA

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
GSSPAPGGG	14,274	SFV3L_P27401-Pro_2mutA
GSSGGGEAAAK	14,275	KORV_Q9TTC1_3mutA
GGSGGGGSS	14,276	PERV_Q4VFZ2_3mutA_WS
GSSGGGEAAAK	14,277	MLVCB_P08361_3mut
GSSEAAAKGGG	14,278	MLVCB_P08361_3mut
GGSGGGGSS	14,279	KORV_Q9TTC1_3mutA
GGSGSSPAP	14,280	PERV_Q4VFZ2_3mutA_WS
GSSPAP	14,281	MLVMS_P03355_3mut
GGGGSSEAAAK	14,282	AVIRE_P03360
GGS	14,283	WMSV_P03359_3mut
EAAAKEAAAK	14,284	PERV_Q4VFZ2_3mut
PAPAPAPAP	14,285	MLVAV_P03356_3mut
GGSEAAAKGGG	14,286	KORV_Q9TTC1_3mutA
PAPGGG	14,287	MLVAV_P03356_3mut
EAAAKGSS	14,288	BAEVM_P10272_3mut
GGGGSGGGGS	14,289	WMSV_P03359_3mutA
GGSGGSGGS	14,290	SFV3L_P27401_2mut
EAAAK	14,291	MLVCB_P08361_3mut
GGGGSSGGS	14,292	WMSV_P03359_3mutA
GGGPAPEAAAK	14,293	MLVAV_P03356_3mutA
EAAAKEAAAKEAAAK	14,294	FFV_O93209
GSSEAAAKGGG	14,295	MLVBM_Q7SVK7_3mut
GGGPAPGGS	14,296	FLV_P10273_3mut
GGSEAAAKGGG	14,297	WMSV_P03359_3mut
EAAAKGGGGS	14,298	XMRV6_A1Z651_3mutA
EAAAKGGSGGG	14,299	FLV_P10273_3mutA
GGSEAAAKGGG	14,300	SFV3L_P27401_2mutA
GGGGS	14,301	PERV_Q4VFZ2_3mutA_WS
GSSGGS	14,302	MLVMS_P03355_3mut
GSSGSS	14,303	MLVAV_P03356_3mutA
GGSPAPGGG	14,304	MLVBM_Q7SVK7_3mutA_WS
GSSGGGGGS	14,305	MLVF5_P26810_3mut
PAPAPAPAP	14,306	MLVCB_P08361_3mut
PAPAP	14,307	PERV_Q4VFZ2_3mutA_WS
PAPGSSGGS	14,308	KORV_Q9TTC1_3mut
PAPGSSGGG	14,309	PERV_Q4VFZ2_3mut
GGGEAAAK	14,310	MLVMS_P03355_PLV919
GGSGGSGGSGGSGGS	14,311	SFV3L_P27401-Pro_2mutA
GGSGGG	14,312	FLV_P10273_3mut

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
PAPEAAAKGGG	14,313	MLVFF_P26809_3mut
PAP	14,314	PERV_Q4VFZ2_3mutA_WS
PAPGGSGSS	14,315	FFV_O93209_2mut
EAAAKEAAAKEAAAKEAAAKEAAAKEAAAK	14,316	FFV_O93209-Pro_2mut
GSSGSSGSSGSS	14,317	FFV_O93209-Pro
GSSGSSGSSGSSGSS	14,318	FLV_P10273_3mutA
GGGEAAAKPAP	14,319	PERV_Q4VFZ2
PAPGSSGGG	14,320	SFV3L_P27401_2mut
PAPGGSGSS	14,321	KORV_Q9TTC1-Pro_3mut
PAPAPAPAPAP	14,322	GALV_P21414_3mutA
GGSGGGEAAAK	14,323	PERV_Q4VFZ2_3mut
GSSPAP	14,324	MLVCB_P08361_3mut
EAAAKPAP	14,325	MLVF5_P26810_3mut
GGGGSGGGGSGGGGSGGGGS	14,326	MLVBM_Q7SVK7_3mut
GGSGGG	14,327	WMSV_P03359_3mut
GGSGGSGGS	14,328	KORV_Q9TTC1_3mut
GGGGGGGG	14,329	MLVFF_P26809_3mut
GGGGSS	14,330	MLVAV_P03356_3mut
GSSGGGGGS	14,331	SFV3L_P27401_2mut
EAAAKEAAAKEAAAKEAAAKEAAAKEAAAK	14,332	GALV_P21414_3mutA
GSSGSSGSS	14,333	PERV_Q4VFZ2_3mut
GSSPAPGGS	14,334	MLVFF_P26809_3mut
PAPAPAP	14,335	AVIRE_P03360_3mutA
EAAAKEAAAKEAAAKEAAAK	14,336	WMSV_P03359_3mutA
PAPAPAPAP	14,337	SFV3L_P27401_2mutA
GGGGSS	14,338	MLVAV_P03356_3mutA
GSSGSSGSSGSSGSS	14,339	SFV3L_P27401_2mutA
PAPGGS	14,340	WMSV_P03359_3mutA
GSSEAAAKGGG	14,341	PERV_Q4VFZ2
GSSGGSPAP	14,342	MLVMS_P03355_PLV919
GSSGSSGSSGSSGSSGSS	14,343	SFV3L_P27401_2mutA
GGSGSSGGG	14,344	MLVCB_P08361_3mut
GGGPAPGSS	14,345	SFV3L_P27401-Pro_2mutA
GSSEAAAKGGS	14,346	WMSV_P03359_3mut
GSSEAAAKGGG	14,347	MLVAV_P03356_3mut
GGSGGGPAP	14,348	FFV_O93209-Pro
GSSGSS	14,349	PERV_Q4VFZ2_3mut
PAPGGGGGS	14,350	GALV_P21414_3mutA
EAAAKPAPGGS	14,351	MLVAV_P03356_3mut

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
GSSGSS	14,352	MLVMS_P03355_3mut
EAAAKPAPGGS	14,353	FFV_O93209-Pro
GGGPAPEAAAK	14,354	MLVMS_P03355_3mutA_WS
GSSEAAAKGGG	14,355	MLVBM_Q7SVK7_3mut
GGGEAAAKGGS	14,356	BAEVM_P10272_3mut
GSSGSS	14,357	KORV_Q9TTC1-Pro_3mutA
EAAAKEAAAKEAAAK	14,358	SFV1_P23074
PAPGSSGGS	14,359	KORV_Q9TTC1-Pro_3mut
PAPAPAPAPAP	14,360	MLVMS_P03355
GSSEAAAK	14,361	SFV3L_P27401_2mut
PAP	14,362	PERV_Q4VFZ2_3mut
GGSEAAAKGGG	14,363	MLVBM_Q7SVK7_3mut
GGSGGGPAP	14,364	MLVBM_Q7SVK7_3mutA_WS
GSSGSS	14,365	MLVMS_P03355_3mut
GGSEAAAK	14,366	MLVMS_P03355
GSSEAAAKGGS	14,367	MLVMS_P03355_PLV919
PAPGGGGGS	14,368	MLVFF_P26809_3mut
GSSGGG	14,369	PERV_Q4VFZ2_3mut
GSSGGS	14,370	PERV_Q4VFZ2_3mutA_WS
PAPGGG	14,371	BAEVM_P10272_3mut
PAPGSSGGG	14,372	MLVBM_Q7SVK7_3mut
GGSEAAAK	14,373	SFV3L_P27401_2mut
GSSPAPEAAAK	14,374	SFV3L_P27401-Pro_2mut
GSSGGSPAP	14,375	BAEVM_P10272_3mut
GGSPAPGSS	14,376	PERV_Q4VFZ2_3mutA_WS
GGSGGSGGS	14,377	PERV_Q4VFZ2
GGSGGGPAP	14,378	FLV_P10273_3mut
GGGPAPEAAAK	14,379	SFV3L_P27401_2mutA
GGGGS	14,380	FLV_P10273_3mutA
GSSGGSGGG	14,381	XMRV6_A1Z651_3mut
EAAAKGGGGSS	14,382	PERV_Q4VFZ2
GGSGSSGGG	14,383	SFV3L_P27401-Pro_2mutA
GGSGGSGGS	14,384	MLVFF_P26809_3mut
GGGPAPEAAAK	14,385	FLV_P10273_3mut
GSSGGGEAAAK	14,386	MLVMS_P03355_3mut
GGG	14,387	SFV3L_P27401_2mut
GSAGSAAGSGEF	14,388	WMSV_P03359_3mut
GSSGGGPAP	14,389	MLVMS_P03355_PLV919
GGGGSS	14,390	KORV_Q9TTC1-Pro_3mut

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
GGGGSSEAAAK	14,391	KORV_Q9TTC1
PAPGGSGGG	14,392	SFV3L_P27401_2mut
GSSGSSGSSGSSGSS	14,393	FFV_O93209
GSSGGSPAP	14,394	MLVMS_P03355_3mut
GGSEAAAK	14,395	KORV_Q9TTC1-Pro_3mutA
GGGGSGGGGS	14,396	BAEVM_P10272_3mut
GSSEAAAKGGG	14,397	AVIRE_P03360_3mut
EAAAKPAPGGG	14,398	FLV_P10273_3mut
EAAAKGGSPAP	14,399	SFV3L_P27401-Pro_2mutA
GSSEAAAKPAP	14,400	MLVBM_Q7SVK7_3mut
GGGPAPGGS	14,401	MLVCB_P08361_3mut
GGG	14,402	SFV3L_P27401_2mutA
EAAAKGGGGSEAAAK	14,403	SFV3L_P27401_2mutA
GGSGSSGGG	14,404	MLVBM_Q7SVK7_3mut
GSAGSAAGSGEF	14,405	BAEVM_P10272_3mut
GGGEAAAK	14,406	FOAMV_P14350_2mutA
PAPEAAAKGGS	14,407	WMSV_P03359_3mut
PAPAPAPAPAP	14,408	MLVF5_P26810_3mutA
GGSGGGGSS	14,409	FLV_P10273_3mutA
PAPGSSGGS	14,410	BAEVM_P10272_3mut
PAPEAAAK	14,411	WMSV_P03359_3mutA
GSSGSSGSSGSSGSSGSS	14,412	FFV_O93209-Pro_2mut
GGGGGSGSS	14,413	FFV_O93209-Pro
GGGGGGGG	14,414	SFV3L_P27401-Pro_2mutA
GGGGGG	14,415	FLV_P10273_3mut
GSSGGSGGG	14,416	MLVAV_P03356_3mutA
GGGGSS	14,417	SFV3L_P27401-Pro_2mutA
GGSGGGPAP	14,418	FOAMV_P14350_2mut
GSSGSS	14,419	AVIRE_P03360_3mutA
EAAAKEAAAKEAAAKEAAAKEAAAK	14,420	SFV3L_P27401-Pro_2mutA
EAAAKEAAAK	14,421	BAEVM_P10272_3mut
GSSPAPEAAAK	14,422	GALV_P21414_3mutA
GGSEAAAKPAP	14,423	SFV3L_P27401_2mutA
GGSGGGEAAAK	14,424	SFV3L_P27401-Pro_2mutA
EAAAKGSSPAP	14,425	FOAMV_P14350_2mut
GGSGSSEAAAK	14,426	SFV3L_P27401_2mut
GGG	14,427	PERV_Q4VFZ2
GGGGGSGSS	14,428	FOAMV_P14350_2mut
GGSGGGEAAAK	14,429	KORV_Q9TTC1-Pro_3mut

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
GSSGGSGGG	14,430	AVIRE_P03360_3mutA
EAAAKPAPGGG	14,431	SFV3L_P27401_2mutA
PAPGGSGGG	14,432	KORV_Q9TTC1-Pro_3mut
PAPAPAP	14,433	WMSV_P03359_3mutA
GSSEAAAKPAP	14,434	SFV1_P23074
SGGSSGGSSGSETPGTSESATPESSGGSSGGSS	14,435	SRV2_P51517
GSSGGSGGG	14,436	PERV_Q4VFZ2_3mutA_WS
GSSGSSGSSGSSGSSGSS	14,437	FFV_O93209
GSSGGGPAP	14,438	WMSV_P03359_3mut
PAPAPAPAPAPAP	14,439	MLVBM_Q7SVK7_3mut
GGGGGSPAP	14,440	KORV_Q9TTC1-Pro_3mutA
PAPGSS	14,441	MLVBM_Q7SVK7_3mutA_WS
PAPEAAAKGGS	14,442	SFV3L_P27401-Pro_2mut
GGGGSSPAP	14,443	MLVMS_P03355_3mut
GGSEAAAK	14,444	FFV_O93209-Pro
EAAAKPAPGGS	14,445	AVIRE_P03360_3mutA
PAPGSS	14,446	WMSV_P03359_3mut
PAPGSSGGG	14,447	SFV3L_P27401-Pro_2mutA
EAAAKEAAAKEAAAK	14,448	SFV3L_P27401_2mut
GGS	14,449	MLVRD_P11227_3mut
GGGGS	14,450	KORV_Q9TTC1-Pro_3mut
GGSGGGGSS	14,451	KORV_Q9TTC1
GGSGGG	14,452	MLVMS_P03355_3mutA_WS
GGGEAAAKPAP	14,453	BAEVM_P10272_3mut
EAAAKEAAAKEAAAKEAAAKEAAAK	14,454	FLV_P10273
PAPGGSGGG	14,455	KORV_Q9TTC1-Pro_3mutA
GSSGSSGSSGSSGSSGSS	14,456	HTL1L_P0C211
GGGEAAAKPAP	14,457	WMSV_P03359
GSSGGSPAP	14,458	FFV_O93209-Pro
PAPAPAPAPAP	14,459	SFV3L_P27401-Pro_2mutA
GSSGGSEAAAK	14,460	SFV3L_P27401_2mutA
GGSPAPGSS	14,461	SFV3L_P27401_2mut
GGSGGSGGS	14,462	KORV_Q9TTC1-Pro_3mut
PAPEAAAKGSS	14,463	KORV_Q9TTC1-Pro_3mut
EAAAKGGS	14,464	KORV_Q9TTC1_3mutA
EAAAKGGGGSEAAAK	14,465	SFV3L_P27401-Pro_2mut
GGGGSSPAP	14,466	FFV_O93209-Pro
EAAAK	14,467	SFV3L_P27401_2mut
EAAAKGGGGSS	14,468	BAEVM_P10272_3mut

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
GGGGGSEAAAK	14,469	MLVBM_Q7SVK7_3mut
GGGG	14,470	PERV_Q4VFZ2
GGGGGSEAAAK	14,471	FLV_P10273_3mut
EAAAKGGGPAP	14,472	KORV_Q9TTC1-Pro
GGGGSGGGGSGGGGSGGGGS	14,473	FFV_O93209_2mutA
GSSGGGSGGG	14,474	PERV_Q4VFZ2_3mut
GGGGSGGGGSGGGGS	14,475	GALV_P21414_3mutA
GGSGGGEAAAK	14,476	AVIRE_P03360_3mutA
PAPEAAAKGGG	14,477	SFV3L_P27401_2mut
GGGGSGGGGS	14,478	AVIRE_P03360
GSSGGGEAAAK	14,479	SFV3L_P27401_2mutA
GGGGG	14,480	AVIRE_P03360_3mutA
GGSGSS	14,481	KORV_Q9TTC1_3mut
PAPAPAPAPAP	14,482	FOAMV_P14350_2mut
GGSEAAAKPAP	14,483	KORV_Q9TTC1-Pro_3mut
GGGGGG	14,484	PERV_Q4VFZ2_3mut
GSSGGGEAAAK	14,485	MLVBM_Q7SVK7
SGGSSGGSSGSETPGTSESATPESSGGSSGGSS	14,486	MLVAV_P03356
GGSPAPGSS	14,487	BAEVM_P10272_3mut
GGGGSSPAP	14,488	BAEVM_P10272
GGGGSEAAAKGGGGS	14,489	SFV3L_P27401_2mut
GGGGGGGG	14,490	GALV_P21414_3mutA
PAPAP	14,491	MLVAV_P03356_3mut
GGGEAAAK	14,492	PERV_Q4VFZ2_3mutA_WS
GSSPAPGGG	14,493	FFV_O93209_2mut
GGSGGSGGSGGSGGS	14,494	BAEVM_P10272
GGGGGS	14,495	MLVF5_P26810_3mutA
PAPGGGGSS	14,496	FLV_P10273_3mutA
GGGEAAAK	14,497	MLVBM_Q7SVK7_3mut
PAPEAAAKGGG	14,498	WMSV_P03359_3mut
GSSEAAAK	14,499	MLVBM_Q7SVK7_3mut
EAAAKEAAAK	14,500	AVIRE_P03360
EAAAKGGGGGS	14,501	MLVBM_Q7SVK7_3mut
GGGEAAAKGGS	14,502	SFV3L_P27401-Pro_2mutA
PAPAPAPAPAP	14,503	MLVF5_P26810_3mut
PAPGSSEAAAK	14,504	SFV3L_P27401-Pro_2mutA
EAAAKEAAAKEAAAK	14,505	BAEVM_P10272_3mutA
GGSPAPGSS	14,506	MLVMS_P03355
PAPGSSGGS	14,507	FLV_P10273_3mutA

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
EAAAKEAAAKEAAAKEAAAK	14,508	FOAMV_P14350-Pro_2mut
EAAAKGGG	14,509	KORV_Q9TTC1_3mutA
EAAAKGGSGGG	14,510	MLVBM_Q7SVK7_3mut
GGGGGS	14,511	KORV_Q9TTC1-Pro_3mutA
PAPGGSGGG	14,512	WMSV_P03359_3mut
GGGPAPGGS	14,513	KORV_Q9TTC1_3mutA
GSS	14,514	FFV_O93209
GGSGGSGGS	14,515	PERV_Q4VFZ2_3mut
GGGGS	14,516	GALV_P21414_3mutA
GGGG	14,517	MLVF5_P26810_3mut
GGSEAAAKPAP	14,518	FFV_O93209-Pro_2mut
PAPAPAPAP	14,519	FFV_O93209-Pro
PAP	14,520	MLVF5_P26810_3mut
EAAAKEAAAKEAAAK	14,521	FFV_O93209_2mut
EAAAKGSS	14,522	MLVCB_P08361_3mut
EAAAKGGG	14,523	MLVBM_Q7SVK7_3mut
PAPEAAAKGGG	14,524	FFV_O93209_2mut
GSSGGGEAAAK	14,525	SFV1_P23074-Pro_2mut
PAPGGGEAAAK	14,526	GALV_P21414_3mutA
GGGGSGGGGSGGGGSGGGGS	14,527	FOAMV_P14350-Pro_2mutA
GSSGGG	14,528	FOAMV_P14350_2mut
GGGGSGGGGSGGGGSGGGGS	14,529	SFV3L_P27401_2mutA
GGSGSS	14,530	AVIRE_P03360_3mut
GGSGSSEAAAK	14,531	MMTVB_P03365_WS
PAPAPAP	14,532	MLVAV_P03356_3mutA
GSSGGSPAP	14,533	SFV3L_P27401-Pro_2mut
GGSPAP	14,534	AVIRE_P03360
GGSGGGPAP	14,535	FFV_O93209
GSSEAAAK	14,536	PERV_Q4VFZ2
GSSGGGPAP	14,537	PERV_Q4VFZ2_3mutA_WS
GGGGSSEAAAK	14,538	KORV_Q9TTC1_3mutA
GGSEAAAKPAP	14,539	SFVCP_Q87040
GGSGGGPAP	14,540	FOAMV_P14350_2mutA
GGGGSGGGGSGGGGSGGGGS	14,541	BLVJ_P03361_2mutB
GGGGSSPAP	14,542	SFV3L_P27401_2mutA
EAAAKGGS	14,543	MLVF5_P26810_3mut
GGSEAAAKGSS	14,544	MLVCB_P08361_3mut
GGGGSSEAAAK	14,545	SFV3L_P27401_2mut
EAAAKGGSGGG	14,546	FOAMV_P14350_2mut

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
GGSGGS	14,547	FLV_P10273_3mut
EAAAKGGG	14,548	FFV_O93209-Pro
GSSGSSGSSGSSGSS	14,549	SFV3L_P27401
GSSGGGPAP	14,550	PERV_Q4VFZ2_3mutA_WS
PAPGGSEAAAK	14,551	SFV3L_P27401-Pro_2mutA
GGSPAP	14,552	KORV_Q9TTC1
EAAAKPAPGSS	14,553	KORV_Q9TTC1_3mutA
SGSETPGTSESATPES	14,554	SFV1_P23074
GSSPAP	14,555	SFV3L_P27401-Pro_2mutA
GSSPAPGGG	14,556	SFV3L_P27401_2mut
GGGEAAAKGSS	14,557	SFV1_P23074_2mut
GGGPAPGGS	14,558	BAEVM_P10272_3mut
EAAAKGGG	14,559	KORV_Q9TTC1-Pro_3mutA
GSSGGG	14,560	SFV3L_P27401-Pro_2mut
GGSPAPEAAAK	14,561	BAEVM_P10272_3mut
EAAAKGSSPAP	14,562	FFV_O93209
EAAAKGGGGSEAAAK	14,563	SFV3L_P27401-Pro_2mutA
GSSGSSGSSGSSGSS	14,564	SFV1_P23074_2mut
EAAAKGGSPAP	14,565	FOAMV_P14350_2mut
GGSGGS	14,566	KORV_Q9TTC1-Pro_3mutA
EAAAKGSSGGS	14,567	GALV_P21414
GSSGGGPAP	14,568	MLVAV_P03356
PAPEAAAKGGS	14,569	FOAMV_P14350_2mut
EAAAKPAPGGG	14,570	AVIRE_P03360_3mut
GGSPAP	14,571	SFV3L_P27401_2mutA
GGGGSGGGGS	14,572	SFV3L_P27401_2mutA
GGGGSS	14,573	AVIRE_P03360_3mutA
GGSPAPGGG	14,574	SFV3L_P27401-Pro_2mutA
EAAAKPAPGSS	14,575	SFV3L_P27401
EAAAKPAP	14,576	FOAMV_P14350-Pro_2mut
PAPEAAAKGSS	14,577	PERV_Q4VFZ2_3mutA_WS
EAAAKGGSGSS	14,578	SFV3L_P27401_2mutA
GGGEAAAKGSS	14,579	GALV_P21414_3mutA
GGGGSEAAAKGGGGS	14,580	PERV_Q4VFZ2_3mut
PAPGGSGSS	14,581	FFV_O93209-Pro_2mutA
GGSEAAAKPAP	14,582	GALV_P21414_3mutA
GGSGGSGGSGGSGGS	14,583	FFV_O93209-Pro
GSSGGSEAAAK	14,584	SFV3L_P27401-Pro_2mut
GGS	14,585	GALV_P21414_3mutA

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
PAPGGSEAAAK	14,586	MLVMS_P03355
PAPEAAAKGGS	14,587	BAEVM_P10272_3mutA
GGSGSSPAP	14,588	SFV3L_P27401-Pro_2mutA
GSSPAP	14,589	WMSV_P03359_3mut
GGGEAAAK	14,590	MMTVB_P03365
GGGGSS	14,591	PERV_Q4VFZ2_3mut
GGSPAPGSS	14,592	SFV3L_P27401-Pro_2mut
PAPGGS	14,593	MLVBM_Q7SVK7_3mut
EAAAKGSSPAP	14,594	MLVBM_Q7SVK7_3mut
GGGGSSGGS	14,595	PERV_Q4VFZ2_3mut
PAPAPAPAPAPAP	14,596	SFV1_P23074
GGSEAAAKGGG	14,597	SFV3L_P27401-Pro_2mut
GGSGGS	14,598	SFV1_P23074_2mut
GSSGGGGGS	14,599	MLVF5_P26810_3mutA
EAAAKGGGPAP	14,600	SFV3L_P27401
EAAAKEAAAKEAAAKEAAAK	14,601	FOAMV_P14350-Pro_2mutA
GGGPAPGSS	14,602	SFV3L_P27401_2mutA
GGGGSGGGGSGGGGSGGGGS	14,603	SFV3L_P27401_2mut
EAAAKEAAAKEAAAKEAAAK	14,604	MMTVB_P03365_WS
PAPGSSGGS	14,605	KORV_Q9TTC1-Pro_3mutA
PAPGSSEAAAK	14,606	FOAMV_P14350-Pro_2mut
GSSPAPEAAAK	14,607	BAEVM_P10272_3mut
EAAAKGGGGSEAAAK	14,608	FFV_O93209-Pro
GGSPAP	14,609	PERV_Q4VFZ2
GGSGSSEAAAK	14,610	XMRV6_A1Z651_3mut
GGSEAAAKGGG	14,611	GALV_P21414_3mutA
PAPGGGGSS	14,612	AVIRE_P03360_3mutA
GGSGGSGGSGGS	14,613	PERV_Q4VFZ2
GGGGSSGGS	14,614	PERV_Q4VFZ2_3mutA_WS
SGGSSGGSSGSETPGTSESATPESSGGSSGGSS	14,615	BAEVM_P10272_3mutA
GGGPAP	14,616	MLVAV_P03356_3mut
GGGGSGGGGSGGGGSGGGGS	14,617	FFV_O93209_2mut
GSSEAAAK	14,618	FFV_O93209
GGSPAPEAAAK	14,619	FOAMV_P14350_2mut
GGGGGSEAAAK	14,620	FOAMV_P14350_2mut
GSSPAPGGS	14,621	MLVBM_Q7SVK7_3mut
GSS	14,622	SFVCP_Q87040_2mut
EAAAKPAP	14,623	FOAMV_P14350-Pro
EAAAKGGG	14,624	SFV3L_P27401_2mut

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
GGGEAAAK	14,625	AVIRE_P03360_3mutA
PAPGSSGGG	14,626	WMSV_P03359_3mut
EAAAKGGSPAP	14,627	SFV3L_P27401
GSSGGSGGG	14,628	SFV3L_P27401-Pro_2mutA
GSSGGGEAAAK	14,629	GALV_P21414_3mutA
GGGPAPGSS	14,630	MLVBM_Q7SVK7_3mutA_WS
PAPGGGEAAAK	14,631	FFV_O93209-Pro_2mut
GSSGSSGSSGSS	14,632	SFV1_P23074_2mut
GGSEAAAK	14,633	PERV_Q4VFZ2_3mutA_WS
GGGEAAAKPAP	14,634	SFV3L_P27401_2mut
EAAAKGGGPAP	14,635	SFV3L_P27401_2mut
GGGGSSPAP	14,636	FLV_P10273_3mut
EAAAKPAPGSS	14,637	FFV_O93209_2mut
GGGGSSPAP	14,638	SFV3L_P27401_2mut
GSSGSS	14,639	KORV_Q9TTC1_3mutA
GGGGSGGGGSGGGGSGGGGSGGGGS	14,640	BLVJ_P03361_2mut
GGGGSSGGS	14,641	GALV_P21414_3mutA
EAAAKGGSGSS	14,642	FFV_O93209-Pro
EAAAKPAP	14,643	PERV_Q4VFZ2
GSSGGGEAAAK	14,644	MLVBM_Q7SVK7_3mut
PAPGGSGGG	14,645	BAEVM_P10272
EAAAKGGGPAP	14,646	MLVF5_P26810
GSSGSSGSS	14,647	MLVBM_Q7SVK7_3mut
GSSGGS	14,648	AVIRE_P03360_3mutA
GGSEAAAKGGG	14,649	FOAMV_P14350_2mut
EAAAKGGS	14,650	MLVF5_P26810_3mutA
GGSGSSGGG	14,651	WMSV_P03359_3mut
EAAAK	14,652	SFV1_P23074_2mut
GSSGGSPAP	14,653	SFV3L_P27401-Pro_2mutA
GGGGSSGGS	14,654	KORV_Q9TTC1_3mut
PAPGGSGGG	14,655	FFV_O93209-Pro_2mut
GGGPAPGGS	14,656	SFV3L_P27401_2mutA
GSSPAPEAAAK	14,657	FLV_P10273_3mut
GGSGSSPAP	14,658	SFV3L_P27401_2mut
GSSEAAAKGGS	14,659	SFV3L_P27401_2mut
PAPGGG	14,660	SFV3L_P27401_2mutA
SGSETPGTSESATPES	14,661	KORV_Q9TTC1-Pro_3mut
GGGGS	14,662	SFV1_P23074-Pro_2mutA
GSSGGGEAAAK	14,663	WMSV_P03359

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
EAAAKGGGGSEAAAK	14,664	MLVF5_P26810_3mutA
GSSEAAAKPAP	14,665	FFV_O93209
GGGGGG	14,666	SFV1_P23074_2mutA
EAAAKEAAAKEAAAK	14,667	MMTVB_P03365-Pro
EAAAKPAPGSS	14,668	MLVBM_Q7SVK7_3mut
GGSGSSEAAAK	14,669	SFV3L_P27401_2mutA
GGSEAAAK	14,670	MLVMS_P03355_3mut
GGSPAPEAAAK	14,671	SFV3L_P27401_2mut
GGGPAPGSS	14,672	SFV1_P23074
GGGGGSEAAAK	14,673	MLVBM_Q7SVK7_3mutA_WS
EAAAKPAPGSS	14,674	KORV_Q9TTC1-Pro
GSSGSSGSSGSS	14,675	SFV3L_P27401_2mut
EAAAKPAP	14,676	SFV3L_P27401_2mut
GGGEAAAK	14,677	PERV_Q4VFZ2_3mut
GGSGGS	14,678	SFV3L_P27401_2mutA
EAAAKGSSGGS	14,679	MMTVB_P03365
SGSETPGTSESATPES	14,680	SFV3L_P27401
EAAAKGSSGGG	14,681	PERV_Q4VFZ2
EAAAKEAAAKEAAAKEAAAKEAAAKEAAAK	14,682	MMTVB_P03365
GGSGGGPAP	14,683	KORV_Q9TTC1_3mutA
PAPAPAPAP	14,684	SFV3L_P27401
GGGEAAAKGGS	14,685	SFV1_P23074_2mut
GSSGGSGGG	14,686	PERV_Q4VFZ2_3mut
PAPEAAAKGGS	14,687	FOAMV_P14350_2mutA
GGGEAAAKGSS	14,688	SFV3L_P27401_2mut
GGGGSGGGGSGGGGSGGGGS	14,689	MLVBM_Q7SVK7
PAPGSSGGG	14,690	FLV_P10273
GGSGSSGGG	14,691	FFV_O93209
EAAAKPAPGSS	14,692	MLVBM_Q7SVK7
GSSEAAAKGGG	14,693	SFV3L_P27401_2mutA
GGSGGSGGSGGSGGS	14,694	MLVF5_P26810
GGSEAAAKPAP	14,695	SFV3L_P27401-Pro_2mutA
EAAAKGGSPAP	14,696	SFV3L_P27401_2mutA
EAAAKGGGGGS	14,697	SFV3L_P27401_2mut
GSSPAPEAAAK	14,698	SFV3L_P27401_2mutA
PAPAP	14,699	MLVBM_Q7SVK7_3mut
PAPGGSEAAAK	14,700	KORV_Q9TTC1-Pro
GGSGSS	14,701	MLVF5_P26810_3mutA
GGSEAAAKPAP	14,702	FFV_O93209_2mut

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
GSS	14,703	MLVMS_P03355
SGGSSGGSSGSETPGTSESATPESSGGSSGGSS	14,704	SFV3L_P27401-Pro
PAPGGGEAAAK	14,705	SFV3L_P27401_2mut
PAPGGGGGS	14,706	SFV3L_P27401-Pro_2mut
PAPGGSGSS	14,707	BAEVM_P10272_3mut
GSSGGGEAAAK	14,708	FFV_O93209
GGSEAAAKPAP	14,709	SFV1_P23074_2mut
GGGGG	14,710	FLV_P10273_3mut
GGGEAAAKGSS	14,711	SFV3L_P27401
GSSGSSGSSGSSGSS	14,712	SFV1_P23074-Pro
SGSETPGTSESATPES	14,713	AVIRE_P03360
PAPGSSGGG	14,714	MLVBM_Q7SVK7_3mut
GGGGSSPAP	14,715	HTL3P_Q4U0X6_2mut
GGGEAAAK	14,716	SFV1_P23074
GGSGGG	14,717	AVIRE_P03360
EAAAKGSSGGG	14,718	SFV3L_P27401_2mutA
GSSPAPEAAAK	14,719	FOAMV_P14350-Pro_2mutA
GGGPAPGSS	14,720	WMSV_P03359
EAAAKGSSGGG	14,721	MLVMS_P03355
GGGGGSEAAAK	14,722	MLVMS_P03355
EAAAKPAPGGS	14,723	SFV3L_P27401
EAAAKGSSPAP	14,724	SFV3L_P27401
GGGGGGG	14,725	FOAMV_P14350_2mutA
EAAAKEAAAKEAAAK	14,726	SFV3L_P27401
GSSPAPGGS	14,727	FFV_O93209_2mutA
GGGGSSEAAAK	14,728	SFV3L_P27401-Pro_2mutA
GGSEAAAKGSS	14,729	GALV_P21414_3mutA
GGSEAAAKGSS	14,730	BAEVM_P10272_3mutA
EAAAKPAPGGG	14,731	MLVCB_P08361
GSSGSSGSSGSSGSSGSS	14,732	SFV1_P23074-Pro
GGGGSEAAAKGGGGS	14,733	FOAMV_P14350_2mut
GSSPAPGGS	14,734	MLVMS_P03355_PLV919
GGGGSGGGGS	14,735	FFV_O93209-Pro
GSSGGSPAP	14,736	KORV_Q9TTC1_3mutA
GGSGGS	14,737	GALV_P21414_3mutA
PAPGSSEAAAK	14,738	WMSV_P03359
PAPGGGGSS	14,739	MMTVB_P03365-Pro
GGGGSSGGS	14,740	PERV_Q4VFZ2_3mutA_WS
GGGGSGGGGS	14,741	FFV_O93209_2mut

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
GGGGSGGGGSGGGGSGGGGS	14,742	XMRV6_A1Z651
GGSGSSEAAAK	14,743	SFV1_P23074_2mut
GGSGGGGSS	14,744	GALV_P21414_3mutA
GGSEAAAKPAP	14,745	MLVBM_Q7SVK7
EAAAKGGSPAP	14,746	SFV1_P23074_2mutA
PAPAPAPAP	14,747	FFV_O93209
GSSGGSPAP	14,748	MMTVB_P03365-Pro
GGGGGSPAP	14,749	KORV_Q9TTC1_3mutA
EAAAKGGGPAP	14,750	PERV_Q4VFZ2
GSSGGSPAP	14,751	BAEVM_P10272
GGGGG	14,752	FFV_O93209
GGGGGS	14,753	FLV_P10273_3mutA
EAAAKEAAAKEAAAK	14,754	FOAMV_P14350
PAPGGG	14,755	MLVCB_P08361_3mut
GSSGGSEAAAK	14,756	FOAMV_P14350_2mutA
GGSPAPGGG	14,757	FLV_P10273_3mut
GSSGSSGSSGSSGSSGSS	14,758	SFV1_P23074-Pro_2mutA
GGSPAPEAAAK	14,759	SFV3L_P27401
PAPGGGGSS	14,760	HTL3P_Q4U0X6_2mutB
GGGGSSEAAAK	14,761	MMTVB_P03365_2mut_WS
PAPGGS	14,762	MLVRD_P11227_3mut
GGSGGSGGSGGSGGS	14,763	MMTVB_P03365
GSAGSAAGSGEF	14,764	AVIRE_P03360
GSSGGS	14,765	BAEVM_P10272_3mutA
GGSGGGGSS	14,766	MMTVB_P03365
GGSGGGGSS	14,767	WMSV_P03359
PAPEAAAKGSS	14,768	SFV1_P23074
GSSGSSGSSGSS	14,769	SFV1_P23074-Pro_2mutA
PAPAPAPAPAPAP	14,770	SFV3L_P27401
PAPGSSGGG	14,771	FLV_P10273_3mut
GGSGSSPAP	14,772	MLVMS_P03355
GGSGGGPAP	14,773	FOAMV_P14350
PAPGGGGGS	14,774	KORV_Q9TTC1_3mutA
EAAAKGSSPAP	14,775	GALV_P21414_3mutA
GGSGSSPAP	14,776	MLVBM_Q7SVK7_3mut
EAAAKGSS	14,777	SFV3L_P27401_2mut
GGGGGSEAAAK	14,778	WMSV_P03359
GGGGGGGG	14,779	SFV1_P23074-Pro
EAAAKEAAAK	14,780	MLVBM_Q7SVK7

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
GGGEAAAKGGS	14,781	MLVBM_Q7SVK7
EAAAKGGSPAP	14,782	SFV3L_P27401_2mut
GSSEAAAK	14,783	XMRV6_A1Z651
PAPGGGEAAAK	14,784	MMTVB_P03365_WS
GGSPAP	14,785	GALV_P21414_3mutA
GSSPAPGGG	14,786	MLVBM_Q7SVK7_3mutA_WS
GGSGSSPAP	14,787	SFV1_P23074_2mutA
GGS	14,788	HTL32_Q0R5R2_2mut
GGSGGGGSS	14,789	MMTVB_P03365-Pro
GGGGSGGGGSGGGGSGGGGS	14,790	SFVCP_Q87040_2mutA
EAAAKGGGPAP	14,791	FOAMV_P14350_2mut
GSSGGGEAAAK	14,792	MMTVB_P03365
SGGSSGGSSGSETPGTSESATPESSGGSSGGSS	14,793	MLVBM_Q7SVK7_3mutA_WS
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	14,794	MMTVB_P03365_WS
EAAAKEAAAK	14,795	FOAMV_P14350-Pro_2mut
GSSPAPEAAAK	14,796	FOAMV_P14350_2mutA
EAAAKPAPGGS	14,797	GALV_P21414_3mutA
GSSGGSPAP	14,798	KORV_Q9TTC1-Pro_3mut
GGGPAPEAAAK	14,799	MLVAV_P03356
GGGEAAAKPAP	14,800	SFV1_P23074-Pro_2mut
GGGGGSEAAAK	14,801	SFV3L_P27401_2mut
GGGPAPGSS	14,802	SFV3L_P27401_2mut
GGSEAAAKPAP	14,803	AVIRE_P03360
GSSGSSGSSGSSGSSGSS	14,804	SFV1_P23074-Pro_2mut
EAAAKGSSGGS	14,805	FOAMV_P14350_2mutA
GGGGGG	14,806	MLVBM_Q7SVK7_3mut
GSSPAPGGS	14,807	PERV_Q4VFZ2
GGSGSSPAP	14,808	GALV_P21414_3mutA
GGGPAPEAAAK	14,809	SFV3L_P27401
GGSGGGEAAAK	14,810	WMSV_P03359
GSAGSAAGSGEF	14,811	SFV1_P23074_2mut
GSSGGGEAAAK	14,812	MLVMS_P03355
GGG	14,813	MMTVB_P03365-Pro
PAPGSSGGS	14,814	FOAMV_P14350_2mut
GGGGSSPAP	14,815	FFV_O93209_2mut
SGGSSGGSSGSETPGTSESATPESSGGSSGGSS	14,816	MMTVB_P03365_WS
GGGGGGG	14,817	XMRV6_A1Z651
PAPAPAPAPAP	14,818	FOAMV_P14350
GGGGSGGGGSGGGGSGGGGS	14,819	MMTVB_P03365_2mut_WS

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
GGSGGGPAP	14,820	SFV3L_P27401_2mut
GGGGGG	14,821	SFV1_P23074-Pro
EAAAKPAPGSS	14,822	SFV3L_P27401_2mut
GGGGSSGGS	14,823	HTL3P_Q4U0X6_2mut
PAPGSSEAAAK	14,824	MMTVB_P03365-Pro
GGGGSSPAP	14,825	FOAMV_P14350-Pro_2mut
PAPGSSGGS	14,826	MMTVB_P03365
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	14,827	SRV2_P51517
PAPAPAP	14,828	MMTVB_P03365_2mut_WS
PAPGGGGGS	14,829	MMTVB_P03365_2mutB
GGGGSS	14,830	SFV1_P23074-Pro_2mutA
EAAAKEAAAKEAAAKEAAAK	14,831	SFV3L_P27401-Pro
GGSGGSGGSGGSGGS	14,832	MMTVB_P03365-Pro
GGGGGGG	14,833	SFV3L_P27401_2mut
PAPGGGEAAAK	14,834	SFV3L_P27401
PAPGSS	14,835	FOAMV_P14350_2mutA
GGGGSGGGGS	14,836	SFVCP_Q87040_2mutA
GSSGGSGGG	14,837	XMRV6_A1Z651
GGGGSGGGGSGGGGSGGGGSGGGGSGGGGS	14,838	MLVBM_Q7SVK7
GSSEAAAKGGG	14,839	FFV_O93209-Pro_2mut
GGSEAAAKPAP	14,840	SFV3L_P27401-Pro
GSSGGSGGG	14,841	SFV1_P23074_2mut
EAAAKGGGGSS	14,842	FOAMV_P14350_2mutA
GGGGGG	14,843	SFV3L_P27401_2mut
GGGGG	14,844	MLVBM_Q7SVK7_3mut
PAPEAAAKGGG	14,845	SFV3L_P27401
EAAAKGGSPAP	14,846	KORV_Q9TTC1_3mutA
GGGEAAAKPAP	14,847	SFV1_P23074_2mut
GSSGSSGSSGSSGSSGSS	14,848	KORV_Q9TTC1-Pro
EAAAKEAAAKEAAAKEAAAK	14,849	SFVCP_Q87040
PAPGSSEAAAK	14,850	MLVBM_Q7SVK7
GSSGSSGSS	14,851	FFV_O93209-Pro_2mut
GSSGGGPAP	14,852	SFV3L_P27401-Pro_2mut
GGGPAPEAAAK	14,853	WMSV_P03359_3mut
GGGEAAAK	14,854	MMTVB_P03365-Pro
GSSGSSGSSGSS	14,855	SFV3L_P27401-Pro_2mutA
PAPAPAPAPAP	14,856	FFV_O93209-Pro
GGSPAPEAAAK	14,857	FFV_O93209-Pro_2mut
GSSGSSGSSGSSGSSGSS	14,858	GALV_P21414

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
EAAAKEAAAKEAAAKEAAAKEAAAK	14,859	FOAMV_P14350
GGGPAPEAAAK	14,860	MMTVB_P03365-Pro
PAPGGSGGG	14,861	MLVF5_P26810_3mutA
PAPGGSGGG	14,862	FLV_P10273_3mut
GGGEAAAKGGS	14,863	SFV3L_P27401
GSAGSAAGSGEF	14,864	MLVBM_Q7SVK7_3mut
GSSPAPGGG	14,865	MPMV_P07572_2mutB
GSSGSSGSSGSSGSSGSS	14,866	FOAMV_P14350
GGSGGGGSS	14,867	BLVJ_P03361_2mut
PAPEAAAKGSS	14,868	SFV1_P23074-Pro
GGG	14,869	FFV_O93209
EAAAKGGGGSS	14,870	SFV1_P23074_2mut
EAAAKEAAAKEAAAKEAAAKEAAAKEAAAK	14,871	SRV2_P51517
GGGGSGGGGSGGGGSGGGGSGGGGSGGGGS	14,872	MMTVB_P03365
GGGEAAAKGGS	14,873	MMTVB_P03365_WS
GSSGSS	14,874	SFV1_P23074
GSSGGGGGS	14,875	SFV3L_P27401
GGGGSSEAAAK	14,876	SFV1_P23074
EAAAKGSSGGS	14,877	HTL1A_P03362_2mutB
GSSEAAAKGGS	14,878	GALV_P21414_3mutA
EAAAKGSSPAP	14,879	SFV1_P23074
EAAAKPAPGSS	14,880	SFV3L_P27401_2mutA
PAPGSSGGG	14,881	SFV3L_P27401-Pro_2mut
GGGGSGGGGSGGGGSGGGGSGGGGSGGGGS	14,882	SFV3L_P27401-Pro
EAAAKEAAAKEAAAKEAAAKEAAAK	14,883	MMTVB_P03365_WS
GGGGSSEAAAK	14,884	MLVF5_P26810_3mutA
EAAAKGGSPAP	14,885	GALV_P21414
PAPEAAAKGSS	14,886	MMTVB_P03365_WS
GSSGGGGGS	14,887	SFVCP_Q87040_2mut
GGGGSSPAP	14,888	SFV1_P23074
EAAAKGGGGSS	14,889	XMRV6_A1Z651
PAPAPAPAP	14,890	MMTVB_P03365
GGSEAAAKGSS	14,891	SFV3L_P27401_2mutA
GSSPAPGGG	14,892	MMTVB_P03365_WS
GGGGGG	14,893	SFV3L_P27401-Pro
GGSGGSGGS	14,894	FOAMV_P14350-Pro_2mut
PAPAPAPAPAP	14,895	WMSV_P03359
GSSPAP	14,896	MLVBM_Q7SVK7
GGGGGSGSS	14,897	MMTVB_P03365_2mut_WS

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
EAAAKGSSGGS	14,898	MMTVB_P03365_2mutB_WS
EAAAK	14,899	FFV_O93209_2mutA
PAPEAAAK	14,900	SFV1_P23074-Pro
EAAAKGGSGSS	14,901	SFV3L_P27401
GGSGGSGGS	14,902	FFV_O93209-Pro
GSSGGGEAAAK	14,903	MMTVB_P03365
SGGSSGGSSGSETPGTSESATPESSGGSSGGSS	14,904	MLVFF_P26809_3mutA
GGSGGSGGSGGSGGSGGS	14,905	HTL1L_P0C211_2mutB
GGGEAAAK	14,906	SFV3L_P27401-Pro_2mutA
GGGGGSGSS	14,907	MMTVB_P03365
GSSPAPGGS	14,908	FOAMV_P14350_2mutA
EAAAKGSS	14,909	MLVMS_P03355
GSSGGSGGG	14,910	FFV_O93209-Pro
GGSGGGGSS	14,911	MMTVB_P03365-Pro_2mut
GGSPAPGSS	14,912	FOAMV_P14350_2mut
GGSGGSGGSGGSGGSGGS	14,913	SFVCP_Q87040-Pro_2mut
GSSEAAAKGGG	14,914	FOAMV_P14350_2mutA
GGSGGSGGS	14,915	MMTVB_P03365-Pro
GSSGSSGSSGSSGSSGSS	14,916	MMTVB_P03365_2mut_WS
GSSGSSGSSGSSGSS	14,917	MMTVB_P03365-Pro
PAPEAAAK	14,918	WDSV_O92815
GSSGSSGSSGSSGSS	14,919	FFV_O93209-Pro_2mut
EAAAKGGGGSEAAAK	14,920	MMTVB_P03365-Pro
GGSPAPEAAAK	14,921	FOAMV_P14350
GSSGSS	14,922	PERV_Q4VFZ2
GGG	14,923	MMTVB_P03365-Pro
GGGGSGGGGSGGGGS	14,924	FFV_O93209_2mut
EAAAKEAAAKEAAAKEAAAKEAAAKEAAAK	14,925	MMTVB_P03365-Pro
GGSGSSPAP	14,926	WMSV_P03359
GGGGGGGG	14,927	SFV3L_P27401_2mut
PAPGSSEAAAK	14,928	FOAMV_P14350-Pro_2mutA
GGGGSSPAP	14,929	FOAMV_P14350_2mut
GSSGGSPAP	14,930	MLVBM_Q7SVK7_3mut
GSSGGGGGS	14,931	GALV_P21414_3mutA
EAAAKEAAAKEAAAKEAAAKEAAAK	14,932	MMTVB_P03365
GSSGGGGGS	14,933	SFV1_P23074_2mut
GGGGSEAAAKGGGGS	14,934	SFV1_P23074
GGGEAAAKPAP	14,935	FFV_O93209
PAPGGGEAAAK	14,936	SFV1_P23074

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
GGSGGGEAAAK	14,937	PERV_Q4VFZ2_3mutA_WS
GSSGGG	14,938	MMTVB_P03365-Pro
EAAAKGSSGGS	14,939	FFV_O93209_2mut
GGGGG	14,940	SFV1_P23074_2mut
GGGPAP	14,941	SFV3L_P27401
GSSGGSEAAAK	14,942	FFV_O93209
SGGSSGGSSGSETPGTSESATPESSGGSSGGSS	14,943	MMTVB_P03365-Pro
GSSGGGEAAAK	14,944	SFV1_P23074_2mutA
GSSGSSGSSGSSGSS	14,945	SFV3L_P27401_2mut
GGSEAAAKPAP	14,946	FLV_P10273
GGGGSGGGGS	14,947	FOAMV_P14350-Pro_2mutA
GSSEAAAKPAP	14,948	SFV3L_P27401
GGGGSEAAAKGGGGS	14,949	MMTVB_P03365-Pro
PAPGSSEAAAK	14,950	MLVF5_P26810_3mut
EAAAKGGSGGG	14,951	SFV3L_P27401
GGGPAPGGS	14,952	SFV3L_P27401
GSSEAAAKGGS	14,953	FOAMV_P14350_2mutA
EAAAKGGSGGG	14,954	HTL1L_P0C211
GSSGGSPAP	14,955	SFV3L_P27401_2mutA
PAPAP	14,956	FFV_O93209
PAPGGSGSS	14,957	MMTVB_P03365_WS
EAAAKGGGGGS	14,958	FOAMV_P14350_2mut
PAPEAAAKGGS	14,959	SFV3L_P27401_2mut
GSSEAAAKPAP	14,960	MMTVB_P03365-Pro
GGSGGS	14,961	PERV_Q4VFZ2_3mut
GSSEAAAKGGG	14,962	FFV_O93209-Pro_2mutA
EAAAK	14,963	HTL1L_P0C211
GSSPAP	14,964	MLVMS_P03355
EAAAKPAPGGG	14,965	FFV_O93209-Pro_2mut
GGGGSEAAAKGGGGS	14,966	SFV1_P23074-Pro_2mut
EAAAKGSSGGS	14,967	SFV3L_P27401
GSAGSAAGSGEF	14,968	FFV_O93209_2mutA
PAPEAAAKGGS	14,969	MMTVB_P03365_2mutB_WS
EAAAKEAAAKEAAAKEAAAKEAAAKEAAAK	14,970	MMTVB_P03365
GGS	14,971	MMTVB_P03365
GGSEAAAKPAP	14,972	SFV1_P23074
EAAAKGSSGGG	14,973	HTLV2_P03363_2mut
GGSEAAAKGGG	14,974	MMTVB_P03365_WS
GGSGGS	14,975	FFV_O93209-Pro

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
GSSEAAAKGGS	14,976	MMTVB_P03365-Pro
PAPAPAPAPAP	14,977	SFV1_P23074_2mutA
GGSEAAAKGGG	14,978	MMTVB_P03365_2mutB_WS
PAPAPAPAP	14,979	MMTVB_P03365_WS
GGGGSGGGGSGGGGSGGGGSGGGGS	14,980	HTL3P_Q4U0X6_2mut
PAPGGSEAAAK	14,981	SFV1_P23074-Pro_2mut
GGSGGGPAP	14,982	MMTVB_P03365
GSSGSSGSSGSSGSSGSS	14,983	MMTVB_P03365-Pro
GGSEAAAKPAP	14,984	SFV1_P23074-Pro
GGGEAAAKGSS	14,985	SFV3L_P27401_2mutA
GGGPAPGGS	14,986	AVIRE_P03360
PAPGGG	14,987	MLVRD_P11227
GGSEAAAKGSS	14,988	SFV3L_P27401_2mut
GGGEAAAKGSS	14,989	FOAMV_P14350_2mut
GGGEAAAKGSS	14,990	SFV1_P23074-Pro
EAAAKEAAAKEAAAKEAAAK	14,991	MLVAV_P03356
EAAAKGGGPAP	14,992	JSRV_P31623_2mutB
EAAAKGGGGSS	14,993	FOAMV_P14350_2mut
EAAAKEAAAKEAAAKEAAAKEAAAK	14,994	SRV2_P51517
GSSGGGGGS	14,995	FFV_O93209
PAPAPAP	14,996	FOAMV_P14350_2mutA
GGSGGSGGSGGS	14,997	FOAMV_P14350
GGGEAAAK	14,998	MMTVB_P03365_WS
GGGGGS	14,999	SFV1_P23074_2mutA
GGSGGS	15,000	WMSV_P03359_3mut
EAAAKGGS	15,001	MMTVB_P03365-Pro
GGGGSS	15,002	BLVJ_P03361_2mut
PAPAP	15,003	MMTVB_P03365-Pro_2mut
PAPGGG	15,004	SMRVH_P03364
EAAAKGGGGSS	15,005	SFV3L_P27401
PAPAPAPAPAP	15,006	MMTVB_P03365
GGGPAP	15,007	MMTVB_P03365-Pro
GSSGGSGGG	15,008	MMTVB_P03365
EAAAKGGGPAP	15,009	FOAMV_P14350_2mutA
GSSGSSGSSGSS	15,010	SFV1_P23074
GGGGSGGGGS	15,011	SFV3L_P27401
GSSGGSGGG	15,012	MLVF5_P26810
GGGEAAAKPAP	15,013	MMTVB_P03365-Pro
PAPEAAAK	15,014	HTLV2_P03363_2mut

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
GSSGSSGSSGSS	15,015	FOAMV_P14350_2mut
GSSEAAAKPAP	15,016	MMTVB_P03365-Pro
PAPEAAAKGGG	15,017	HTL3P_Q4U0X6_2mut
GGSEAAAKGSS	15,018	MMTVB_P03365-Pro
EAAAKPAPGGS	15,019	MMTVB_P03365_2mut_WS
GSSGGSEAAAK	15,020	MLVF5_P26810_3mutA
GGGGSGGGGSGGGGSGGGGSGGGGSGGGGS	15,021	MLVF5_P26810_3mut
EAAAKGGGGSS	15,022	MMTVB_P03365-Pro
GGGGGSGSS	15,023	HTL1A_P03362_2mutB
PAPAP	15,024	FFV_O93209-Pro_2mut
GGGGGSPAP	15,025	HTL1C_P14078_2mut
GGGPAP	15,026	HTLV2_P03363_2mut
EAAAKGGGGSEAAAK	15,027	SFVCP_Q87040
GGSEAAAKGGG	15,028	FFV_O93209-Pro_2mutA
GSSPAPGGS	15,029	FOAMV_P14350-Pro_2mut
GGGGGGG	15,030	MMTVB_P03365-Pro
EAAAKGSS	15,031	SFV3L_P27401_2mutA
EAAAKGGGGSEAAAK	15,032	MMTVB_P03365-Pro
GGGGSEAAAKGGGGS	15,033	SFV1_P23074-Pro_2mutA
EAAAKGGGGSS	15,034	MMTVB_P03365
GGGEAAAKGGS	15,035	SFV1_P23074
PAPEAAAKGGG	15,036	MLVF5_P26810
GGGGSSGGS	15,037	MMTVB_P03365
GGSGSS	15,038	MMTVB_P03365
PAPAPAPAPAPAP	15,039	KORV_Q9TTC1
EAAAKGGG	15,040	SFV1_P23074-Pro_2mut
PAPAPAPAPAPAP	15,041	SRV2_P51517
GSSGSSGSSGSSGSS	15,042	FFV_O93209-Pro_2mutA
GGGGSS	15,043	FOAMV_P14350_2mut
PAPGGGEAAAK	15,044	MMTVB_P03365_WS
GGSGGGEAAAK	15,045	FFV_O93209-Pro_2mut
PAPAPAPAPAP	15,046	MMTVB_P03365_WS
GGGEAAAKGGS	15,047	MMTVB_P03365-Pro
GGGEAAAKGSS	15,048	MMTVB_P03365_2mutB
GSSPAPEAAAK	15,049	MMTVB_P03365_WS
EAAAKEAAAKEAAAKEAAAKEAAAK	15,050	SFV1_P23074-Pro_2mutA
PAPGGG	15,051	SFV3L_P27401
GSSEAAAKGGG	15,052	MMTVB_P03365_WS
GGGGSSEAAAK	15,053	FOAMV_P14350_2mut

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
PAPGSSGGS	15,054	SFV1_P23074-Pro_2mut
GSSGSSGSSGSSGSSGSS	15,055	SFV3L_P27401
EAAAKGSSGGG	15,056	MMTVB_P03365
PAPGGGGSS	15,057	WDSV_O92815_2mutA
GGSPAP	15,058	MMTVB_P03365-Pro
GGSGGSGGSGGSGGS	15,059	SFVCP_Q87040-Pro_2mut
PAPAPAPAP	15,060	MMTVB_P03365-Pro
GGGGG	15,061	HTL1A_P03362
GGSGGSGGSGGS	15,062	SFV1_P23074_2mutA
GSSGSSGSSGSSGSS	15,063	FOAMV_P14350-Pro_2mut
PAPGGSEAAAK	15,064	MMTVB_P03365_2mutB_WS
PAPAPAPAP	15,065	SFV1_P23074_2mut
PAPGGGGSS	15,066	MMTVB_P03365
GGSGSS	15,067	SFV3L_P27401_2mut
EAAAKEAAAKEAAAKEAAAK	15,068	MMTVB_P03365_2mut
EAAAKGGSGGG	15,069	HTL3P_Q4U0X6_2mut
PAPGGGGSS	15,070	SFVCP_Q87040-Pro_2mutA
EAAAKGGGGGS	15,071	MLVAV_P03356
GGGGGS	15,072	FOAMV_P14350_2mut
GGGEAAAKGGS	15,073	FFV_O93209-Pro_2mutA
EAAAKPAPGGG	15,074	MMTVB_P03365_2mutB
GGSGGGPAP	15,075	FFV_O93209_2mut
GSSEAAAKPAP	15,076	MMTVB_P03365
PAPAPAPAPAPAP	15,077	SFV1_P23074_2mut
GGSPAPGGG	15,078	MMTVB_P03365-Pro
GGSGGGEAAAK	15,079	MMTVB_P03365
PAPAP	15,080	SFVCP_Q87040
GSSEAAAK	15,081	SFVCP_Q87040
GGGGSGGGGSGGGGS	15,082	MMTVB_P03365-Pro
GSSGSSGSS	15,083	SFV3L_P27401
EAAAKGGSGGG	15,084	MMTVB_P03365-Pro
GSSPAP	15,085	SFV1_P23074_2mut
GGGEAAAK	15,086	SFV1_P23074-Pro
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	15,087	MMTVB_P03365-Pro
PAPGGS	15,088	HTL1C_P14078_2mut
PAPGSSGGS	15,089	SFV1_P23074_2mut
PAPEAAAK	15,090	MMTVB_P03365_WS
PAPAP	15,091	MMTVB_P03365-Pro
EAAAKGGS	15,092	HTL1A_P03362_2mut

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
GGGGSEAAAKGGGGS	15,093	HTL1C_P14078
EAAAKGSSGGS	15,094	FOAMV_P14350-Pro
PAPGGSGSS	15,095	MMTVB_P03365-Pro
PAPGGSEAAAK	15,096	SFV1_P23074_2mut
PAPGSSEAAAK	15,097	FFV_O93209-Pro_2mut
PAPGSSGGG	15,098	FOAMV_P14350-Pro_2mutA
GSSGGGEAAAK	15,099	AVIRE_P03360
GGGGGG	15,100	SMRVH_P03364_2mut
PAPEAAAKGGG	15,101	MMTVB_P03365-Pro
GGGEAAAKGGS	15,102	SFVCP_Q87040_2mutA
PAPAPAPAPAP	15,103	SRV2_P51517
GSSGSSGSSGSSGSSGSS	15,104	MMTVB_P03365
EAAAKGGGPAP	15,105	MLVAV_P03356
PAPAPAPAPAP	15,106	FOAMV_P14350-Pro_2mutA
PAPGGSEAAAK	15,107	FOAMV_P14350
GSSGGGPAP	15,108	HTL32_Q0R5R2_2mutB
GGGGGSPAP	15,109	HTL3P_Q4U0X6_2mutB
GSSGGSGGG	15,110	MMTVB_P03365-Pro
PAPAP	15,111	SFVCP_Q87040-Pro
GSSGGGPAP	15,112	MMTVB_P03365-Pro
GGSGSS	15,113	MMTVB_P03365-Pro_2mut
GGSPAPEAAAK	15,114	SFV1_P23074-Pro_2mut
EAAAKGGSGGG	15,115	SFV3L_P27401_2mut
GGGGSSEAAAK	15,116	MMTVB_P03365_WS
GGGGGSGSS	15,117	MMTVB_P03365_2mut
GGGGSSGGS	15,118	SFV1_P23074-Pro_2mutA
EAAAKGGGGSEAAAK	15,119	MMTVB_P03365_WS
PAPGGGEAAAK	15,120	SFV1_P23074-Pro
PAPEAAAKGGG	15,121	MMTVB_P03365
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	15,122	MMTVB_P03365
GSSGGSEAAAK	15,123	FOAMV_P14350-Pro_2mut
GGSPAP	15,124	MLVBM_Q7SVK7_3mut
GSSEAAAK	15,125	FOAMV_P14350
GSSEAAAK	15,126	MMTVB_P03365-Pro
EAAAKGSSGGS	15,127	HTL1A_P03362_2mut
GGGEAAAKPAP	15,128	FOAMV_P14350-Pro_2mut
EAAAKGGSPAP	15,129	FOAMV_P14350
GSSEAAAKPAP	15,130	MMTVB_P03365_WS
GSSGSSGSS	15,131	FOAMV_P14350_2mut

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
EAAAKEAAAKEAAAKEAAAK	15,132	MMTVB_P03365_WS
EAAAK	15,133	MMTVB_P03365
PAPGSS	15,134	BAEVM_P10272
PAPGGS	15,135	FFV_O93209-Pro_2mut
GGSGGS	15,136	SFV1_P23074-Pro_2mutA
SGGSSGGSSGSETPGTSESATPESSGGSSGGSS	15,137	HTLV2_P03363_2mut
GGSGGGEAAAK	15,138	MMTVB_P03365_WS
PAPGSSGGG	15,139	HTL1A_P03362
GGSGGS	15,140	SFV3L_P27401-Pro
GSSGSS	15,141	SFV1_P23074-Pro
PAPGGSEAAAK	15,142	MMTVB_P03365
GSAGSAAGSGEF	15,143	MMTVB_P03365-Pro
PAPGGG	15,144	FOAMV_P14350_2mut
EAAAKGGSGSS	15,145	MMTVB_P03365_WS
GSSGGGEAAAK	15,146	SFV3L_P27401-Pro
GGSGGGPAP	15,147	FOAMV_P14350-Pro_2mut
PAPAPAPAPAPAP	15,148	WDSV_O92815
SGSETPGTSESATPES	15,149	SFVCP_Q87040-Pro_2mutA
GGSGGSGGS	15,150	SFV1_P23074
GGGGSS	15,151	SFVCP_Q87040_2mut
GGGGGSEAAAK	15,152	MMTVB_P03365
SGSETPGTSESATPES	15,153	MMTVB_P03365_WS
PAPAPAP	15,154	SFV3L_P27401
PAPEAAAKGSS	15,155	MMTVB_P03365_2mutB_WS
GSSGSSGSSGSSGSS	15,156	SRV2_P51517
GGGPAPGSS	15,157	HTL32_Q0R5R2_2mutB
GGSGGGGSS	15,158	MMTVB_P03365-Pro
SGSETPGTSESATPES	15,159	SRV2_P51517
EAAAKGSSGGS	15,160	MMTVB_P03365-Pro
GSSPAPEAAAK	15,161	MMTVB_P03365-Pro
GSSPAPEAAAK	15,162	SRV2_P51517
GGGGSSPAP	15,163	MMTVB_P03365-Pro
PAPGGGEAAAK	15,164	SFV1_P23074-Pro_2mutA
PAPEAAAKGGS	15,165	MMTVB_P03365
GSSGSSGSSGSSGSSGSS	15,166	FOAMV_P14350-Pro
GGSPAPGSS	15,167	SFV3L_P27401
GGGPAPGGS	15,168	SFV1_P23074-Pro_2mutA
GGGPAPGSS	15,169	MMTVB_P03365-Pro
EAAAKPAP	15,170	MLVBM_Q7SVK7

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
EAAAKEAAAKEAAAK	15,171	HTL1C_P14078
GSSGGSEAAAK	15,172	SRV2_P51517
PAPGGGGGS	15,173	SRV2_P51517
GGGEAAAK	15,174	FFV_O93209-Pro_2mut
EAAAKGGGPAP	15,175	HTL32_Q0R5R2
GGSGSSGGG	15,176	MMTVB_P03365
PAPEAAAKGSS	15,177	MMTVB_P03365-Pro
PAPGGGGGS	15,178	MMTVB_P03365-Pro
EAAAKGGGGGS	15,179	MMTVB_P03365_WS
GGGGGS	15,180	MMTVB_P03365-Pro
GGGGSGGGGSGGGGSGGGGSGGGGS	15,181	HTL1C_P14078
EAAAKGGSPAP	15,182	MMTVB_P03365
GGGGSSPAP	15,183	FFV_O93209-Pro_2mut
GGGGSSGGS	15,184	MMTVB_P03365-Pro
PAPGSSGGS	15,185	MMTVB_P03365-Pro
GGGGGS	15,186	SRV2_P51517
GGSGSSGGG	15,187	MMTVB_P03365
GSSGGSEAAAK	15,188	MMTVB_P03365-Pro
EAAAKEAAAKEAAAKEAAAK	15,189	GALV_P21414
GGSEAAAKGGG	15,190	MMTVB_P03365-Pro
SGGSSGGSSGSETPGTSESATPESSGGSSGGSS	15,191	MMTVB_P03365-Pro
GSSEAAAKGGS	15,192	MMTVB_P03365
GGGGSGGGGSGGGGSGGGGSGGGGSGGGGS	15,193	HTL3P_Q4U0X6_2mutB
GGGEAAAK	15,194	MMTVB_P03365-Pro
PAPAPAPAP	15,195	MMTVB_P03365-Pro
PAPGSSGGG	15,196	MMTVB_P03365
GSSGSSGSSGSSGSS	15,197	GALV_P21414
GGSPAP	15,198	MMTVB_P03365_WS
GGGGSGGGGSGGGGSGGGGSGGGGSGGGGS	15,199	MMTVB_P03365-Pro
PAPEAAAK	15,200	MMTVB_P03365-Pro
PAPGSSGGG	15,201	SFV1_P23074-Pro_2mutA
GGGGGSEAAAK	15,202	MMTVB_P03365_2mutB_WS
PAPAPAPAPAP	15,203	MMTVB_P03365-Pro
EAAAKGGSGSS	15,204	MMTVB_P03365-Pro
EAAAKEAAAKEAAAKEAAAK	15,205	MLVRD_P11227_3mut
PAPAPAPAP	15,206	FOAMV_P14350_2mutA
GGGPAPGSS	15,207	SFVCP_Q87040_2mut
PAPEAAAKGSS	15,208	SFVCP_Q87040_2mut
GGSPAPGGG	15,209	MMTVB_P03365-Pro

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
GGGGSGGGGSGGGGSGGGGS	15,210	MMTVB_P03365
EAAAKGGS	15,211	HTL3P_Q4U0X6_2mut
PAPGSSGGS	15,212	MMTVB_P03365_WS
GGGGSGGGGS	15,213	MMTVB_P03365
GGSGGS	15,214	FOAMV_P14350
EAAAKGGGGSEAAAK	15,215	SFVCP_Q87040-Pro_2mut
EAAAKEAAAKEAAAKEAAAK	15,216	MMTVB_P03365-Pro_2mutB
PAPGGGEAAAK	15,217	SFVCP_Q87040-Pro
GSSGSS	15,218	JSRV_P31623_2mutB
EAAAKGGGGGS	15,219	MMTVB_P03365_2mut_WS
GSSPAPEAAAK	15,220	MMTVB_P03365-Pro
GGGEAAAK	15,221	HTL1C_P14078
PAPEAAAKGSS	15,222	HTL32_Q0R5R2_2mutB
GGGGSSEAAAK	15,223	MMTVB_P03365-Pro
PAPGSSGGS	15,224	MMTVB_P03365-Pro
EAAAKGGGGGS	15,225	MMTVB_P03365
GGGGSGGGGSGGGGSGGGGS	15,226	MMTVB_P03365
EAAAKGGGGSS	15,227	HTL3P_Q4U0X6_2mut
GGGEAAAKGGS	15,228	SFVCP_Q87040-Pro
GGGGGSPAP	15,229	MMTVB_P03365-Pro_2mutB
GGSGGGEAAAK	15,230	SFV3L_P27401-Pro
PAPGGGGGS	15,231	SFV3L_P27401-Pro
EAAAKGGGGSEAAAK	15,232	MMTVB_P03365
PAPEAAAKGSS	15,233	MMTVB_P03365-Pro
GGSEAAAKGGG	15,234	MMTVB_P03365-Pro
GGSGGSGGSGGSGGS	15,235	SMRVH_P03364_2mutB
GGSGGSGGSGGSGGS	15,236	HTL1L_P0C211_2mut
GGGGGG	15,237	WDSV_O92815
GGGGGSGSS	15,238	MMTVB_P03365-Pro
GGSEAAAKPAP	15,239	SFV3L_P27401-Pro_2mut
GGGPAPGSS	15,240	MMTVB_P03365_2mut_WS
GGGGGS	15,241	MMTVB_P03365_WS
GGSPAPEAAAK	15,242	MMTVB_P03365
PAPEAAAKGGS	15,243	HTL1A_P03362
EAAAKGGSGSS	15,244	MMTVB_P03365_2mut_WS
GGGPAPEAAAK	15,245	SFV3L_P27401-Pro_2mut
PAPGGGGSS	15,246	HTL32_Q0R5R2_2mut
GSSPAPGGG	15,247	HTL3P_Q4U0X6_2mut
GGGGSSGGS	15,248	BLVAU_P25059_2mut

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
EAAAKGGGGGS	15,249	HTL1L_P0C211
GGSEAAAKGSS	15,250	JSRV_P31623_2mutB
GSSGGG	15,251	JSRV_P31623
GGSGGSGGSGGS	15,252	MMTVB_P03365-Pro
EAAAKPAP	15,253	SFV1_P23074-Pro_2mutA
GGGGSSGGS	15,254	MMTVB_P03365_WS
GGSGGS	15,255	MMTVB_P03365_WS
EAAAKGGGGGS	15,256	MMTVB_P03365-Pro
GGGGSGGGGSGGGGSGGGGSGGGGSGGGGS	15,257	MMTVB_P03365
GGSGGSGGS	15,258	MMTVB_P03365
GGGGGSEAAAK	15,259	MLVBM_Q7SVK7
GGSGSSPAP	15,260	MMTVB_P03365_WS
EAAAKEAAAKEAAAK	15,261	JSRV_P31623
PAPEAAAKGGS	15,262	MMTVB_P03365-Pro
GGSGSSEAAAK	15,263	FOAMV_P14350
GGGGGSGSS	15,264	MMTVB_P03365-Pro_2mut
GGGPAPGGS	15,265	MMTVB_P03365
SGSETPGTSESATPES	15,266	SFVCP_Q87040_2mut
GSSPAPGGS	15,267	SFV1_P23074-Pro_2mutA
GSSGSSGSSGSSGSS	15,268	MMTVB_P03365
EAAAKGGGPAP	15,269	MMTVB_P03365
GSSGGG	15,270	MMTVB_P03365_2mut_WS
GGGEAAAKPAP	15,271	MMTVB_P03365
PAPGGSGGG	15,272	MMTVB_P03365-Pro
GSSGGSGGG	15,273	WDSV_O92815_2mut
GGSGGG	15,274	HTL32_Q0R5R2_2mut
EAAAKGGSPAP	15,275	HTLV2_P03363_2mut
GGSPAPEAAAK	15,276	MMTVB_P03365-Pro
GSSGGSEAAAK	15,277	MMTVB_P03365_2mut
GSAGSAAGSGEF	15,278	MMTVB_P03365_WS
PAPGGSGSS	15,279	FFV_O93209
GGSEAAAKGGG	15,280	MMTVB_P03365
GGSPAPGSS	15,281	MMTVB_P03365-Pro
GSSGGSGGG	15,282	SFV3L_P27401
PAPEAAAKGGG	15,283	HTL1A_P03362_2mutB
GGGEAAAKPAP	15,284	MMTVB_P03365-Pro
GGSEAAAK	15,285	HTL32_Q0R5R2_2mutB
GGGEAAAKGSS	15,286	MPMV_P07572
GGGGGSEAAAK	15,287	MMTVB_P03365-Pro

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
PAPAPAPAPAP	15,288	SFVCP_Q87040-Pro_2mutA
PAPAPAPAPAP	15,289	HTL1L_P0C211_2mut
GGGGSSGGS	15,290	HTL3P_Q4U0X6
PAPGGSEAAAK	15,291	MMTVB_P03365_2mut_WS
PAPAPAPAPAP	15,292	HTL1A_P03362
EAAAKPAPGGG	15,293	MMTVB_P03365_2mut_WS
GGSEAAAK	15,294	MMTVB_P03365_2mut_WS
GGGEAAAKGSS	15,295	SFV1_P23074-Pro_2mutA
GGSPAPGSS	15,296	MMTVB_P03365-Pro
GGSEAAAKPAP	15,297	MLVBM_Q7SVK7
PAPEAAAKGGG	15,298	MMTVB_P03365_2mut_WS
GSSEAAAKPAP	15,299	MMTVB_P03365-Pro_2mutB
GGGGSEAAAKGGGGS	15,300	MMTVB_P03365-Pro_2mut
GSSEAAAKGGS	15,301	MMTVB_P03365-Pro_2mutB
GSSGSSGSSGSSGSS	15,302	SRV2_P51517_2mutB
GGGGGSPAP	15,303	HTL1L_P0C211_2mut
GGSEAAAK	15,304	MMTVB_P03365
GSSPAPEAAAK	15,305	SMRVH_P03364_2mutB
GGGPAPGGS	15,306	HTL1C_P14078_2mut
GGSPAPEAAAK	15,307	MMTVB_P03365_WS
GGSEAAAKPAP	15,308	HTL1A_P03362_2mut
PAPAPAPAP	15,309	HTLV2_P03363_2mut
GSSPAPGGG	15,310	MMTVB_P03365
GSSGSSGSSGSS	15,311	MMTVB_P03365-Pro
GGSEAAAKGSS	15,312	MMTVB_P03365_WS
GGSGSSGGG	15,313	MMTVB_P03365_2mutB
GSSGSSGSSGSSGSSGSS	15,314	JSRV_P31623_2mutB
GGSEAAAKPAP	15,315	MMTVB_P03365-Pro
GSSGGSGGG	15,316	HTLV2_P03363_2mut
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	15,317	WDSV_O92815_2mut
GGSPAPEAAAK	15,318	MMTVB_P03365
GGGGSSEAAAK	15,319	MMTVB_P03365
GGSGGGEAAAK	15,320	SFV1_P23074-Pro_2mutA
GGGGSEAAAKGGGGS	15,321	WDSV_O92815_2mut
GGSGSSEAAAK	15,322	MMTVB_P03365_2mutB_WS
GGSEAAAKPAP	15,323	MMTVB_P03365_WS
GSSGGGEAAAK	15,324	SFVCP_Q87040-Pro
GSSGGS	15,325	SFVCP_Q87040-Pro_2mut
GGSEAAAKPAP	15,326	SFVCP_Q87040_2mut

Linker amino acid sequence	Linker SEQ ID NO:	RT domain name
GSSGGSEAAAK	15,327	SFVCP_Q87040_2mut
GSSPAPEAAAK	15,328	SRV2_P51517_2mutB
GGSGGSGGSGGSGGSGGS	15,329	BLVAU_P25059
GSSGSSGSSGSSGSS	15,330	HTL1C_P14078_2mut
EAAAKGGGGSS	15,331	MMTVB_P03365_2mutB
GGGEAAAKGSS	15,332	SFVCP_Q87040-Pro

Example 3: Screening configurations of template RNAs that install the SCD mutation into the endogenous HBB gene in human cells

This example describes the use of a gene modifying system containing a gene modifying polypeptide and template RNAs comprising varied lengths of heterologous object sequences and primer binding site sequences to identify favorable configurations for editing of the endogenous HBB gene in human cells. In this example, a template RNA contains:

(1) a gRNA spacer;

(2) a gRNA scaffold;

(3) a heterologous object sequence; and

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

The template RNAs were designed to contain 8 – 17 nt PBS sequences and 9 – 20 nt heterologous object sequences. Two different gRNA spacer sequences were used to target sites proximal to the SCD mutation in the endogenous HBB genomic site. The heterologous object sequences and PBS sequences were designed to install the SCD mutation (an E6V mutation) into the endogenous gene by replacing an "A" nucleotide with a "T" nucleotide at the mutation site using a gene modifying system described herein. The template RNA sequences used are those shown in Table A (HBB5 sequences) and Table B (HBB8 sequences), with the following exceptions. First, the mutation region of the RT template sequence was designed to install the mutation (A→T) rather than to correct back to the wild-type sequence. In particular, RT template regions for SCD installation using template HBB5 comprise at least a portion of the following sequence: Install RT Template (PAM-kill): AACGGCAGACTTCTCTACAG (SEQ ID NO: 21672), of which the no PAM-kill equivalent would be: Install RT Template (no PAM-kill): AACGGCAGACTTCTCCACAG (SEQ ID NO: 21673). In addition, the installation

version of the HBB8 spacer had the following sequence that differed from the HBB8 mutation correction spacer due to the SCD mutation falling within the target protospacer, resulting in a single nt difference relative to the WT sequence without the SCD mutation: GTAACGGCAGACTTCTCCTC (SEQ ID NO: 21674). In particular, RT template regions for SCD mutation installation using template HBB8 comprise at least a portion of the following sequence: Install RT Template (293T SNP): TGGTGCACCTGACTCCTGTG (SEQ ID NO: 21676), of which the equivalent template lacking the 293T SNP and targeted to the hg38 reference sequence would be: Install RT Template (no SNP): TGGTGCATCTGACTCCTGTG (SEQ ID NO: 21675).

A gene modifying system comprising a gene modifying polypeptide (see Table C) and a template RNA was transfected into HEK293T cells. The gene modifying polypeptide and the template RNAs were delivered by nucleofection in RNA format. Specifically, 1μg of gene modifying polypeptide mRNA was combined with 10μM template RNAs. The mRNA and template RNAs were added to 25μL SF buffer containing 250,000 HEK293T cells and cells were nucleofected using program DS-150. After nucleofection, cells were grown at 37˚C, 5% CO_2 for 3 days prior to cell lysis and genomic DNA extraction. To analyze gene editing activity, primers flanking the HBB genomic target site were used to amplify across the locus. Amplicons are analyzed via short read sequencing using an Illumina MiSeq. Gene editing activity with high editing efficiency was detected in the configurations with 9 – 12nt PBS sequence and 13 – 16 nt heterologous object sequence. These results indicate that template RNAs comprising gRNA spacers and gRNA scaffolds described herein successfully directed a gene modifying polypeptide to the endogenous HBB gene in human cells, such that specific gene editing occurred. Results are shown in Table E.

Although this experiment demonstrates installation of the mutation rather than correction of the mutation, it indicates that editing may be performed at the native HBB locus.

Table E. HBB5 and HBB8 Sequences for installing mutation. *The columns indicate, from left to right: 1) Name of the HBB5 template RNA, 2) Full HBB5 template RNA sequence depicted as RNA, further showing chemical modifications as used in Example 3, 3) observed activity of template RNA of column 2 as defined in Example 3, 4) Name of the HBB8 template RNA, 5) Full*

HBB8 template RNA sequence depicted as RNA, further showing chemical modifications as used in Example 3, 6) observed activity of template RNA of column 5 as defined in Example 3.

Installation of SCD mutation using HBB5 protospacer region				Installation of SCD mutation using HBB8 protospacer region			
Name	**Template Sequence**	**SEQ ID NO**	**Activity**	**Name**	**Template Sequence**	**SEQ ID NO**	**Activity**
HBB5_inst_RT20_PBS17	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArCrUrCrCrUrGrGrUrUrUrUrArGrArGrCrUrArGrArArArUrArGrCrArArGrUrUrArArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrArArCrCrUrCrUrCrUrArArCrArGrGrArGrUrCrArGrGrUrGrCrArCrC*mA*mU*mG	20637	+	HBB8_inst_RT20_PBS17	mG*mU*mA*rArCrGrGrCrArGrArCrUrUrCrUrCrCrUrCrGrUrUrUrUrArGrArGrCrUrArGrArArArUrArGrCrArArGrUrUrArArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrUrGrGrUrGrCrArCrCrUrGrArCrUrCrCrUrGrUrGrGrArGrArArGrUrCrUrGrCrCrGrU*mU*mA*mC	20727	+
HBB5_inst_RT20_PBS16	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArCrUrCrCrUrGrGrUrUrUrUrArGrArGrCrUrArGrArArArUrArGrCrArArGrUrUrArArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrArArCrCrUrCrUrCrUrArArCrArGrGrArGrUrCrArGrGrUrGrCrArC*mC*mA*mU	20638	+	HBB8_inst_RT20_PBS16	mG*mU*mA*rArCrGrGrCrArGrArCrUrUrCrUrCrCrUrCrGrUrUrUrUrArGrArGrCrUrArGrArArArUrArGrCrArArGrUrUrArArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrUrGrGrUrGrCrArCrCrUrGrArCrUrCrCrUrGrUrGrGrArGrArArGrUrCrUrGrCrCrG*mU*mU*mA	20728	+
HBB5_inst_RT20_PBS15	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArCrUrCrCrUrGrGrUrUrUrUrArGrArGrCrUrArGrArArArUrArGrCrArArGrUrUrArArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrArArCrCrUrCrUrCrUrArArCrArGrGrArGrUrCrArGrGrUrGrCrA*mC*mC*mA	20639	+	HBB8_inst_RT20_PBS15	mG*mU*mA*rArCrGrGrCrArGrArCrUrUrCrUrCrCrUrCrGrUrUrUrUrArGrArGrCrUrArGrArArArUrArGrCrArArGrUrUrArArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrUrGrGrUrGrCrArCrCrUrGrArCrUrCrCrUrGrUrGrGrArGrArArGrUrCrUrGrCrC*mG*mU*mU	20729	+
HBB5_inst_RT20_PBS14	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArCrUrCrCrUrGrGrUrUrUrUrArGrArGrCrUrArGrArArArUrArGrCrArArGrUrUrArArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrArArCrCrUrCrUrCrUrArArCrArGrGrArGrUrCrArGrGrUrGrCrArCrC	20640	+	HBB8_inst_RT20_PBS14	mG*mU*mA*rArCrGrGrCrArGrArCrUrUrCrUrCrCrUrCrGrUrUrUrUrArGrArGrCrUrArGrArArArUrArGrCrArArGrUrUrArArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrUrGrGrUrGrCrArCrCrUrGrArCrUrCrCrUrGrUrGrGrArGrArArGrUrCrUrGrCrCrGrAr	20730	+

	GrUrCrGrGrUrGrCrArArCrGrGr CrArGrArCrUrUrCrUrCrUrArCr ArGrGrArGrUrCrArGrGrUrGrC *mA*mC*mC				GrUrCrGrGrUrGrCrUrGrGrUrGr CrArCrCrUrGrArCrUrCrCrUrGr UrGrGrArGrArArGrUrCrUrGrC *mC*mG*mU		
HBB 5_inst _RT2 0_PB S13	mC*mA*mU*rGrGrUrGrCrArCr CrUrGrArCrUrCrCrUrGrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrArArCrGrGr CrArGrArCrUrUrCrUrCrUrArCr ArGrGrArGrUrCrArGrGrUrG*m C*mA*mC	2064 1	+ +	HBB 8_inst _RT2 0_PB S13	mG*mU*mA*rArCrGrGrCrArGr ArCrUrUrCrUrCrCrUrCrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrUrGrGrUrGr CrArCrCrUrGrArCrUrCrCrUrGr UrGrGrArGrArArGrUrCrUrG*m C*mC*mG	2073 1	+
HBB 5_inst _RT2 0_PB S12	mC*mA*mU*rGrGrUrGrCrArCr CrUrGrArCrUrCrCrUrGrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrArArCrGrGr CrArGrArCrUrUrCrUrCrUrArCr ArGrGrArGrUrCrArGrGrU*mG* mC*mA	2064 2	+ + +	HBB 8_inst _RT2 0_PB S12	mG*mU*mA*rArCrGrGrCrArGr ArCrUrUrCrUrCrCrUrCrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrUrGrGrUrGr CrArCrCrUrGrArCrUrCrCrUrGr UrGrGrArGrArArGrUrCrU*mG* mC*mC	2073 2	+ +
HBB 5_inst _RT2 0_PB S11	mC*mA*mU*rGrGrUrGrCrArCr CrUrGrArCrUrCrCrUrGrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrArArCrGrGr CrArGrArCrUrUrCrUrCrUrArCr ArGrGrArGrUrCrArGrG*mU*m G*mC	2064 3	+ + +	HBB 8_inst _RT2 0_PB S11	mG*mU*mA*rArCrGrGrCrArGr ArCrUrUrCrUrCrCrUrCrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrUrGrGrUrGr CrArCrCrUrGrArCrUrCrCrUrGr UrGrGrArGrArArGrUrC*mU*m G*mC	2073 3	+ +
HBB 5_inst _RT2 0_PB S10	mC*mA*mU*rGrGrUrGrCrArCr CrUrGrArCrUrCrCrUrGrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrArArCrGrGr CrArGrArCrUrUrCrUrCrUrArCr ArGrGrArGrUrCrArG*mG*mU* mG	2064 4	+ + +	HBB 8_inst _RT2 0_PB S10	mG*mU*mA*rArCrGrGrCrArGr ArCrUrUrCrUrCrCrUrCrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrUrGrGrUrGr CrArCrCrUrGrArCrUrCrCrUrGr UrGrGrArGrArArGrU*mC*mU* mG	2073 4	+
HBB 5_inst _RT2 0_PB S9	mC*mA*mU*rGrGrUrGrCrArCr CrUrGrArCrUrCrCrUrGrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrArArCrGrGr	2064 5	+ +	HBB 8_inst _RT2 0_PB S9	mG*mU*mA*rArCrGrGrCrArGr ArCrUrUrCrUrCrCrUrCrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrUrGrGrUrGr	2073 5	+

	CrArGrArCrUrUrCrUrCrUrArCrArGrGrArGrUrCrA*mG*mG*mU				CrArCrCrUrGrArCrUrCrCrUrGrUrGrGrArGrArArG*mU*mC*mU		
HBB5_inst_RT20_PBS8	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArCrUrCrCrUrGrGrUrUrUrUrArGrArGrCrUrArGrArArArUrArGrCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrArArCrGrGrCrArGrArArCrUrUrCrUrCrUrArCrArArGrGrArGrUrC*mA*mG*mG	20646	+	HBB8_inst_RT20_PBS8	mG*mU*mA*rArCrGrGrCrArGrArCrUrUrCrUrCrCrUrCrGrUrUrUrUrArGrArGrCrUrArGrArArArUrArGrCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrUrGrGrUrGrCrArCrCrUrGrArCrUrCrCrUrGrUrGrGrArGrArArA*mG*mU*mC	20736	+
HBB5_inst_RT19_PBS17	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArCrUrCrCrUrGrGrUrUrUrUrArGrArGrCrUrArGrArArArUrArGrCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrArCrCrUrGrArCrUrCrCrUrGrUrGrGrArGrArArCrC*mA*mU*mG	20647	+	HBB8_inst_RT19_PBS17	mG*mU*mA*rArCrGrGrCrArGrArCrUrUrCrUrCrCrUrCrGrUrUrUrUrArGrArGrCrUrArGrArArArUrArGrCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrGrGrUrGrCrArCrCrUrGrArCrUrCrCrUrGrUrGrGrArGrArArCrG*mU*mA*mC	20737	+
HBB5_inst_RT19_PBS16	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArCrUrCrCrUrGrGrUrUrUrUrArGrArGrCrUrArGrArArArUrArGrCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrArCrCrUrGrArCrUrCrCrUrGrUrGrGrArGrArArCrC*mC*mA*mU	20648	+	HBB8_inst_RT19_PBS16	mG*mU*mA*rArCrGrGrCrArGrArCrUrUrCrUrCrCrUrCrGrUrUrUrUrArGrArGrCrUrArGrArArArUrArGrCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrGrGrUrGrCrArCrCrUrGrArCrUrCrCrUrGrUrGrGrArGrArArCrG*mU*mU*mA	20738	+
HBB5_inst_RT19_PBS15	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArCrUrCrCrUrGrGrUrUrUrUrArGrArGrCrUrArGrArArArUrArGrCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrArCrCrUrGrArCrUrCrCrUrGrUrGrGrArGrArArCrC*mC*mA	20649	+	HBB8_inst_RT19_PBS15	mG*mU*mA*rArCrGrGrCrArGrArCrUrUrCrUrCrCrUrCrGrUrUrUrUrArGrArGrCrUrArGrArArArUrArGrCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrGrGrUrGrCrArCrCrUrGrArCrUrCrCrUrGrUrGrGrArGrArArCrC*mG*mU*mU	20739	+
HBB5_inst_RT19_PBS14	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArCrUrCrCrUrGrGrUrUrUrUrArGrArGrCrUrArGrArArArUrArGrCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrArCrCrUrGrArCrUrCrCrUrGrUrGrGrArGrArArCrC	20650	+ +	HBB8_inst_RT19_PBS14	mG*mU*mA*rArCrGrGrCrArGrArCrUrUrCrUrCrCrUrCrGrUrUrUrUrArGrArGrCrUrArGrArArArUrArGrCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrGrGrUrGrCrArCrCrUrGrArCrUrCrCrUrGrUr	20740	+

	GrGrArGrUrCrArGrGrUrGrC*mA*mC*mC				GrGrArGrArArGrUrCrUrGrC*mC*mG*mU		
HBB5_inst_RT19_PBS13	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArCrUrCrCrUrGrGrUrUrUrUrArGrArGrCrUrArGrGrArArArUrArGrCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrArCrGrGrCrArGrUrArCrArCrUrCrUrArCrArGrGrArGrUrCrArGrGrUrG*mC*mA*mC	20651	+ +	HBB8_inst_RT19_PBS13	mG*mU*mA*rArCrGrGrCrArGrArCrUrUrCrUrCrCrUrCrGrUrUrUrUrArGrArGrCrUrArGrGrArArArUrArGrCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrGrGrUrGrCrArCrCrUrGrArCrUrCrCrUrGrUrGrGrArGrArArArGrUrCrUrG*mC*mC*mG	20741	+
HBB5_inst_RT19_PBS12	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArCrUrCrCrUrGrGrUrUrUrUrArGrArGrCrUrArGrGrArArArUrArGrCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrArCrGrGrCrArGrUrArCrArCrUrCrUrArCrArGrGrArGrUrCrArGrGrU*mG*mC*mA	20652	+ + +	HBB8_inst_RT19_PBS12	mG*mU*mA*rArCrGrGrCrArGrArCrUrUrCrUrCrCrUrCrGrUrUrUrUrArGrArGrCrUrArGrGrArArArUrArGrCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrGrGrUrGrCrArCrCrUrGrArCrUrCrCrUrGrUrGrGrArGrArArArGrUrCrU*mG*mC*mC	20742	+ +
HBB5_inst_RT19_PBS11	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArCrUrCrCrUrGrGrUrUrUrUrArGrArGrCrUrArGrGrArArArUrArGrCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrArCrGrGrCrArGrUrArCrArCrUrCrUrArCrArGrGrArGrUrCrArGrG*mU*mG*mC	20653	+ + +	HBB8_inst_RT19_PBS11	mG*mU*mA*rArCrGrGrCrArGrArCrUrUrCrUrCrCrUrCrGrUrUrUrUrArGrArGrCrUrArGrGrArArArUrArGrCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrGrGrUrGrCrArCrCrUrGrArCrUrCrCrUrGrUrGrGrArGrArArArGrU*mC*mU*mG*mC	20743	+
HBB5_inst_RT19_PBS10	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArCrUrCrCrUrGrGrUrUrUrUrArGrArGrCrUrArGrGrArArArUrArGrCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrArCrGrGrCrArGrUrArCrArCrUrCrUrArCrArGrGrArGrUrCrArG*mG*mU*mG	20654	+ + +	HBB8_inst_RT19_PBS10	mG*mU*mA*rArCrGrGrCrArGrArCrUrUrCrUrCrCrUrCrGrUrUrUrUrArGrArGrCrUrArGrGrArArArUrArGrCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrGrGrUrGrCrArCrCrUrGrArCrUrCrCrUrGrUrGrGrArGrArArArGrU*mC*mU*mG	20744	+
HBB5_inst_RT19_PBS9	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArCrUrCrCrUrGrGrUrUrUrUrArGrArGrCrUrArGrGrArArArUrArGrCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrArCrGrGrCrArGrUrArCrArCrUrCrUrArCrArGrGrArGrUrCrA*mG*mG*mU	20655	+ +	HBB8_inst_RT19_PBS9	mG*mU*mA*rArCrGrGrCrArGrArCrUrUrCrUrCrCrUrCrGrUrUrUrUrArGrArGrCrUrArGrGrArArArUrArGrCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrGrGrUrGrCrArCrCrUrGrArCrUrCrCrUrGrUrGrGrArGrArArG*mU*mC*mU	20745	+

HBB 5_inst _RT1 9_PB S8	mC*mA*mU*rGrGrUrGrCrArCr CrUrGrArCrUrCrCrUrGrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrArCrGrGrCr ArGrArCrUrUrCrUrCrUrArCrAr GrGrArGrUrC*mA*mG*mG	2065 6	+	HBB 8_inst _RT1 9_PB S8	mG*mU*mA*rArCrGrGrCrArGr ArCrUrUrCrUrCrCrUrCrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrGrGrUrGrCr ArCrCrUrGrArCrUrCrCrUrGrUr GrGrArGrArA*mG*mU*mC	2074 6	+
HBB 5_inst _RT1 7_PB S17	mC*mA*mU*rGrGrUrGrCrArCr CrUrGrArCrUrCrCrUrGrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrGrGrCrArGr ArCrUrUrCrUrCrUrArCrArGrGr ArGrUrCrArGrGrUrGrCrArCrC* mA*mU*mG	2065 7	+	HBB 8_inst _RT1 8_PB S17	mG*mU*mA*rArCrGrGrCrArGr ArCrUrUrCrUrCrCrUrCrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrGrUrGrCrAr CrCrUrGrArCrUrCrCrUrGrUrGr GrArGrArArGrUrCrUrGrCrCrGr U*mU*mA*mC	2074 7	+
HBB 5_inst _RT1 7_PB S16	mC*mA*mU*rGrGrUrGrCrArCr CrUrGrArCrUrCrCrUrGrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrGrGrCrArGr ArCrUrUrCrUrCrUrArCrArGrGr ArGrUrCrArGrGrUrGrCrArC*m C*mA*mU	2065 8	+	HBB 8_inst _RT1 8_PB S16	mG*mU*mA*rArCrGrGrCrArGr ArCrUrUrCrUrCrCrUrCrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrGrUrGrCrAr CrCrUrGrArCrUrCrCrUrGrUrGr GrArGrArArGrUrCrUrGrCrCrG* mU*mU*mA	2074 8	+
HBB 5_inst _RT1 7_PB S15	mC*mA*mU*rGrGrUrGrCrArCr CrUrGrArCrUrCrCrUrGrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrGrGrCrArGr ArCrUrUrCrUrCrUrArCrArGrGr ArGrUrCrArGrGrUrGrCrA*mC* mC*mA	2065 9	+ +	HBB 8_inst _RT1 8_PB S15	mG*mU*mA*rArCrGrGrCrArGr ArCrUrUrCrUrCrCrUrCrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrGrUrGrCrAr CrCrUrGrArCrUrCrCrUrGrUrGr GrArGrArArGrUrCrUrGrCrC*m G*mU*mU	2074 9	+
HBB 5_inst _RT1 7_PB S14	mC*mA*mU*rGrGrUrGrCrArCr CrUrGrArCrUrCrCrUrGrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrGrGrCrArGr ArCrUrUrCrUrCrUrArCrArGrGr ArGrUrCrArGrGrUrGrC*mA*m C*mC	2066 0	+ +	HBB 8_inst _RT1 8_PB S14	mG*mU*mA*rArCrGrGrCrArGr ArCrUrUrCrUrCrCrUrCrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrGrUrGrCrAr CrCrUrGrArCrUrCrCrUrGrUrGr GrArGrArArGrUrCrUrGrC*mC* mG*mU	2075 0	+

HBB 5_inst _RT1 7_PB S13	mC*mA*mU*rGrGrUrGrCrArCr CrUrGrArCrUrCrCrUrGrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrGrGrCrArGr ArCrUrUrCrUrCrUrArCrArGrGr ArGrUrCrArGrGrUrG*mC*mA* mC	20661	+ + +	HBB 8_inst _RT1 8_PB S13	mG*mU*mA*rArCrGrGrCrArGr ArCrUrUrCrUrCrCrUrCrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrGrUrGrCrAr CrCrUrGrArCrUrCrCrUrGrUrGr GrArGrArArGrUrCrUrG*mC*m C*mG	20751	+
HBB 5_inst _RT1 7_PB S12	mC*mA*mU*rGrGrUrGrCrArCr CrUrGrArCrUrCrCrUrGrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrGrGrCrArGr ArCrUrUrCrUrCrUrArCrArGrGr ArGrUrCrArGrGrU*mG*mC*m A	20662	+ + +	HBB 8_inst _RT1 8_PB S12	mG*mU*mA*rArCrGrGrCrArGr ArCrUrUrCrUrCrCrUrCrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrGrUrGrCrAr CrCrUrGrArCrUrCrCrUrGrUrGr GrArGrArArGrUrCrU*mG*mC* mC	20752	+ +
HBB 5_inst _RT1 7_PB S11	mC*mA*mU*rGrGrUrGrCrArCr CrUrGrArCrUrCrCrUrGrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrGrGrCrArGr ArCrUrUrCrUrCrUrArCrArGrGr ArGrUrCrArGrG*mU*mG*mC	20663	+ + +	HBB 8_inst _RT1 8_PB S11	mG*mU*mA*rArCrGrGrCrArGr ArCrUrUrCrUrCrCrUrCrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrGrUrGrCrAr CrCrUrGrArCrUrCrCrUrGrUrGr GrArGrArArGrUrC*mU*mG*m C	20753	+
HBB 5_inst _RT1 7_PB S10	mC*mA*mU*rGrGrUrGrCrArCr CrUrGrArCrUrCrCrUrGrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrGrGrCrArGr ArCrUrUrCrUrCrUrArCrArGrGr ArGrUrCrArG*mG*mU*mG	20664	+ + +	HBB 8_inst _RT1 8_PB S10	mG*mU*mA*rArCrGrGrCrArGr ArCrUrUrCrUrCrCrUrCrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrGrUrGrCrAr CrCrUrGrArCrUrCrCrUrGrUrGr GrArGrArArGrU*mC*mU*mG	20754	+
HBB 5_inst _RT1 7_PB S9	mC*mA*mU*rGrGrUrGrCrArCr CrUrGrArCrUrCrCrUrGrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrGrGrCrArGr ArCrUrUrCrUrCrUrArCrArGrGr ArGrUrCrA*mG*mG*mU	20665	+ +	HBB 8_inst _RT1 8_PB S9	mG*mU*mA*rArCrGrGrCrArGr ArCrUrUrCrUrCrCrUrCrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrGrUrGrCrAr CrCrUrGrArCrUrCrCrUrGrUrGr GrArGrArArG*mU*mC*mU	20755	+
HBB 5_inst _RT1	mC*mA*mU*rGrGrUrGrCrArCr CrUrGrArCrUrCrCrUrGrGrUrUr UrUrArGrArGrCrUrArGrArArAr	20666	+	HBB 8_inst _RT1	mG*mU*mA*rArCrGrGrCrArGr ArCrUrUrCrUrCrCrUrCrGrUrUr UrUrArGrArGrCrUrArGrArArAr	20756	+

7_PBS8	UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrGrGrCrArGr ArCrUrUrCrUrCrUrArCrArGrGr ArGrUrC*mA*mG*mG			8_PBS8	UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrGrUrGrCrAr CrCrUrGrArCrUrCrCrUrGrUrGr GrArGrArA*mG*mU*mC		
HBB5_inst_RT16_PBS17	mC*mA*mU*rGrGrUrGrCrArCr CrUrGrArCrUrCrCrUrGrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrGrCrArGrAr CrUrUrCrUrCrUrArCrArGrGrAr GrUrCrArGrGrUrGrCrArCrC*mA*mU*mG	20667	+	HBB8_inst_RT17_PBS17	mG*mU*mA*rArCrGrGrCrArGr ArCrUrUrCrUrCrCrUrCrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrUrGrCrArCr CrUrGrArCrUrCrCrUrGrUrGrGr ArGrArArGrUrCrUrGrCrCrGrU*mU*mA*mC	20757	+
HBB5_inst_RT16_PBS16	mC*mA*mU*rGrGrUrGrCrArCr CrUrGrArCrUrCrCrUrGrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrGrCrArGrAr CrUrUrCrUrCrUrArCrArGrGrAr GrUrCrArGrGrUrGrCrArC*mC*mA*mU	20668	+	HBB8_inst_RT17_PBS16	mG*mU*mA*rArCrGrGrCrArGr ArCrUrUrCrUrCrCrUrCrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrUrGrCrArCr CrUrGrArCrUrCrCrUrGrUrGrGr ArGrArArGrUrCrUrGrCrCrG*mU*mU*mA	20758	+
HBB5_inst_RT16_PBS15	mC*mA*mU*rGrGrUrGrCrArCr CrUrGrArCrUrCrCrUrGrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrGrCrArGrAr CrUrUrCrUrCrUrArCrArGrGrAr GrUrCrArGrGrUrGrCrA*mC*mC*mA	20669	+	HBB8_inst_RT17_PBS15	mG*mU*mA*rArCrGrGrCrArGr ArCrUrUrCrUrCrCrUrCrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrUrGrCrArCr CrUrGrArCrUrCrCrUrGrUrGrGr ArGrArArGrUrCrUrGrCrC*mG*mU*mU	20759	+
HBB5_inst_RT16_PBS14	mC*mA*mU*rGrGrUrGrCrArCr CrUrGrArCrUrCrCrUrGrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrGrCrArGrAr CrUrUrCrUrCrUrArCrArGrGrAr GrUrCrArGrGrUrGrC*mA*mC*mC	20670	+	HBB8_inst_RT17_PBS14	mG*mU*mA*rArCrGrGrCrArGr ArCrUrUrCrUrCrCrUrCrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrUrGrCrArCr CrUrGrArCrUrCrCrUrGrUrGrGr ArGrArArGrUrCrUrGrC*mC*mG*mU	20760	+
HBB5_inst_RT16_PBS13	mC*mA*mU*rGrGrUrGrCrArCr CrUrGrArCrUrCrCrUrGrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr	20671	+ +	HBB8_inst_RT17_PBS13	mG*mU*mA*rArCrGrGrCrArGr ArCrUrUrCrUrCrCrUrCrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr	20761	+

	UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrGrCrArGrAr CrUrUrCrUrCrUrArCrArGrGrAr GrUrCrArGrGrUrG*mC*mA*m C				UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrUrGrCrArCr CrUrGrArCrUrCrCrUrGrUrGrGr ArGrArArGrUrCrUrG*mC*mC* mG		
HBB 5_inst _RT1 6_PB S12	mC*mA*mU*rGrGrUrGrCrArCr CrUrGrArCrUrCrCrUrGrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrGrCrArGrAr CrUrUrCrUrCrUrArCrArGrGrAr GrUrCrArGrGrU*mG*mC*mA	2067 2	+ + +	HBB 8_inst _RT1 7_PB S12	mG*mU*mA*rArCrGrGrCrArGr ArCrUrUrCrUrCrCrUrCrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrUrGrCrArCr CrUrGrArCrUrCrCrUrGrUrGrGr ArGrArArGrUrCrU*mG*mC*m C	2076 2	+ +
HBB 5_inst _RT1 6_PB S11	mC*mA*mU*rGrGrUrGrCrArCr CrUrGrArCrUrCrCrUrGrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrGrCrArGrAr CrUrUrCrUrCrUrArCrArGrGrAr GrUrCrArGrG*mU*mG*mC	2067 3	+ + +	HBB 8_inst _RT1 7_PB S11	mG*mU*mA*rArCrGrGrCrArGr ArCrUrUrCrUrCrCrUrCrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrUrGrCrArCr CrUrGrArCrUrCrCrUrGrUrGrGr ArGrArArGrUrC*mU*mG*mC	2076 3	+ +
HBB 5_inst _RT1 6_PB S10	mC*mA*mU*rGrGrUrGrCrArCr CrUrGrArCrUrCrCrUrGrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrGrCrArGrAr CrUrUrCrUrCrUrArCrArGrGrAr GrUrCrArG*mG*mU*mG	2067 4	+ + +	HBB 8_inst _RT1 7_PB S10	mG*mU*mA*rArCrGrGrCrArGr ArCrUrUrCrUrCrCrUrCrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrUrGrCrArCr CrUrGrArCrUrCrCrUrGrUrGrGr ArGrArArGrU*mC*mU*mG	2076 4	+
HBB 5_inst _RT1 6_PB S9	mC*mA*mU*rGrGrUrGrCrArCr CrUrGrArCrUrCrCrUrGrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrGrCrArGrAr CrUrUrCrUrCrUrArCrArGrGrAr GrUrCrA*mG*mG*mU	2067 5	+ +	HBB 8_inst _RT1 7_PB S9	mG*mU*mA*rArCrGrGrCrArGr ArCrUrUrCrUrCrCrUrCrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrUrGrCrArCr CrUrGrArCrUrCrCrUrGrUrGrGr ArGrArArG*mU*mC*mU	2076 5	+
HBB 5_inst _RT1 6_PB S8	mC*mA*mU*rGrGrUrGrCrArCr CrUrGrArCrUrCrCrUrGrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrGrCrArGrAr	2067 6	+	HBB 8_inst _RT1 7_PB S8	mG*mU*mA*rArCrGrGrCrArGr ArCrUrUrCrUrCrCrUrCrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrUrGrCrArCr	2076 6	+

	CrUrUrCrUrCrUrArCrArGrGrAr GrUrC*mA*mG*mG				CrUrGrArCrUrCrCrUrGrUrGrGr ArGrArA*mG*mU*mC		
HBB 5_inst _RT1 4_PB S17	mC*mA*mU*rGrGrUrGrCrArCr CrUrGrArCrUrCrCrUrGrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrArGrArCrUr UrCrUrCrUrArCrArGrGrArGrUr CrArGrGrUrGrCrArCrC*mA*m U*mG	20677	+	HBB 8_inst _RT1 6_PB S17	mG*mU*mA*rArCrGrGrCrArGr ArCrUrUrCrUrCrCrUrCrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrGrCrArCrCr UrGrArCrUrCrCrUrGrUrGrGrAr GrArArGrUrCrUrGrCrCrGrU*m U*mA*mC	20767	+
HBB 5_inst _RT1 4_PB S16	mC*mA*mU*rGrGrUrGrCrArCr CrUrGrArCrUrCrCrUrGrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrArGrArCrUr UrCrUrCrUrArCrArGrGrArGrUr CrArGrGrUrGrCrArC*mC*mA* mU	20678	+	HBB 8_inst _RT1 6_PB S16	mG*mU*mA*rArCrGrGrCrArGr ArCrUrUrCrUrCrCrUrCrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrGrCrArCrCr UrGrArCrUrCrCrUrGrUrGrGrAr GrArArGrUrCrUrGrCrCrG*mU* mU*mA	20768	+
HBB 5_inst _RT1 4_PB S15	mC*mA*mU*rGrGrUrGrCrArCr CrUrGrArCrUrCrCrUrGrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrArGrArCrUr UrCrUrCrUrArCrArGrGrArGrUr CrArGrGrUrGrCrA*mC*mC*m A	20679	+	HBB 8_inst _RT1 6_PB S15	mG*mU*mA*rArCrGrGrCrArGr ArCrUrUrCrUrCrCrUrCrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrGrCrArCrCr UrGrArCrUrCrCrUrGrUrGrGrAr GrArArGrUrCrUrGrCrC*mG*m U*mU	20769	+
HBB 5_inst _RT1 4_PB S14	mC*mA*mU*rGrGrUrGrCrArCr CrUrGrArCrUrCrCrUrGrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrArGrArCrUr UrCrUrCrUrArCrArGrGrArGrUr CrArGrGrUrGrC*mA*mC*mC	20680	+ +	HBB 8_inst _RT1 6_PB S14	mG*mU*mA*rArCrGrGrCrArGr ArCrUrUrCrUrCrCrUrCrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrGrCrArCrCr UrGrArCrUrCrCrUrGrUrGrGrAr GrArArGrUrCrUrGrC*mC*mG* mU	20770	+
HBB 5_inst _RT1 4_PB S13	mC*mA*mU*rGrGrUrGrCrArCr CrUrGrArCrUrCrCrUrGrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrArGrArCrUr UrCrUrCrUrArCrArGrGrArGrUr CrArGrGrUrG*mC*mA*mC	20681	+ +	HBB 8_inst _RT1 6_PB S13	mG*mU*mA*rArCrGrGrCrArGr ArCrUrUrCrUrCrCrUrCrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrGrCrArCrCr UrGrArCrUrCrCrUrGrUrGrGrAr	20771	+ +

					GrArArGrUrCrUrG*mC*mC*mG		
HBB5_inst_RT14_PBS12	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArCrUrCrCrUrGrGrUrUrUrUrArGrArGrCrUrArGrArArArUrArGrCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrArGrArCrUrUrCrUrCrArCrArGrGrArGrUrCrArArGrGrU*mG*mC*mA	20682	+++	HBB8_inst_RT16_PBS12	mG*mU*mA*rArCrGrGrCrArGrArCrUrUrCrUrCrCrUrCrGrUrUrUrUrArGrArGrCrUrArGrArArArUrArGrCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrGrCrArCrCrUrGrArCrUrCrCrUrGrUrGrGrArGrArGrUrCrU*mG*mC*mC	20772	++
HBB5_inst_RT14_PBS11	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArCrUrCrCrUrGrGrUrUrUrUrArGrArGrCrUrArGrArArArUrArGrCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrArGrArCrUrUrCrUrCrArCrArGrGrArGrUrCrArArGrGrU*mG*mC	20683	+++	HBB8_inst_RT16_PBS11	mG*mU*mA*rArCrGrGrCrArGrArCrUrUrCrUrCrCrUrCrGrUrUrUrUrArGrArGrCrUrArGrArArArUrArGrCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrGrCrArCrCrUrGrArCrUrCrCrUrGrUrGrGrArGrArGrUrC*mU*mG*mC	20773	++
HBB5_inst_RT14_PBS10	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArCrUrCrCrUrGrGrUrUrUrUrArGrArGrCrUrArGrArArArUrArGrCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrArGrArCrUrUrCrUrCrArCrArGrGrArGrUrCrArArGrG*mG*mU*mG	20684	+++	HBB8_inst_RT16_PBS10	mG*mU*mA*rArCrGrGrCrArGrArCrUrUrCrUrCrCrUrCrGrUrUrUrUrArGrArGrCrUrArGrArArArUrArGrCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrGrCrArCrCrUrGrArCrUrCrCrUrGrUrGrGrArGrArGrU*mC*mU*mG	20774	+
HBB5_inst_RT14_PBS9	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArCrUrCrCrUrGrGrUrUrUrUrArGrArGrCrUrArGrArArArUrArGrCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrArGrArCrUrUrCrUrCrArCrArGrGrArGrUrCrArArGrA*mG*mG*mU	20685	+++	HBB8_inst_RT16_PBS9	mG*mU*mA*rArCrGrGrCrArGrArCrUrUrCrUrCrCrUrCrGrUrUrUrUrArGrArGrCrUrArGrArArArUrArGrCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrGrCrArCrCrUrGrArCrUrCrCrUrGrUrGrGrArGrArG*mU*mC*mU	20775	+
HBB5_inst_RT14_PBS8	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArCrUrCrCrUrGrGrUrUrUrUrArGrArGrCrUrArGrArArArUrArGrCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrArGrArCrUrUrCrUrCrArCrArGrGrArGrUrCrArArGrC*mA*mG*mG	20686	++	HBB8_inst_RT16_PBS8	mG*mU*mA*rArCrGrGrCrArGrArCrUrUrCrUrCrCrUrCrGrUrUrUrUrArGrArGrCrUrArGrArArArUrArGrCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrGrCrArCrCrUrGrArCrUrCrCrUrGrUrGrGrArGrArA*mG*mU*mC	20776	+
HBB5_inst_RT1	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArCrUrCrCrUrGrGrUrUrUrUrArGrArGrCrUrArGrArArArUrArGrCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrArGrArCrUrUrCrUrCrArCrArGrGrArGrUrCrArArGrA	20687	+	HBB8_inst_RT1	mG*mU*mA*rArCrGrGrCrArGrArCrUrUrCrUrCrCrUrCrGrUrUrUrUrArGrArGrCrUrArGrArArArUrArGrCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrGrCrArCrCrUrGrArCrUrCrCrUrGrUrGrGrArGrArA	20777	+

3_PBS17	UrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrGrArCrUrUrCrUrCrUrArCrArGrGrArGrUrCrArGrGrUrGrCrArCrC*mA*mU*mG			4_PBS17	UrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrArCrCrUrGrArCrUrCrCrUrGrUrGrGrArGrArArGrUrCrUrGrCrCrGrU*mU*mA*mC		
HBB5_inst_RT13_PBS16	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArCrUrCrCrUrGrGrUrUrUrUrArGrArGrCrUrArGrArArArUrArGrCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrGrArCrUrUrCrUrCrUrArCrArGrGrArGrUrCrArGrGrUrGrCrArC*mC*mA*mU	20688	+	HBB8_inst_RT14_PBS16	mG*mU*mA*rArCrGrGrCrArGrArCrUrUrCrUrCrCrUrCrGrUrUrUrUrArGrArGrCrUrArGrArArArUrArGrCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrGrArCrUrUrCrUrCrUrArCrArGrGrArGrUrCrArGrGrUrGrCrArG*mU*mU*mA	20778	+
HBB5_inst_RT13_PBS15	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArCrUrCrCrUrGrGrUrUrUrUrArGrArGrCrUrArGrArArArUrArGrCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrGrArCrUrUrCrUrCrUrArCrArGrGrArGrUrCrArGrGrUrGrCrA*mC*mC*mA	20689	+	HBB8_inst_RT14_PBS15	mG*mU*mA*rArCrGrGrCrArGrArCrUrUrCrUrCrCrUrCrGrUrUrUrUrArGrArGrCrUrArGrArArArUrArGrCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrGrArCrUrUrCrUrCrUrArCrArGrGrArGrUrCrArGrGrUrGrCrC*mG*mU*mU	20779	+
HBB5_inst_RT13_PBS14	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArCrUrCrCrUrGrGrUrUrUrUrArGrArGrCrUrArGrArArArUrArGrCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrGrArCrUrUrCrUrCrUrArCrArGrGrArGrUrCrArGrGrUrGrCrA*mC*mC	20690	+	HBB8_inst_RT14_PBS14	mG*mU*mA*rArCrGrGrCrArGrArCrUrUrCrUrCrCrUrCrGrUrUrUrUrArGrArGrCrUrArGrArArArUrArGrCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrGrArCrUrUrCrUrCrUrArCrArGrGrArGrUrCrArGrGrUrGrCrC*mC*mG*mU	20780	+ +
HBB5_inst_RT13_PBS13	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArCrUrCrCrUrGrGrUrUrUrUrArGrArGrCrUrArGrArArArUrArGrCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrGrArCrUrUrCrUrCrUrArCrArGrGrArGrUrCrArGrGrUrGrCrA*mC*mC	20691	+ +	HBB8_inst_RT14_PBS13	mG*mU*mA*rArCrGrGrCrArGrArCrUrUrCrUrCrCrUrCrGrUrUrUrUrArGrArGrCrUrArGrArArArUrArGrCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrGrArCrUrUrCrUrCrUrArCrArGrGrArGrUrCrArGrGrUrGrCrG*mC*mC*mG	20781	+ +
HBB5_inst_RT13_PBS12	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArCrUrCrCrUrGrGrUrUrUrUrArGrArGrCrUrArGrArArArUrArGrCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrGrArCrUrUrCrUrCrUrArCrArGrGrArGrUrCrArGrGrUrGrCrG*mC*mA*mC	20692	+ + +	HBB8_inst_RT14_PBS12	mG*mU*mA*rArCrGrGrCrArGrArCrUrUrCrUrCrCrUrCrGrUrUrUrUrArGrArGrCrUrArGrArArArUrArGrCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrGrArCrUrUrCrUrCrUrArCrArGrGrArGrUrCrArGrGrUrGrCrG*mC*mC*mG	20782	+ +

	GrUrCrGrGrUrGrCrGrArCrUrUr CrUrCrUrArCrArGrGrArGrUrCr ArGrGrU*mG*mC*mA				GrUrCrGrGrUrGrCrArCrCrUrGr ArCrUrCrCrUrGrUrGrGrArGrAr ArGrUrCrU*mG*mC*mC		
HBB 5_inst _RT1 3_PB S11	mC*mA*mU*rGrGrUrGrCrArCr CrUrGrArCrUrCrCrUrGrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrGrArCrUrUr CrUrCrUrArCrArGrGrArGrUrCr ArGrG*mU*mG*mC	2069 3	+ + +	HBB 8_inst _RT1 4_PB S11	mG*mU*mA*rArCrGrGrCrArGr ArCrUrUrCrUrCrCrUrCrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrArCrCrUrGr ArCrUrCrCrUrGrUrGrGrArGrAr ArGrUrC*mU*mG*mC	2078 3	+ +
HBB 5_inst _RT1 3_PB S10	mC*mA*mU*rGrGrUrGrCrArCr CrUrGrArCrUrCrCrUrGrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrGrArCrUrUr CrUrCrUrArCrArGrGrArGrUrCr ArG*mG*mU*mG	2069 4	+ + +	HBB 8_inst _RT1 4_PB S10	mG*mU*mA*rArCrGrGrCrArGr ArCrUrUrCrUrCrCrUrCrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrArCrCrUrGr ArCrUrCrCrUrGrUrGrGrArGrAr ArGrU*mC*mU*mG	2078 4	+ +
HBB 5_inst _RT1 3_PB S9	mC*mA*mU*rGrGrUrGrCrArCr CrUrGrArCrUrCrCrUrGrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrGrArCrUrUr CrUrCrUrArCrArGrGrArGrUrCr A*mG*mG*mU	2069 5	+ + +	HBB 8_inst _RT1 4_PB S9	mG*mU*mA*rArCrGrGrCrArGr ArCrUrUrCrUrCrCrUrCrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrArCrCrUrGr ArCrUrCrCrUrGrUrGrGrArGrAr ArG*mU*mC*mU	2078 5	+
HBB 5_inst _RT1 3_PB S8	mC*mA*mU*rGrGrUrGrCrArCr CrUrGrArCrUrCrCrUrGrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrGrArCrUrUr CrUrCrUrArCrArGrGrArGrUrC* mA*mG*mG	2069 6	+ +	HBB 8_inst _RT1 4_PB S8	mG*mU*mA*rArCrGrGrCrArGr ArCrUrUrCrUrCrCrUrCrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrArCrCrUrGr ArCrUrCrCrUrGrUrGrGrArGrAr A*mG*mU*mC	2078 6	+ +
HBB 5_inst _RT1 2_PB S17	mC*mA*mU*rGrGrUrGrCrArCr CrUrGrArCrUrCrCrUrGrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrArCrUrUrCr UrCrUrArCrArGrGrArGrUrCrAr GrGrUrGrCrArCrC*mA*mU*m G	2069 7	+	HBB 8_inst _RT1 1_PB S17	mG*mU*mA*rArCrGrGrCrArGr ArCrUrUrCrUrCrCrUrCrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrUrGrArCrUr CrCrUrGrUrGrGrArGrArArGrUr CrUrGrCrCrGrU*mU*mA*mC	2078 7	+
HBB 5_inst	mC*mA*mU*rGrGrUrGrCrArCr CrUrGrArCrUrCrCrUrGrGrUrUr	2069 8	+	HBB 8_inst	mG*mU*mA*rArCrGrGrCrArGr ArCrUrUrCrUrCrCrUrCrGrUrUr	2078 8	+

_RT12_PBS16	UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrArCrUrUrCr UrCrUrArCrArGrGrArGrUrCrAr GrGrUrGrCrArC*mC*mA*mU			_RT11_PBS16	UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrUrGrArCrUr CrCrUrGrUrGrGrArGrArArGrUr CrUrGrCrCrG*mU*mU*mA		
HBB5_inst_RT12_PBS15	mC*mA*mU*rGrGrUrGrCrArCr CrUrGrArCrUrCrCrUrGrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrArCrUrUrCr UrCrUrArCrArGrGrArGrUrCrAr GrGrUrGrCrA*mC*mC*mA	20699	+	HBB8_inst_RT11_PBS15	mG*mU*mA*rArCrGrGrCrArGr ArCrUrUrCrUrCrCrUrCrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrUrGrArCrUr CrCrUrGrUrGrGrArGrArArGrUr CrUrGrCrC*mG*mU*mU	20789	+
HBB5_inst_RT12_PBS14	mC*mA*mU*rGrGrUrGrCrArCr CrUrGrArCrUrCrCrUrGrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrArCrUrUrCr UrCrUrArCrArGrGrArGrUrCrAr GrGrUrGrC*mA*mC*mC	20700	+	HBB8_inst_RT11_PBS14	mG*mU*mA*rArCrGrGrCrArGr ArCrUrUrCrUrCrCrUrCrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrUrGrArCrUr CrCrUrGrUrGrGrArGrArArGrUr CrUrGrC*mC*mG*mU	20790	+
HBB5_inst_RT12_PBS13	mC*mA*mU*rGrGrUrGrCrArCr CrUrGrArCrUrCrCrUrGrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrArCrUrUrCr UrCrUrArCrArGrGrArGrUrCrAr GrGrUrG*mC*mA*mC	20701	+	HBB8_inst_RT11_PBS13	mG*mU*mA*rArCrGrGrCrArGr ArCrUrUrCrUrCrCrUrCrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrUrGrArCrUr CrCrUrGrUrGrGrArGrArArGrUr CrUrG*mC*mC*mG	20791	+ +
HBB5_inst_RT12_PBS12	mC*mA*mU*rGrGrUrGrCrArCr CrUrGrArCrUrCrCrUrGrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrArCrUrUrCr UrCrUrArCrArGrGrArGrUrCrAr GrGrU*mG*mC*mA	20702	+ +	HBB8_inst_RT11_PBS12	mG*mU*mA*rArCrGrGrCrArGr ArCrUrUrCrUrCrCrUrCrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrUrGrArCrUr CrCrUrGrUrGrGrArGrArArGrUr CrU*mG*mC*mC	20792	+ +
HBB5_inst_RT12_PBS11	mC*mA*mU*rGrGrUrGrCrArCr CrUrGrArCrUrCrCrUrGrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrArCrUrUrCr	20703	+ +	HBB8_inst_RT11_PBS11	mG*mU*mA*rArCrGrGrCrArGr ArCrUrUrCrUrCrCrUrCrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrUrGrArCrUr	20793	+ +

	UrCrUrArCrArGrGrArGrUrCrAr GrG*mU*mG*mC				CrCrUrGrUrGrGrArGrArArGrUr C*mU*mG*mC		
HBB 5_inst _RT1 2_PB S10	mC*mA*mU*rGrGrUrGrCrArCr CrUrGrArCrUrCrCrUrGrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrArCrUrUrCr UrCrUrArCrArGrGrArGrUrCrAr G*mG*mU*mG	2070 4	+ +	HBB 8_inst _RT1 1_PB S10	mG*mU*mA*rArCrGrGrCrArGr ArCrUrUrCrUrCrCrUrCrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrUrGrArCrUr CrCrUrGrUrGrGrArGrArArGrU *mC*mU*mG	2079 4	+ +
HBB 5_inst _RT1 2_PB S9	mC*mA*mU*rGrGrUrGrCrArCr CrUrGrArCrUrCrCrUrGrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrArCrUrUrCr UrCrUrArCrArGrGrArGrUrCrA* mG*mG*mU	2070 5	+ +	HBB 8_inst _RT1 1_PB S9	mG*mU*mA*rArCrGrGrCrArGr ArCrUrUrCrUrCrCrUrCrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrUrGrArCrUr CrCrUrGrUrGrGrArGrArArG*m U*mC*mU	2079 5	+
HBB 5_inst _RT1 2_PB S8	mC*mA*mU*rGrGrUrGrCrArCr CrUrGrArCrUrCrCrUrGrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrArCrUrUrCr UrCrUrArCrArGrGrArGrUrC*m A*mG*mG	2070 6	+ +	HBB 8_inst _RT1 1_PB S8	mG*mU*mA*rArCrGrGrCrArGr ArCrUrUrCrUrCrCrUrCrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrUrGrArCrUr CrCrUrGrUrGrGrArGrArA*mG* mU*mC	2079 6	+
HBB 5_inst _RT1 0_PB S17	mC*mA*mU*rGrGrUrGrCrArCr CrUrGrArCrUrCrCrUrGrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrUrUrCrUrCr UrArCrArGrGrArGrUrCrArGrGr UrGrCrArCrC*mA*mU*mG	2070 7	+	HBB 8_inst _RT1 0_PB S17	mG*mU*mA*rArCrGrGrCrArGr ArCrUrUrCrUrCrCrUrCrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrGrArCrUrCr CrUrGrUrGrGrArGrArArGrUrCr UrGrCrCrGrU*mU*mA*mC	2079 7	+
HBB 5_inst _RT1 0_PB S16	mC*mA*mU*rGrGrUrGrCrArCr CrUrGrArCrUrCrCrUrGrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrUrUrCrUrCr UrArCrArGrGrArGrUrCrArGrGr UrGrCrArC*mC*mA*mU	2070 8	+	HBB 8_inst _RT1 0_PB S16	mG*mU*mA*rArCrGrGrCrArGr ArCrUrUrCrUrCrCrUrCrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrGrArCrUrCr CrUrGrUrGrGrArGrArArGrUrCr UrGrCrCrG*mU*mU*mA	2079 8	+
HBB 5_inst _RT1	mC*mA*mU*rGrGrUrGrCrArCr CrUrGrArCrUrCrCrUrGrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr	2070 9	+	HBB 8_inst _RT1	mG*mU*mA*rArCrGrGrCrArGr ArCrUrUrCrUrCrCrUrCrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr	2079 9	+

0_PBS15	UrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrUrUrCrUrCrUrArCrArGrGrArGrUrCrArGrGrUrGrCrA*mC*mC*mA			0_PBS15	UrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrGrArCrUrCrCrUrGrUrGrUrGrGrArGrArArGrUrCrUrGrC*mG*mU*mU		
HBB5_inst_RT10_PBS14	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArCrUrCrCrUrGrGrUrUrUrUrArGrArGrCrUrArArGrArGrUrUrArArArArArUrArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrUrUrCrUrCrUrArCrArGrGrArGrUrCrArGrGrUrGrC*mA*mC*mC	20710	+	HBB8_inst_RT10_PBS14	mG*mU*mA*rArCrGrGrCrArGrArCrUrUrCrUrCrCrUrCrGrUrUrUrUrArGrArGrCrUrArArGrArGrUrUrArArArArArUrArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrGrArCrUrCrCrUrGrUrGrUrGrGrArGrArArGrUrCrUrGrC*mC*mG*mU	20800	+
HBB5_inst_RT10_PBS13	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArCrUrCrCrUrGrGrUrUrUrUrArGrArGrCrUrArArGrArGrUrUrArArArArArUrArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrUrUrCrUrCrUrArCrArGrGrArGrUrCrArGrGrUrG*mC*mA*mC	20711	+	HBB8_inst_RT10_PBS13	mG*mU*mA*rArCrGrGrCrArGrArCrUrUrCrUrCrCrUrCrGrUrUrUrUrArGrArGrCrUrArArGrArGrUrUrArArArArArUrArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrGrArCrUrCrCrUrGrUrGrUrGrGrArGrArArGrUrCrUrGrC*mC*mC*mG	20801	+ +
HBB5_inst_RT10_PBS12	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArCrUrCrCrUrGrGrUrUrUrUrArGrArGrCrUrArArGrArGrUrUrArArArArArUrArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrUrUrCrUrCrUrArCrArGrGrArGrUrCrArGrGrU*mG*mC*mA	20712	+	HBB8_inst_RT10_PBS12	mG*mU*mA*rArCrGrGrCrArGrArCrUrUrCrUrCrCrUrCrGrUrUrUrUrArGrArGrCrUrArArGrArGrUrUrArArArArArUrArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrGrArCrUrCrCrUrGrUrGrUrGrGrArGrArArGrUrCrUrGrU*mG*mC*mC	20802	+
HBB5_inst_RT10_PBS11	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArCrUrCrCrUrGrGrUrUrUrUrArGrArGrCrUrArArGrArGrUrUrArArArArArUrArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrUrUrCrUrCrUrArCrArGrGrArGrUrCrArGrG*mU*mG*mC	20713	+	HBB8_inst_RT10_PBS11	mG*mU*mA*rArCrGrGrCrArGrArCrUrUrCrUrCrCrUrCrGrUrUrUrUrArGrArGrCrUrArArGrArGrUrUrArArArArArUrArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrGrArCrUrCrCrUrGrUrGrUrGrGrArGrArArGrUrC*mU*mG*mC	20803	+
HBB5_inst_RT10_PBS10	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArCrUrCrCrUrGrGrUrUrUrUrArGrArGrCrUrArArGrArGrUrUrArArArArArUrArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrUrUrCrUrCrUrArCrArGrGrArGrUrCrArG*mG*mU*mG	20714	+	HBB8_inst_RT10_PBS10	mG*mU*mA*rArCrGrGrCrArGrArCrUrUrCrUrCrCrUrCrGrUrUrUrUrArGrArGrCrUrArArGrArGrUrUrArArArArArUrArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrGrArCrUrCrCrUrGrUrGrUrGrGrArGrArArGrU*mC*mU*mG	20804	+

HBB 5_inst_RT10_PBS9	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArCrUrCrCrUrGrGrUrUrUrUrArGrArGrCrUrArGrArArArUrArGrCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrUrUrCrUrCrUrArCrArGrGrArGrUrCrA*mG*mG*mU	20715	+	HBB 8_inst_RT10_PBS9	mG*mU*mA*rArCrGrGrCrArGrArCrUrUrCrUrCrCrUrCrGrUrUrUrUrArGrArGrCrUrArGrArArArUrArGrCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrGrArCrUrCrCrUrGrUrGrUrGrArGrArArG*mU*mC*mU	20805	+
HBB 5_inst_RT10_PBS8	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArCrUrCrCrUrGrGrUrUrUrUrArGrArGrCrUrArGrArArArUrArGrCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrUrUrCrUrCrUrArCrArGrGrArGrUrC*mA*mG*mG	20716	+	HBB 8_inst_RT10_PBS8	mG*mU*mA*rArCrGrGrCrArGrArCrUrUrCrUrCrCrUrCrGrUrUrUrUrArGrArGrCrUrArGrArArArUrArGrCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrGrArCrUrCrCrUrGrUrGrUrGrArGrArA*mG*mU*mC	20806	+
HBB 5_inst_RT9_PBS17	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArCrUrCrCrUrGrGrUrUrUrUrArGrArGrCrUrArGrArArArUrArGrCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrUrUrCrUrCrUrArCrArGrGrArGrUrCrArGrGrUrGrCrArArC*mA*mU*mG	20717	+	HBB 8_inst_RT9_PBS17	mG*mU*mA*rArCrGrGrCrArGrArCrUrUrCrUrCrCrUrCrGrUrUrUrUrArGrArGrCrUrArGrArArArUrArGrCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrArCrUrCrCrUrGrUrGrUrGrArGrArArGrUrCrUrGrCrCrGrU*mU*mA*mC	20807	+
HBB 5_inst_RT9_PBS16	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArCrUrCrCrUrGrGrUrUrUrUrArGrArGrCrUrArGrArArArUrArGrCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrUrUrCrUrCrUrArCrArGrGrArGrUrCrArGrGrUrGrCrArC*mC*mA*mU	20718	+	HBB 8_inst_RT9_PBS16	mG*mU*mA*rArCrGrGrCrArGrArCrUrUrCrUrCrCrUrCrGrUrUrUrUrArGrArGrCrUrArGrArArArUrArGrCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrArCrUrCrCrUrGrUrGrUrGrArGrArArGrUrCrUrGrCrCrG*mU*mU*mA	20808	+
HBB 5_inst_RT9_PBS15	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArCrUrCrCrUrGrGrUrUrUrUrArGrArGrCrUrArGrArArArUrArGrCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrUrUrCrUrCrUrArCrArGrGrArGrUrCrArGrGrUrGrCrA*mC*mC*mA	20719	+	HBB 8_inst_RT9_PBS15	mG*mU*mA*rArCrGrGrCrArGrArCrUrUrCrUrCrCrUrCrGrUrUrUrUrArGrArGrCrUrArGrArArArUrArGrCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrArCrUrCrCrUrGrUrGrUrGrArGrArArGrUrCrUrGrCrC*mG*mU*mU	20809	+
HBB 5_inst_RT9_PBS14	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArCrUrCrCrUrGrGrUrUrUrUrArGrArGrCrUrArGrArArArUrArGrCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrUrUrCrUrCrUrArCrArGrGrArGrUrCrArGrGrUrGrCrA*mC*mU*mA	20720	+	HBB 8_inst_RT9_PBS14	mG*mU*mA*rArCrGrGrCrArGrArCrUrUrCrUrCrCrUrCrGrUrUrUrUrArGrArGrCrUrArGrArArArUrArGrCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrArCrUrCrCrUrGrUrGrUrGrArGrArArGrUrCrUrGrCrC*mU*mC	20810	+

	ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrUrCrUrCrUr ArCrArGrGrArGrUrCrArGrGrUr GrC*mA*mC*mC				ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrArCrUrCrCr UrGrUrGrGrArGrArArGrUrCrUr GrC*mC*mG*mU		
HBB 5_inst _RT9 _PBS 13	mC*mA*mU*rGrGrUrGrCrArCr CrUrGrArCrUrCrCrUrGrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrUrCrUrCrUr ArCrArGrGrArGrUrCrArGrGrUr G*mC*mA*mC	20721	+	HBB 8_inst _RT9 _PBS 13	mG*mU*mA*rArCrGrGrCrArGr ArCrUrUrCrUrCrCrUrCrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrArCrUrCrCr UrGrUrGrGrArGrArArGrUrCrUr G*mC*mC*mG	20811	+
HBB 5_inst _RT9 _PBS 12	mC*mA*mU*rGrGrUrGrCrArCr CrUrGrArCrUrCrCrUrGrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrUrCrUrCrUr ArCrArGrGrArGrUrCrArGrGrU *mG*mC*mA	20722	+	HBB 8_inst _RT9 _PBS 12	mG*mU*mA*rArCrGrGrCrArGr ArCrUrUrCrUrCrCrUrCrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrArCrUrCrCr UrGrUrGrGrArGrArArGrUrCrU *mG*mC*mC	20812	+
HBB 5_inst _RT9 _PBS 11	mC*mA*mU*rGrGrUrGrCrArCr CrUrGrArCrUrCrCrUrGrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrUrCrUrCrUr ArCrArGrGrArGrUrCrArGrG*m U*mG*mC	20723	+	HBB 8_inst _RT9 _PBS 11	mG*mU*mA*rArCrGrGrCrArGr ArCrUrUrCrUrCrCrUrCrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrArCrUrCrCr UrGrUrGrGrArGrArArGrUrC*m U*mG*mC	20813	+
HBB 5_inst _RT9 _PBS 10	mC*mA*mU*rGrGrUrGrCrArCr CrUrGrArCrUrCrCrUrGrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrUrCrUrCrUr ArCrArGrGrArGrUrCrArG*mG* mU*mG	20724	+	HBB 8_inst _RT9 _PBS 10	mG*mU*mA*rArCrGrGrCrArGr ArCrUrUrCrUrCrCrUrCrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrArCrUrCrCr UrGrUrGrGrArGrArArGrU*mC* mU*mG	20814	
HBB 5_inst _RT9 _PBS 9	mC*mA*mU*rGrGrUrGrCrArCr CrUrGrArCrUrCrCrUrGrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrUrCrUrCrUr ArCrArGrGrArGrUrCrA*mG*m G*mU	20725	+	HBB 8_inst _RT9 _PBS 9	mG*mU*mA*rArCrGrGrCrArGr ArCrUrUrCrUrCrCrUrCrGrUrUr UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrArCrUrCrCr UrGrUrGrGrArGrArArG*mU*m C*mU	20815	+
HBB 5_inst	mC*mA*mU*rGrGrUrGrCrArCr CrUrGrArCrUrCrCrUrGrGrUrUr	20726	+	HBB 8_inst	mG*mU*mA*rArCrGrGrCrArGr ArCrUrUrCrUrCrCrUrCrGrUrUr	20816	+

_RT9_PBS8	UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrUrCrUrCrUr ArCrArGrGrArGrUrC*mA*mG* mG			_RT9_PBS8	UrUrArGrArGrCrUrArGrArArAr UrArGrCrArArGrUrUrArArArAr UrArArGrGrCrUrArGrUrCrCrGr UrUrArUrCrArArCrUrUrGrArAr ArArArGrUrGrGrCrArCrCrGrAr GrUrCrGrGrUrGrCrArCrUrCrCr UrGrUrGrGrArGrArA*mG*mU* mC		

Example 4: Screening configurations of template RNAs that correct the SCD mutation in a genomic landing pad in human cells

This example describes the use of gene modifying system containing a gene modifying polypeptide and template RNAs comprising varied lengths of heterologous object sequences and PBS sequences to identify favorable configurations for correction of the SCD mutation. In this example, a template RNA contains:

(1) a gRNA spacer;

(2) a gRNA scaffold;

(3) a heterologous object sequence; and

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

The template RNAs were designed to contain 8 – 17 nt PBS sequences and 9 – 20 nt heterologous object sequences (Tables A and B). Two different gRNA spacer sequences, designated HBB5 (see Table A) and HBB8 (see Table B), were used to target sites proximal to the SCD mutation in the custom genomic landing pad in human cells. The heterologous object sequences and PBS sequences were designed to correct the SCD mutation in the landing pad by replacing a "T" nucleotide with an "A" nucleotide at the mutation site using a gene modifying system described herein.

A cell line was created to have a "landing pad" or a stable integration that mimic a region of the HBB gene that contains sequences flanking the SCD mutation site. The DNA for the landing pad was chemically synthesized and cloned into the pLenti-N-tGFP vector. The cloned landing pad into the lentiviral expression vector was confirmed and the sequence was verified by Sanger sequencing of the landing pad. The sequence verified plasmids (9μg) along with the lentiviral packaging mix (9μg, obtained from Biosettia) were transfected using Lipofectamine2000™ according to the manufacturer instructions into a packaging cell line, LentiX-293T (Takara Bio). The transfected cells were incubated at 37°C, 5% CO_2 for 48 hours (including one medium change at 24hrs) and the viral particle containing medium was collected

from the cell culture dish. The collected medium was filtered through a 0.2 μm filter to remove cell debris and prepared for transduction of HEK293T cells. The virus-containing medium was diluted in DMEM and mixed with polybrene to prepare a dilution series for transduction of HEK293T cells where the final concentration of polybrene was 8 μg/ml. The HEK293T cells were grown in viral containing medium for 48 hour and then split with fresh medium. The split cells were grown to confluence and transduction efficiency of the different dilutions of virus were measured by GFP expression via flow cytometry and ddPCR detection of the genomic integrated lentivirus that contained GFP and the HBB landing pads.

A gene modifying system comprising a gene modifying polypeptide (see Table C) and a template RNA was transfected into the HEK293T landing pad cell line. The gene modifying polypeptide and the template RNAs were delivered by nucleofection in RNA format. Specifically, 1μg of gene modifying polypeptide mRNA was combined with 10μM template RNAs. The mRNA and template RNAs were added to 25μL SF buffer containing 250,000 HEK293T landing pad cells and cells were nucleofected using program DS-150. After nucleofection, cells were grown at 37˚C, 5% CO_2 for 3 days prior to cell lysis and genomic DNA extraction. To analyze gene editing activity, primers flanking the HBB genomic target site were used to amplify across the locus. Amplicons are analyzed via short read sequencing using an Illumina MiSeq. Gene editing activity with high editing efficiency was detected in the configurations with 9 – 12nt PBS sequence and 12 – 14 nt heterologous object sequence, and is shown in Tables A and B. In particular, in Tables A and B, "+" indicates an editing frequency of <3%, "++" indicates an editing frequency of 3-7%, and "+++" indicates an editing frequency of >=7%.

It is understood that the template RNA sequences shown in Tables A and may be customized depending on the cell being targeted. For example, HEK293T cells have a SNP in the HBB gene (NC_000011.10:g.5227013A>G (T>C in HBB coding strand) relative to human hg38 reference genome), and thus the template RNA sequences shown in Tables A and B are suitable for use in a cell with that SNP. Template RNAs suitable for use in a cell with a different sequence at that SNP position ("no SNP") may utilize the sequences below, wherein capital letters indicate core sequences and lower case letters indicate flanking sequences, and underlining indicates the mutation region. Similarly, in some embodiments it is desired to inactive a PAM sequence upon editing ("PAM-kill") and in other embodiments it is preferred to

leave the PAM sequence intact (no PAM-kill). The RT template can be designed as a "PAM-kill" or "no PAM-kill" version, for example, as shown below.

HBB5 Spacer (no SNP): CATGGTGCATCTGACTCCTG (SEQ ID NO: 21668)

HBB5 PBS (no SNP): GAGTCAGAtgcaccatg (SEQ ID NO: 21669)

HBB5 RT template (no PAM-kill): aacggcagactTCTCGTCAG (SEQ ID NO: 21670)

HBB8 RT template (no SNP): tggtgcatctgACTCCTGAG (SEQ ID NO: 21671)

Table A: HBB5 Sequences. *The columns indicate, from left to right: 1) Name of the template RNA, 2) gRNA spacer sequence of the template RNA, which contains a SNP relative to hg38 that is present in HEK293T cells, 3) SpCas9 gRNA scaffold sequence of the template RNA, 4) PBS sequence of the template RNA, which contains a SNP relative to hg38 that is present in HEK293T cells, 5) RT template sequence of the template RNA, wherein the PAM-kill mutation is bolded and the mutation region is underlined, 6) full template RNA sequence comprising HEK293T SNP and PAM-kill edit, 7) Full template RNA sequence depicted as RNA corresponding to column 6, further showing chemical modifications as used in Example 4, 8) alternative template RNA sequence designed relative to hg38 reference genome (lacking HEK293T SNP) and comprising PAM-kill edit, 9) alternative template RNA sequence designed relative to hg38 reference genome (lacking HEK293T SNP) and lacking PAM-kill edit and 10) observed activity of template RNA of column 7 as defined in Example 4.*

Name	Spacer	SEQ ID NO	gRNA Scaffold	SEQ ID NO	PBS	SEQ ID NO	RT Template: (**PAM-kill**; Correction)	SEQ ID NO	Template Sequence (+SNP +PAM-kill)	SEQ ID NO	Template Sequence (+SNP +PAM-kill) (RNA)	SEQ ID NO	Template Sequence (no SNP +PAM-kill)	SEQ ID NO	Template Sequence (no SNP no PAM-kill)	SEQ ID NO	Activity
HBB5_RT20_PBS17	CATGGTGCACCTGACTCCTG	19251	GTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCG	19341	GAGTCAGGTGCACCATG	19431	AACGGCAGACTTCTC**T**TCAG	19521	CATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACGGCAGACTTCTCTTCAGGAGTCAGGTGCACCATG	19611	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArCrUrCrCrUrGrGrUrUrUrUrArGrGrArArArArUrArGrCrArArGrGrUrUrArArArArUrArArArGrGrCrUrArGrGrUrCrCrGrUrUrArUrCrArArCrUrUrGrGrArArArArArArGrUrGrGrCrArCrCrCrGrArGrUrCrGrGrUrGrCrArArCrGrGrCrArGrArCrUrUrCrUrCrArGrGrArGrUrCrArGrGrUrGrCrArCrCrArG*mA*mU*mG	19701	CATGGTGCATCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACGGCAGACTTCTCTTCAGGA	19791	CATGGTGCATCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC	19881	++

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HBB 5_RT 19_P BS14	CAT GG TGC AC CTG ACT CCT G	19 26 4	GTTT TAGA GCTA GAA ATAG CAA GTTA AAAT AAG GCTA GTCC GTTA TCAA CTTG AAA AAGT GGC ACCG AGTC GGTG C	19 35 4	GAGT CAGG TGCA CC	19 44 4	ACGGC AGACT TCTCT**T** T̲CAG	19 53 4	CATGGTGCACCT GACTCCTGGTTT TAGAGCTAGAAA TAGCAAGTTAAA ATAAGGCTAGTC CGTTATCAACTT GAAAAAGTGGC ACCGAGTCGGTG CACGGCAGACTT CTCTTCAGGAGT CAGGTGCACC	19 62 4	mC*mA*mU*rGrGr UrGrCrArCrCrUrGr ArCrUrCrCrUrGrGr UrUrUrUrArGrArArUr CrUrArGrArArArUr ArGrCrArArGrUrUr ArArArArUrArArGr GrCrUrArGrUrCrCr GrUrUrArUrCrArAr CrUrUrGrArArArAr ArGrUrGrGrCrArCr CrGrArGrUrCrGrGr UrGrCrArCrGrGrCr ArGrArCrUrUrCrUr CrUrUrCrArGrGrAr GrUrCrArGrGrUrGr C*mA*mC*mC	197 14	CATGGTG CATCTGA CTCCTGG TTTTAGA GCTAGA AATAGC AAGTTA AAATAA GGCTAGT CCGTTAT CAACTTG AAAAAG TGGCACC GAGTCG GTGCAC GGCAGA CTTCTCT TCAGGA GTCAGAT GCACC	198 04	AGATG CACCA CATGG TGCAT CTGAC TCCTG GTTTT AGAGC TAGAA ATAGC AAGTT AAAAT AAGGC TAGTC CGTTA TCAAC TTGAA AAAGT GGCAC CGAGT CGGTG CACGG CAGAC TTCTC GTCAG GAGTC AGATG CACC	198 94	+++
HBB 5_RT 19_P BS13	CAT GG TGC AC CTG ACT CCT G	19 26 5	GTTT TAGA GCTA GAA ATAG CAA GTTA AAAT AAG GCTA GTCC GTTA TCAA	19 35 5	GAGT CAGG TGCA C	19 44 5	ACGGC AGACT TCTCT**T** T̲CAG	19 53 5	CATGGTGCACCT GACTCCTGGTTT TAGAGCTAGAAA TAGCAAGTTAAA ATAAGGCTAGTC CGTTATCAACTT GAAAAAGTGGC ACCGAGTCGGTG CACGGCAGACTT CTCTTCAGGAGT CAGGTGCAC	19 62 5	mC*mA*mU*rGrGr UrGrCrArCrCrUrGr ArCrUrCrCrUrGrGr UrUrUrUrArGrArArUr CrUrArGrArArArUr ArGrCrArArGrUrUr ArArArArUrArArGr GrCrUrArGrUrCrCr GrUrUrArUrCrArAr CrUrUrGrArArArAr ArGrUrGrGrCrArCr CrGrArGrUrCrGrGr UrGrCrArCrGrGrCr	197 15	CATGGTG CATCTGA CTCCTGG TTTTAGA GCTAGA AATAGC AAGTTA AAATAA GGCTAGT CCGTTAT CAACTTG AAAAAG TGGCACC	198 05	AGATG CACCA CATGG TGCAT CTGAC TCCTG GTTTT AGAGC TAGAA ATAGC AAGTT AAAAT AAGGC TAGTC	198 95	+++

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Name	Teplate Sequence (+SNP +PA-kill) (NA)	SEQ ID NO
HBB5_RT20_PBS17	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCAACGGCAGACUUCUCUUCAGGAGUCAGGUGCACCAUG	21677
HBB5_RT20_PBS16	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCAACGGCAGACUUCUCUUCAGGAGUCAGGUGCACCAU	21678
HBB5_RT20_PBS15	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCAACGGCAGACUUCUCUUCAGGAGUCAGGUGCACCA	21679
HBB5_RT20_PBS14	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCAACGGCAGACUUCUCUUCAGGAGUCAGGUGCACC	21680
HBB5_RT20_PBS13	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCAACGGCAGACUUCUCUUCAGGAGUCAGGUGCAC	21681
HBB5_RT20_PBS12	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCAACGGCAGACUUCUCUUCAGGAGUCAGGUGCA	21682
HBB5_RT20_PBS11	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCAACGGCAGACUUCUCUUCAGGAGUCAGGUGC	21683
HBB5_RT20_PBS10	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCAACGGCAGACUUCUCUUCAGGAGUCAGGUG	21684
HBB5_RT20_PBS9	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCAACGGCAGACUUCUCUUCAGGAGUCAGGU	21685
HBB5_RT20_PBS8	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCAACGGCAGACUUCUCUUCAGGAGUCAGG	21686
HBB5_RT19_PBS17	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCACGGCAGACUUCUCUUCAGGAGUCAGGUGCACCAUG	21687
HBB5_RT19_PBS16	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCACGGCAGACUUCUCUUCAGGAGUCAGGUGCACCAU	21688
HBB5_RT19_PBS15	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCACGGCAGACUUCUCUUCAGGAGUCAGGUGCACCA	21689
HBB5_RT19_PBS14	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCACGGCAGACUUCUCUUCAGGAGUCAGGUGCACC	21690
HBB5_RT19_PBS13	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCACGGCAGACUUCUCUUCAGGAGUCAGGUGCAC	21691
HBB5_RT19_PBS12	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCACGGCAGACUUCUCUUCAGGAGUCAGGUGCA	21692
HBB5_RT19_PBS11	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCACGGCAGACUUCUCUUCAGGAGUCAGGUGC	21693
HBB5_RT19_PBS10	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCACGGCAGACUUCUCUUCAGGAGUCAGGUG	21694
HBB5_RT19_PBS9	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCACGGCAGACUUCUCUUCAGGAGUCAGGU	21695
HBB5_RT19_PBS8	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCACGGCAGACUUCUCUUCAGGAGUCAGG	21696

HBB5_RT17_PBS17	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCGCAGACUUCUCUUCAGGAGUCAGGUGCACCAUG	21697
HBB5_RT17_PBS16	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCGCAGACUUCUCUUCAGGAGUCAGGUGCACCAU	21698
HBB5_RT17_PBS15	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCGCAGACUUCUCUUCAGGAGUCAGGUGCACCA	21699
HBB5_RT17_PBS14	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCGCAGACUUCUCUUCAGGAGUCAGGUGCACC	21700
HBB5_RT17_PBS13	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCGCAGACUUCUCUUCAGGAGUCAGGUGCAC	21701
HBB5_RT17_PBS12	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCGCAGACUUCUCUUCAGGAGUCAGGUGCA	21702
HBB5_RT17_PBS11	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCGCAGACUUCUCUUCAGGAGUCAGGUGC	21703
HBB5_RT17_PBS10	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCGCAGACUUCUCUUCAGGAGUCAGGUG	21704
HBB5_RT17_PBS9	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCGCAGACUUCUCUUCAGGAGUCAGGU	21705
HBB5_RT17_PBS8	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCGCAGACUUCUCUUCAGGAGUCAGG	21706
HBB5_RT16_PBS17	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCGCAGACUUCUCUUCAGGAGUCAGGUGCACCAUG	21707
HBB5_RT16_PBS16	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCGCAGACUUCUCUUCAGGAGUCAGGUGCACCAU	21708
HBB5_RT16_PBS15	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCGCAGACUUCUCUUCAGGAGUCAGGUGCACCA	21709
HBB5_RT16_PBS14	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCGCAGACUUCUCUUCAGGAGUCAGGUGCACC	21710
HBB5_RT16_PBS13	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCGCAGACUUCUCUUCAGGAGUCAGGUGCAC	21711
HBB5_RT16_PBS12	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCGCAGACUUCUCUUCAGGAGUCAGGUGCA	21712
HBB5_RT16_PBS11	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCGCAGACUUCUCUUCAGGAGUCAGGUGC	21713
HBB5_RT16_PBS10	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCGCAGACUUCUCUUCAGGAGUCAGGUG	21714
HBB5_RT16_PBS9	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCGCAGACUUCUCUUCAGGAGUCAGGU	21715
HBB5_RT16_PBS8	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCGCAGACUUCUCUUCAGGAGUCAGG	21716
HBB5_RT14_PBS17	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCAGACUUCUCUUCAGGAGUCAGGUGCACCAUG	21717

HBB5_RT14_PBS16	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCAGACUUCUCUUCAGGAGUCAGGUGCACCAU	21718
HBB5_RT14_PBS15	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCAGACUUCUCUUCAGGAGUCAGGUGCACCA	21719
HBB5_RT14_PBS14	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCAGACUUCUCUUCAGGAGUCAGGUGCACC	21720
HBB5_RT14_PBS13	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCAGACUUCUCUUCAGGAGUCAGGUGCAC	21721
HBB5_RT14_PBS12	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCAGACUUCUCUUCAGGAGUCAGGUGCA	21722
HBB5_RT14_PBS11	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCAGACUUCUCUUCAGGAGUCAGGUGC	21723
HBB5_RT14_PBS10	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCAGACUUCUCUUCAGGAGUCAGGUG	21724
HBB5_RT14_PBS9	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCAGACUUCUCUUCAGGAGUCAGGU	21725
HBB5_RT14_PBS8	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCAGACUUCUCUUCAGGAGUCAGG	21726
HBB5_RT13_PBS17	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCGACUUCUCUUCAGGAGUCACCAU	21727
HBB5_RT13_PBS16	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCGACUUCUCUUCAGGAGUCAGGUGCACCAU	21728
HBB5_RT13_PBS15	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCGACUUCUCUUCAGGAGUCAGGUGCACCA	21729
HBB5_RT13_PBS14	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCGACUUCUCUUCAGGAGUCAGGUGCACC	21730
HBB5_RT13_PBS13	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCGACUUCUCUUCAGGAGUCAGGUGCAC	21731
HBB5_RT13_PBS12	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCGACUUCUCUUCAGGAGUCAGGUGCA	21732
HBB5_RT13_PBS11	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCGACUUCUCUUCAGGAGUCAGGUGC	21733
HBB5_RT13_PBS10	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCGACUUCUCUUCAGGAGUCAGGUG	21734
HBB5_RT13_PBS9	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCGACUUCUCUUCAGGAGUCAGGU	21735
HBB5_RT13_PBS8	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCGACUUCUCUUCAGGAGUCAGG	21736
HBB5_RT12_PBS17	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCACUUCUCUUCAGGAGUCAGGUGCACCAUG	21737
HBB5_RT12_PBS16	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCACUUCUCUUCAGGAGUCAGGUGCACCAU	21738

HBB5_RT12_PBS15	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCACUUCUUCUUCAGGAGUCAGGUGCACCA	21739
HBB5_RT12_PBS14	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCACUUCUUCUUCAGGAGUCAGGUGCACC	21740
HBB5_RT12_PBS13	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCACUUCUUCUUCAGGAGUCAGGUGCAC	21741
HBB5_RT12_PBS12	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCACUUCUUCUUCAGGAGUCAGGUGCA	21742
HBB5_RT12_PBS11	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCACUUCUUCUUCAGGAGUCAGGUGC	21743
HBB5_RT12_PBS10	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCACUUCUUCUUCAGGAGUCAGGUG	21744
HBB5_RT12_PBS9	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCACUUCUUCUUCAGGAGUCAGGU	21745
HBB5_RT12_PBS8	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCACUUCUUCUUCAGGAGUCAGG	21746
HBB5_RT10_PBS17	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCUUCUCUUCAGGAGUCAGGUGCACCAUG	21747
HBB5_RT10_PBS16	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCUUCUCUUCAGGAGUCAGGUGCACCAU	21748
HBB5_RT10_PBS15	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCUUCUCUUCAGGAGUCAGGUGCACCA	21749
HBB5_RT10_PBS14	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCUUCUCUUCAGGAGUCAGGUGCACC	21750
HBB5_RT10_PBS13	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCUUCUCUUCAGGAGUCAGGUGCAC	21751
HBB5_RT10_PBS12	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCUUCUCUUCAGGAGUCAGGUGCA	21752
HBB5_RT10_PBS11	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCUUCUCUUCAGGAGUCAGGUGC	21753
HBB5_RT10_PBS10	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCUUCUCUUCAGGAGUCAGGUG	21754
HBB5_RT10_PBS9	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCUUCUCUUCAGGAGUCAGGU	21755
HBB5_RT10_PBS8	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCUUCUCUUCAGGAGUCAGG	21756
HBB5_RT9_PBS17	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCUCUCUUCAGGAGUCAGGUGCACCAUG	21757
HBB5_RT9_PBS16	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCUCUCUUCAGGAGUCAGGUGCACCAU	21758
HBB5_RT9_PBS15	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCUCUCUUCAGGAGUCAGGUGCACCA	21759

HBB5_RT9_PBS14	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUCUCUUCAGGAGUCAGGUGCACC	21760
HBB5_RT9_PBS13	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUCUCUUCAGGAGUCAGGUGCAC	21761
HBB5_RT9_PBS12	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUCUCUUCAGGAGUCAGGUGCA	21762
HBB5_RT9_PBS11	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUCUCUUCAGGAGUCAGGUGC	21763
HBB5_RT9_PBS10	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUCUCUUCAGGAGUCAGGUG	21764
HBB5_RT9_PBS9	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUCUCUUCAGGAGUCAGGU	21765
HBB5_RT9_PBS8	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUCUCUUCAGGAGUCAGG	21766

Table B: HBB8 Sequences. *The columns indicate, from left to right: 1) Name of the template RNA, 2) gRNA spacer sequence of the template RNA, 3) SpCas9 gRNA scaffold sequence of the template RNA, 4) PBS sequence of the template RNA, 5) RT template sequence of the template RNA, wherein a SNP relative to hg38 that is present in HEK293T cells is bolded, and wherein the mutation region is underlined, 6) full template RNA sequence comprising HEK293T SNP, 7) Full template RNA sequence depicted as RNA corresponding to column 6, further showing chemical modifications as used in Example 4, 8) alternative template RNA sequence designed relative to hg38 reference genome (lacking HEK293T SNP) and 9) observed activity of template RNA of column 7 as defined in Example 4.*

Name	Spacer	SEQ ID NO	gRNA Scaffold (SpCas9 scaffold)	SEQ ID NO	PBS	SEQ ID NO	RT Template (293T SNP; Correction)	SEQ ID NO	Template Sequence (+SNP)	SEQ ID NO	Template Sequence (+SNP) (RNA)	SEQ ID NO	Template Sequence (no SNP)	SEQ ID NO	Activity
HBB8_RT20_PBS17	GTAACGGCAGACTTCTCCAC	1971	GTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCG	2061	GAGAAGTCTGCC	2015	TGGTGCACCTGACTCCTGAG	2024	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGT	2033	mG*mU*mA*rArCrGrGrCrArGrArCrUrUrCrUrCrCrArCrGrUrUrUrUrArGrArGrCrUrArGrArArArUrArA	2042	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATA	2051	+

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HBB8_RT19_PBS12	GTAACG GCAGA CTTCTC CAC	19 98 6	AGTCGGTG C	GTTTTAGAG CTAGAAAT AGCAAGTT AAAATAAG GCTAGTCCG TTATCAACT TGAAAAAG TGGCACCG AGTCGGTG C	20 07 6	GAG AAG TCT GCC	20 16 6	GGTGCA CCTGAC TCCTGA G	20 25 6	ACTCCTGAGGAG AAGTCTGCCG	GTAACGGCAGA CTTCTCCACGTT TTAGAGCTAGAA ATAGCAAGTTAA AATAAGGCTAGT CCGTTATCAACT TGAAAAAGTGG CACCGAGTCGGT GCGGTGCACCTG ACTCCTGAGGAG AAGTCTGCC	20 34 6	CrGrUrUrArArUrCr ArArCrUrUrUrGrAr ArArArArGrUrGr GrCrArCrCrGrAr GrUrCrGrGrUrGr CrGrGrUrGrCrAr CrCrUrGrArCrUr CrCrUrGrArGrGr ArGrArArArGrUrCr UrG*mC*mC*m G	mG*mU*mA*rAr CrGrGrCrArArGrAr CrUrUrCrUrCrCr ArCrGrUrUrUrUrUr ArGrArArGrCrUrAr GrArArArUrArArGr CrArArGrUrUrAr ArArArUrArArArGr GrCrUrArArGrUrCr CrGrUrUrArArUrCr ArArCrUrUrUrGrAr ArArArArArGrUrGr GrCrArCrCrGrAr GrUrCrGrGrUrGrUr CrGrGrUrUrGrCrAr CrCrUrGrArCrUr CrCrUrGrArGrGr ArGrArArGrUrCr U*mG*mC*mC*mC	20 43 6	AACTTGA AAAAGTG GCACCGA GTCGGTG CGGTGCA TCTGACTC CTGAGGA GAAGTCT GCCG	20 52 6	++
HBB8_RT19_PBS11	GTAACG GCAGA CTTCTC CAC	19 98 7	AGTCGGTG C	GTTTTAGAG CTAGAAAT AGCAAGTT AAAATAAG GCTAGTCCG TTATCAACT TGAAAAAG TGGCACCG AGTCGGTG C	20 07 7	GAG AAG TCT GC	20 16 7	GGTGCA CCTGAC TCCTGA G	20 25 7	GTAACGGCAGA CTTCTCCACGTT TTAGAGCTAGAA ATAGCAAGTTAA AATAAGGCTAGT CCGTTATCAACT TGAAAAAGTGG CACCGAGTCGGT GCGGTGCACCTG	20 34 7	CrGrUrUrArArUrCr ArArCrUrUrUrGrAr ArArArArGrUrGr GrCrArCrCrGrAr GrUrCrGrGrUrGrUr CrGrGrUrUrGrCrAr CrCrUrGrArCrUr CrCrUrGrArGrGr ArGrArArGrUrCr U*mG*mC*mC*mC	mG*mU*mA*rAr CrGrGrCrArArGrAr CrUrUrCrUrCrCr ArCrGrUrUrUrUrUr ArGrArArGrCrUrAr GrArArArUrArArGr CrArArGrUrUrAr ArArArUrArArArGr GrCrUrArArGrUrCr CrGrUrUrArArUrCr	20 43 7	GTAACGG CAGACTTC TCCACGTT TTAGAGCT AGAAATA GCAAGTT AAAATAA GGCTAGT CCGTTATC AACTTGA	20 52 7	++ +

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HBB8_RT18_PBS10	GTAACG GCAGA CTTCTC CAC	19 99 8	GTTTTAGAG CTAGAAAT AGCAAGTT AAAATAAG GCTAGTCCG TTATCAACT TGAAAAAG TGGCACCG AGTCGGTG C	20 08 8	GAG AAG TCT G	20 17 8	GTGCAC CTGACT CCTGAG	20 26 8	GTAACGGCAGA CTTCTCCACGTT TTAGAGCTAGAA ATAGCAAGTTAA AATAAGGCTAGT CCGTTATCAACT TGAAAAAGTGG CACCGAGTCGGT GCGTGCACCTGA CTCCTGAGGAGA AGTCTG	20 35 8	mG*mU*mA*rAr CrGrGrCrArGrAr CrUrUrCrUrCrCr ArCrGrUrUrUrUr ArGrArGrCrUrAr GrArArArUrArGr CrArArGrUrUrAr ArArArUrArArGr GrCrUrArGrUrCr CrGrUrUrArArUrCr ArArCrUrUrUrGrAr ArArArArGrUrGr GrCrArCrCrGrAr GrUrCrGrGrUrGr CrGrUrGrCrArCr CrUrGrArCrCrUr CrUrGrArGrGrAr GrArArGrU*mC* mU*mG	20 44 8	GAGGAGA AGTCTGC	GTAACGG CAGACTTC TCCACGTT TTAGAGCT AGAAATA GCAAGTT AAAATAA GGCTAGT CCGTTATC AACTTGA AAAAGTG GCACCGA GTCGGTG CGTGCATC TGACTCCT GAGGAGA AGTCTG	20 53 8	+ ‡
HBB8_RT18_PBS9	GTAACG GCAGA CTTCTC CAC	19 99 9	GTTTTAGAG CTAGAAAT AGCAAGTT AAAATAAG GCTAGTCCG TTATCAACT TGAAAAAG TGGCACCG AGTCGGTG C	20 08 9	GAG AAG TCT	20 17 9	GTGCAC CTGACT CCTGAG	20 26 9	GTAACGGCAGA CTTCTCCACGTT TTAGAGCTAGAA ATAGCAAGTTAA AATAAGGCTAGT CCGTTATCAACT TGAAAAAGTGG CACCGAGTCGGT GCGTGCACCTGA CTCCTGAGGAGA AGTCT	20 35 9	mG*mU*mA*rAr CrGrGrCrArGrAr CrUrUrCrUrCrCr ArCrGrUrUrUrUr ArGrArGrCrUrAr GrArArArUrArGr CrArArGrUrUrAr ArArArUrArArGr GrCrUrArGrUrCr CrGrUrUrArArUrCr ArArCrUrUrUrGrAr ArArArArGrUrGr GrCrArCrCrGrAr GrUrCrGrGrUrGr CrGrUrGrCrArCr CrUrGrArCrCrUr CrUrGrArGrGrAr	20 44 9	GAGGAGA AGTCTGC	GTAACGG CAGACTTC TCCACGTT TTAGAGCT AGAAATA GCAAGTT AAAATAA GGCTAGT CCGTTATC AACTTGA AAAAGTG GCACCGA GTCGGTG CGTGCATC TGACTCCT GAGGAGA AGTCT	20 53 9	+ ‡

HBB8_RT18_PBS8	GTAACGGCAGACTTCTCCAC	20 00 0	GTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	20 09 0	GAG AAG TC	20 18 0	GTGCAC CTGACT CCTGAG	20 27 0	GTAACGGCAGACTTCTCCACGTTCTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTGAGGAGAAGTC	20 36 0	mG*mU*mA*rArCrGrGrCrArGrArArUrCrUrUrCrUrCrCrArCrGrUrUrArGrArGrCrUrArGrArArArUrArGrCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrC	20 45 0	GTAACGG CAGACTTC TCCACGTT TTAGAGCT AGAAATA GCAAGTT AAAATAA GGCTAGT CCGTTATC AACTTGA AAAAGTG GCACCGA GTCGGTG CGTGCATC TGACTCCT GAGGAGA AGTC	20 54 0	++
HBB8_RT17_PBS17	GTAACGGCAGACTTCTCCAC	20 00 1	GTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	20 09 1	GAG AAG TCT GCC GTT AC	20 18 1	TGCAC TGACTC CTGAG	20 27 1	GTAACGGCAGACTTCTCCACGTTCTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTGAGGAGAAGTCTGCCGTTA C	20 36 1	mG*mU*mA*rArCrGrGrCrArGrArArUrCrUrUrCrUrCrCrArCrGrUrUrArGrArGrCrUrArGrArArArUrArGrCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrC	20 45 1	GTAACGG CAGACTTC TCCACGTT TTAGAGCT AGAAATA GCAAGTT AAAATAA GGCTAGT CCGTTATC AACTTGA AAAAGTG GCACCGA GTCGGTG CTGCATCT GACTCCTG AGGAGAA GTCTGCCG TTAC	20 54 1	+

HBB8_RT17_PBS16	GTAACGGCAGACTTCTCCAC	2000 2	GTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	2009 2	GAG AAG TCT GCC GTT A	20 18 2	TGCACC TGACTC CTGAG	20 27 2	GTAACGGCAGACTTCTCCACGTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCCTGAGGAGAAGTCTGCCGTTA	20 36 2	mG*mU*mA*rArCrGrGrCrArGrArCrUrUrCrUrCrCrArCrGrUrUrArGrArGrCrUrArGrArArArUrArArArArGrUrUrArArArArUrArArArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrUrCrCrUrGrArGrGrArGrArArGrUrCrUrGrCrCrGrUrUrA	20 54 2	+
HBB8_RT17_PBS15	GTAACGGCAGACTTCTCCAC	2003 3	GTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	2009 3	GAG AAG TCT GCC GTT	20 18 3	TGCACC TGACTC CTGAG	20 27 3	GTAACGGCAGACTTCTCCACGTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCCTGAGGAGAAGTCTGCCGTT	20 36 3	mG*mU*mA*rArCrGrGrCrArGrArCrUrUrCrUrCrCrArCrGrUrUrArGrArGrCrUrArGrArArArUrArArArArGrUrUrArArArArUrArArArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrUrCrCrUrGrArGrGrArGrArArGrUrCrUrGrCrCrGrUrU	20 45 3	GTAACGG CAGACTTC TCCACGTT TTAGAGCT AGAAATA GCAAGTT AAAATAA GGCTAG CCGTTATC AACTTGA AAAAGTG GCACCGA GTCGGTG CTGCATCT GACTCCTG AGGAGAA GTCTGCCG TT	20 54 3	+

HBB8_RT17_PBS14	GTAACGGCAGACTTCTCCAC	20 00 4	GTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	20 09 4	GAG AAG TCT GCC GT	20 18 4	TGCACC TGACTC CTGAG	20 27 4	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGTCTGCCGT	20 36 4	mG*mU*mA*rArCrGrGrCrArGrArArUrCrUrUrCrUrCrCrArCrGrUrUrArGrCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrArGrArArGrUrCrUrGrCrCrGrU	20 54 4	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGTCTGCCGT	++
HBB8_RT17_PBS13	GTAACGGCAGACTTCTCCAC	20 00 5	GTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	20 09 5	GAG AAG TCT GCC G	20 18 5	TGCACC TGACTC CTGAG	20 27 5	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGTCTGCCG	20 36 5	mG*mU*mA*rArCrGrGrCrArGrArArUrCrUrUrCrUrCrCrArCrGrUrUrArGrCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrArGrArArGrUrCrUrGrCrCrG	20 54 5	GTAACGGCAGACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGTCTGCCG	+

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HBB8_RT14_PBS9	GTAACGGCAGAAGGCACCGGTGAT	20	AGTCGGTGC	GTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	20	GAG	AAG	TCT	20	ACCTGA	CTCCTG	AG	20	TGAGGAGAAAGTCTG	20	CrGrUrUrArUrUrCr	ArArCrUrUrUrGrAr	ArArArArGrUrUrGr	GrCrArCrCrGrArGr	GrUrCrGrGrUrUrGr	CrArCrCrUrUrGrAr	CrUrCrCrUrUrGrAr	GrGrArGrArArArGr	U*mC*mU*mG	20	mG*mU*mA*rAr	CrGrGrCrArGrArGr	CrUrUrCrUrCrCr	ArCrGrUrUrUrUrUr	ArGrArGrCrCrUrAr	GrArArArUrArArGr	CrArArGrUrUrUrAr	ArArArUrArArArGr	GrCrUrArGrUrCr	CrGrUrUrArArUrCr	ArArCrUrUrGrGrAr	ArArArArGrUrUrGr	GrCrArCrCrGrArGr	GrUrCrGrGrUrUrGr	CrArCrCrUrUrGrAr	CrUrCrCrUrUrGrAr	GrGrArGrArArArG*	mU*mC*mU	20	GTAACGG	CAGACTTC	TCCACGTT	TTAGAGCT	AGAAATA	GCAAGTT	AAAATAA	GGCTAGT	CCGTTATC	AACTTGA	AAAAGTG	GCACCGA	GTCGGTG	CATCTGAC	TCCTGAG	GAGAAGT	CT	20	56	9	‡	+
HBB8_RT14_PBS8	GTAACGGCAGAAGGCACCGGTGAT	20	AGTCGGTGC	GTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	20	GAG	AAG	TC	20	ACCTGA	CTCCTG	AG	20	TGAGGAGAAAGTC	20	CrGrUrUrArUrUrCr	ArArCrUrUrUrGrAr	ArArArArGrUrUrGr	GrCrArCrCrGrArGr	GrUrCrGrGrUrUrGr	CrArCrCrUrUrGrAr	CrUrCrCrUrUrGrAr	GrGrArGrArArArG*	mU*mC*mU	20	mG*mU*mA*rAr	CrGrGrCrArGrArGr	CrUrUrCrUrCrCr	ArCrGrUrUrUrUrUr	ArGrArGrCrCrUrAr	GrArArArUrArArGr	CrArArGrUrUrUrAr	ArArArUrArArArGr	GrCrUrArGrUrCr	CrGrUrUrArArUrCr	ArArCrUrUrGrGrAr	ArArArArGrUrUrGr	GrCrArCrCrGrArGr	GrUrCrGrGrUrUrGr	CrArCrCrUrUrGrAr	CrUrCrCrUrUrGrAr	GrGrArGrArArArG*	mU*mC*mU	20	GTAACGG	CAGACTTC	TCCACGTT	TTAGAGCT	AGAAATA	GCAAGTT	AAAATAA	GGCTAGT	CCGTTATC	AACTTGA	AAAAGTG	GCACCGA	GTCGGTG	CATCTGAC	TCCTGAG	GAGAAGT	CT	20	57	0	‡	

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HBB8_RT11_PBS15	GTAACGGCAGACTTCTCCAC	20	GTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	20	GAG AAG TCT GCC GTT	20 21 3	TGACTC CTGAG	20 30 3	GTAACGGCAGACTTCTCCACGTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCGTT	20 39 3	GrArArGrUrCrUr GrCrCrG*mU*m U*mA	mG*mU*mA*rAr CrGrGrCrArGrArAr CrUrUrCrUrCrCr ArCrGrUrUrUrUr ArGrArGrCrUrAr GrArArArUrArGr CrArArGrGrUrUr ArArArUrArArGr GrCrUrArGrUrCr CrGrUrUrArArUrCr ArArCrUrUrGrAr ArArArArGrUrGr GrCrArCrCrGrAr GrUrCrGrGrUrGr CrUrGrArCrUrCr CrUrGrArGrGrAr GrArArGrUrCrUr GrCrC*mG*mU* mU	20 48 3	AAGTCTG CCGTTA	20 57 3	++
HBB8_RT11_PBS14	GTAACGGCAGACTTCTCCAC	20	GTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	20	GAG AAG TCT GCC GT	20 21 4	TGACTC CTGAG	20 30 4	GTAACGGCAGACTTCTCCACGTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGT	20 39 4	GrArArGrUrCrUr GrCrCrG*mU*m U*mA	mG*mU*mA*rAr CrGrGrCrArGrArAr CrUrUrCrUrCrCr ArCrGrUrUrUrUr ArGrArGrCrUrAr GrArArArUrArGr CrArArGrGrUrUr ArArArUrArArGr GrCrUrArGrUrCr CrGrUrUrArArUrCr ArArCrUrUrGrAr ArArArArGrUrGr GrCrArCrCrGrAr GrUrCrGrGrUrGr CrUrGrArCrUrCr CrUrGrArGrGrAr GrArArGrUrCrUr	20 48 4	AAGTCTG CCGT	20 57 4	++ +

HBB8_RT11_PBS13	GTAACGGCAGACTTCTCCAC	20 03 5	GTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	20 12 5	GAG AAG TCT GCC G	20 21 5	TGACTC CTGAG	20 30 5	GTAACGGCAGACTTCTCCACGTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGGAGAAGTCTGCCG	20 39 5	mG*mU*mA*rArCrGrGrCrArGrArArUrUrCrUrUrCrCrArCrGrUrUrArArGrArArArUrArArGrCrArArGrUrUrArArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrC	20 48 5	GTAACGGCAGACTTCTCCACGTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCG	20 57 5	+ + +
HBB8_RT11_PBS12	GTAACGGCAGACTTCTCCAC	20 03 6	GTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	20 12 6	GAG AAG TCT GCC	20 21 6	TGACTC CTGAG	20 30 6	GTAACGGCAGACTTCTCCACGTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGGAGAAGTCTGCC	20 39 6	mG*mU*mA*rArCrGrGrCrArGrArArUrUrCrUrUrCrCrArCrGrUrUrArArGrArArArUrArArGrCrArArGrUrUrArArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrU*mG*mC*mC	20 48 6	GTAACGGCAGACTTCTCCACGTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGACTCCTGAGGAGAAGTCTGCC	20 57 6	+ + +

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HBB8_RT10_PBS15	GTAACGGCAGACTTCTCCAC	20 04 3	AGTCGGTGC	GTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	20 13 3	GAG AAG TCT GCC GTT	20 22 3	GACTCC TGAG	20 31 3	GTAACGGCAGACTTCTCCACGTTCTAGAGCTAGAAATAGCAAGTTAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	20 40 3	mG*mU*mA*rArCrGrGrCrArGrArArUrCrArArGrGrUrArArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrG	20 49 3	CCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAGGAGAAGTCTGCCGTTAC	++	20 58 2
HBB8_RT10_PBS16	GTAACGGCAGACTTCTCCAC	20 04 2	AGTCGGTGC	GTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	20 13 2	GAG AAG TCT GCC GTT A	20 22 2	GACTCC TGAG	20 31 2	GTAACGGCAGACTTCTCCACGTTCTAGAGCTAGAAATAGCAAGTTAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	20 40 2	mG*mU*mA*rArCrGrGrCrArGrArArUrCrArArGrGrUrArArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrG	20 49 2	CCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAGGAGAAGTCTGCCGTTAC	++	20 58 2

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HBB8_RT10_PBS12	GTAACGGCAGAACTTCTCCAC	20046	GTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	20136	GAGAAGTCT GCC	20226	GACTCC TGAG	20316	GTAACGGCAGACTTCTCCACGTTCTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAGAAGTCTGCC	20406	GrUrCrGrGrUrGr CrGrArCrUrCrCr UrGrArGrGrArGr ArArGrUrCrUrG* mC*mC*mG	CGACTCCT GAGGAGA AGTCTGCC G	20586	++
HBB8_RT10_PBS11	GTAACGGCAGACTTCTCCAC	20047	GTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	20137	GAG AAG TCT GC	20227	GACTCC TGAG	20317	GTAACGGCAGACTTCTCCACGTTCTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAGAAGTCTGC	20407	mG*mU*mA*rAr CrGrGrCrArGrGrAr CrUrUrCrUrCrCrCr ArCrGrUrUrUrUrUr ArGrArArGrCrUrAr GrArArArUrArArGr CrArArGrUrUrAr ArArArUrArArArGr GrCrUrArArGrUrCr CrGrUrUrArArUrCr ArArCrUrUrGrAr ArArArArArGrUrGr GrCrArArCrCrGrAr GrUrCrGrGrUrGr CrGrArCrUrCrCrCr UrGrArGrGrArGr ArArGrUrCrU*m G*mC*mC	GTAACGG CAGACTTC TCCACGTT TTAGAGCT AGAAATA GCAAGTT AAAATAA GGCTAGT CCGTTATC AACTTGA AAAAGTG GCACCGA GTCGGTG CGACTCCT GAGGAGA AGTCTGCC	20587	++

HBB8_RT10_PBS10	GTAACGGCAGACTTCTCCAC	20 04 8	GTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	20 13 8	GAG AAG TCT G	20 22 8	GACTCC TGAG	20 31 8	GTAACGGCAGACTTCTCCACGTTCTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAGAAGTCTG	20 40 8	ArArArGrU*mC*mU*mG*mC	20 49 8	GTAACGGCAGACTTCTCCACGTTCTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAGTGGCACCGAGTCGGTGCGAGAAGTCTG	20 58 8	‡
HBB8_RT10_PBS9	GTAACGGCAGACTTCTCCAC	20 04 9	GTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	20 13 9	GAG AAG TCT	20 22 9	GACTCC TGAG	20 31 9	GTAACGGCAGACTTCTCCACGTTCTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAGAAGTCT	20 40 9	mG*mU*mA*rArCrGrGrCrArGrArCrUrUrCrUrCrCrArCrGrUrUrUrUrArArGrArGrCrUrArGrArArArUrArGrCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrC	20 49 9	GTAACGGCAGACTTCTCCACGTTCTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAGTGGCACCGAGTCGGTGCGAGAAGTCT	20 58 9	‡

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HBB8_RT9_PBS9	GTAACGGCAGACTTCTCCAC	2005 9	GTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	2014 9	GAGAAGTCT	2023 9	ACTCCTGAG	2032 9	GTAACGGCAGACTTCTCCACGTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGAAGTCT	2041 9	mG*mU*mA*rArCrGrGrCrArGrArCrUrUrCrUrUrCrCrArCrGrUrUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrC	2050 9	AGGAGAAGTCTG
HBB8_RT9_PBS8	GTAACGGCAGACTTCTCCAC	2006 0	GTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	2015 0	GAGAAGTC	2024 0	ACTCCTGAG	2033 0	GTAACGGCAGACTTCTCCACGTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGAAGTC	2042 0	mG*mU*mA*rArCrGrGrCrArGrArCrUrUrCrUrUrCrCrArCrGrUrUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrArGrGrArArGrUrC	2051 0	AGGAGAAGTCTG

+		2059 9	GTAACGGCAGACTTCTCCACGTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGAAGTCT									
++		2060 0	GTAACGGCAGACTTCTCCACGTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGAAGTC									

Table B1: Table B Sequences Reproduced without Nucleotide Modifications. *The Template Sequence (+SNP +PAM-kill) (RNA) sequences from Table B are reproduced below without nucleotide modifications. In some embodiments, In some embodiments, the sequences used in this table can be used without chemical modifications.*

Name	Template Sequence (+SNP) (RNA)	SEQ ID NO
HBB8_RT20_PBS17	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUGGUGCACCUGACUCCUGAGGAGAAGUCUGCCGUUAC	21907
HBB8_RT20_PBS16	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUGGUGCACCUGACUCCUGAGGAGAAGUCUGCCGUUA	21908
HBB8_RT20_PBS15	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUGGUGCACCUGACUCCUGAGGAGAAGUCUGCCGUU	21909
HBB8_RT20_PBS14	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUGGUGCACCUGACUCCUGAGGAGAAGUCUGCCGU	21910
HBB8_RT20_PBS13	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUGGUGCACCUGACUCCUGAGGAGAAGUCUGCCG	21911
HBB8_RT20_PBS12	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUGGUGCACCUGACUCCUGAGGAGAAGUCUGCC	21912
HBB8_RT20_PBS11	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUGGUGCACCUGACUCCUGAGGAGAAGUCUGC	21913
HBB8_RT20_PBS10	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUGGUGCACCUGACUCCUGAGGAGAAGUCUG	21914
HBB8_RT20_PBS9	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUGGUGCACCUGACUCCUGAGGAGAAGUCU	21915
HBB8_RT20_PBS8	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUGGUGCACCUGACUCCUGAGGAGAAGUC	21916

HBB8_RT19_PBS17	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAA AGUGGCACCGAGUCGGUGCGGUGCACCUGACUCCUGAGGAGAAGUCUGCCGUUAC	21917
HBB8_RT19_PBS16	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAA AGUGGCACCGAGUCGGUGCGGUGCACCUGACUCCUGAGGAGAAGUCUGCCGUUA	21918
HBB8_RT19_PBS15	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAA AGUGGCACCGAGUCGGUGCGGUGCACCUGACUCCUGAGGAGAAGUCUGCCGUU	21919
HBB8_RT19_PBS14	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAA AGUGGCACCGAGUCGGUGCGGUGCACCUGACUCCUGAGGAGAAGUCUGCCGU	21920
HBB8_RT19_PBS13	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAA AGUGGCACCGAGUCGGUGCGGUGCACCUGACUCCUGAGGAGAAGUCUGCCG	21921
HBB8_RT19_PBS12	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAA AGUGGCACCGAGUCGGUGCGGUGCACCUGACUCCUGAGGAGAAGUCUGCC	21922
HBB8_RT19_PBS11	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAA AGUGGCACCGAGUCGGUGCGGUGCACCUGACUCCUGAGGAGAAGUCUGC	21923
HBB8_RT19_PBS10	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAA AGUGGCACCGAGUCGGUGCGGUGCACCUGACUCCUGAGGAGAAGUCUG	21924
HBB8_RT19_PBS9	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAA AGUGGCACCGAGUCGGUGCGGUGCACCUGACUCCUGAGGAGAAGUCU	21925
HBB8_RT19_PBS8	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAA AGUGGCACCGAGUCGGUGCGGUGCACCUGACUCCUGAGGAGAAGUC	21926
HBB8_RT18_PBS17	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAA AGUGGCACCGAGUCGGUGCGUGCACCUGACUCCUGAGGAGAAGUCUGCCGUUAC	21927
HBB8_RT18_PBS16	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAA AGUGGCACCGAGUCGGUGCGUGCACCUGACUCCUGAGGAGAAGUCUGCCGUUA	21928
HBB8_RT18_PBS15	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAA AGUGGCACCGAGUCGGUGCGUGCACCUGACUCCUGAGGAGAAGUCUGCCGUU	21929

HBB8_RT18_PBS14	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAA AGUGGCACCGAGUCGGUGCGUGCACCUGACUCCUGAGGAGAAGUCUGCCGU	21930
HBB8_RT18_PBS13	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAA AGUGGCACCGAGUCGGUGCGUGCACCUGACUCCUGAGGAGAAGUCUGCCG	21931
HBB8_RT18_PBS12	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAA AGUGGCACCGAGUCGGUGCGUGCACCUGACUCCUGAGGAGAAGUCUGCC	21932
HBB8_RT18_PBS11	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAA AGUGGCACCGAGUCGGUGCGUGCACCUGACUCCUGAGGAGAAGUCUGC	21933
HBB8_RT18_PBS10	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAA AGUGGCACCGAGUCGGUGCGUGCACCUGACUCCUGAGGAGAAGUCUG	21934
HBB8_RT18_PBS9	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAA AGUGGCACCGAGUCGGUGCGUGCACCUGACUCCUGAGGAGAAGUCU	21935
HBB8_RT18_PBS8	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAA AGUGGCACCGAGUCGGUGCGUGCACCUGACUCCUGAGGAGAAGUC	21936
HBB8_RT17_PBS17	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAA AGUGGCACCGAGUCGGUGCUGCACCUGACUCCUGAGGAGAAGUCUGCCGUUAC	21937
HBB8_RT17_PBS16	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAA AGUGGCACCGAGUCGGUGCUGCACCUGACUCCUGAGGAGAAGUCUGCCGUUA	21938
HBB8_RT17_PBS15	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAA AGUGGCACCGAGUCGGUGCUGCACCUGACUCCUGAGGAGAAGUCUGCCGUU	21939
HBB8_RT17_PBS14	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAA AGUGGCACCGAGUCGGUGCUGCACCUGACUCCUGAGGAGAAGUCUGCCGU	21940
HBB8_RT17_PBS13	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAA AGUGGCACCGAGUCGGUGCUGCACCUGACUCCUGAGGAGAAGUCUGCCG	21941
HBB8_RT17_PBS12	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAA AGUGGCACCGAGUCGGUGCUGCACCUGACUCCUGAGGAGAAGUCUGCC	21942

HBB8_RT17_PBS11	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAA AGUGGCACCGAGUCGGUGCUGCACCUGACUCCUGAGGGAGAAGUCUGC	21943
HBB8_RT17_PBS10	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAA AGUGGCACCGAGUCGGUGCUGCACCUGACUCCUGAGGAGAAGUCUG	21944
HBB8_RT17_PBS9	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAA AGUGGCACCGAGUCGGUGCUGCACCUGACUCCUGAGGAGAAGUCU	21945
HBB8_RT17_PBS8	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAA AGUGGCACCGAGUCGGUGCUGCACCUGACUCCUGAGGAGAAGUC	21946
HBB8_RT16_PBS17	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAA AGUGGCACCGAGUCGGUGCGCACCUGACUCCUGAGGAGAAGUCUGCCGUUAC	21947
HBB8_RT16_PBS16	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAA AGUGGCACCGAGUCGGUGCGCACCUGACUCCUGAGGAGAAGUCUGCCGUUA	21948
HBB8_RT16_PBS15	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAA AGUGGCACCGAGUCGGUGCGCACCUGACUCCUGAGGAGAAGUCUGCCGUU	21949
HBB8_RT16_PBS14	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAA AGUGGCACCGAGUCGGUGCGCACCUGACUCCUGAGGAGAAGUCUGCCGU	21950
HBB8_RT16_PBS13	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAA AGUGGCACCGAGUCGGUGCGCACCUGACUCCUGAGGAGAAGUCUGCCG	21951
HBB8_RT16_PBS12	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAA AGUGGCACCGAGUCGGUGCGCACCUGACUCCUGAGGAGAAGUCUGCC	21952
HBB8_RT16_PBS11	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAA AGUGGCACCGAGUCGGUGCGCACCUGACUCCUGAGGAGAAGUCUGC	21953
HBB8_RT16_PBS10	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAA AGUGGCACCGAGUCGGUGCGCACCUGACUCCUGAGGAGAAGUCUG	21954
HBB8_RT16_PBS9	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAA AGUGGCACCGAGUCGGUGCGCACCUGACUCCUGAGGAGAAGUCU	21955

HBB8_RT16_PBS8	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAA AGUGGCACCGAGUCGGUGCGCACCUGACUCCUGAGGAGAAGUC	21956
HBB8_RT14_PBS17	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAA AGUGGCACCGAGUCGGUGCACCUGACUCCUGAGGAGAAGUCUGCCGUUAC	21957
HBB8_RT14_PBS16	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAA AGUGGCACCGAGUCGGUGCACCUGACUCCUGAGGAGAAGUCUGCCGUUA	21958
HBB8_RT14_PBS15	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAA AGUGGCACCGAGUCGGUGCACCUGACUCCUGAGGAGAAGUCUGCCGUU	21959
HBB8_RT14_PBS14	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAA AGUGGCACCGAGUCGGUGCACCUGACUCCUGAGGAGAAGUCUGCCGU	21960
HBB8_RT14_PBS13	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAA AGUGGCACCGAGUCGGUGCACCUGACUCCUGAGGAGAAGUCUGCCG	21961
HBB8_RT14_PBS12	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAA AGUGGCACCGAGUCGGUGCACCUGACUCCUGAGGAGAAGUCUGCC	21962
HBB8_RT14_PBS11	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAA AGUGGCACCGAGUCGGUGCACCUGACUCCUGAGGAGAAGUCUGC	21963
HBB8_RT14_PBS10	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAA AGUGGCACCGAGUCGGUGCACCUGACUCCUGAGGAGAAGUCUG	21964
HBB8_RT14_PBS9	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAA AGUGGCACCGAGUCGGUGCACCUGACUCCUGAGGAGAAGUCU	21965
HBB8_RT14_PBS8	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAA AGUGGCACCGAGUCGGUGCACCUGACUCCUGAGGAGAAGUC	21966
HBB8_RT11_PBS17	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAA AGUGGCACCGAGUCGGUGCUGACUCCUGAGGAGAAGUCUGCCGUUAC	21967
HBB8_RT11_PBS16	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAA AGUGGCACCGAGUCGGUGCUGACUCCUGAGGAGAAGUCUGCCGUUA	21968

HBB8_RT11_PBS15	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAA AGUGGCACCGAGUCGGUGCUGACUCCUGAGGGAGAAGUCUGCCGUU	21969
HBB8_RT11_PBS14	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAA AGUGGCACCGAGUCGGUGCUGACUCCUGAGGGAGAAGUCUGCCGU	21970
HBB8_RT11_PBS13	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAA AGUGGCACCGAGUCGGUGCUGACUCCUGAGGGAGAAGUCUGCCG	21971
HBB8_RT11_PBS12	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAA AGUGGCACCGAGUCGGUGCUGACUCCUGAGGGAGAAGUCUGCC	21972
HBB8_RT11_PBS11	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAA AGUGGCACCGAGUCGGUGCUGACUCCUGAGGGAGAAGUCUGC	21973
HBB8_RT11_PBS10	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAA AGUGGCACCGAGUCGGUGCUGACUCCUGAGGGAGAAGUCUG	21974
HBB8_RT11_PBS9	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAA AGUGGCACCGAGUCGGUGCUGACUCCUGAGGGAGAAGUCU	21975
HBB8_RT11_PBS8	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAA AGUGGCACCGAGUCGGUGCUGACUCCUGAGGGAGAAGUC	21976
HBB8_RT10_PBS17	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAA AGUGGCACCGAGUCGGUGCGACUCCUGAGGAGAAGUCUGCCGUUAC	21977
HBB8_RT10_PBS16	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAA AGUGGCACCGAGUCGGUGCGACUCCUGAGGAGAAGUCUGCCGUUA	21978
HBB8_RT10_PBS15	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAA AGUGGCACCGAGUCGGUGCGACUCCUGAGGAGAAGUCUGCCGUU	21979
HBB8_RT10_PBS14	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAA AGUGGCACCGAGUCGGUGCGACUCCUGAGGAGAAGUCUGCCGU	21980
HBB8_RT10_PBS13	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAA AGUGGCACCGAGUCGGUGCGACUCCUGAGGAGAAGUCUGCCG	21981

HBB8_RT10_PBS12	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAA AGUGGCACCGAGUCGGUGCGACUCCUGAGGAGAAGUCUGCC	21982
HBB8_RT10_PBS11	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAA AGUGGCACCGAGUCGGUGCGACUCCUGAGGAGAAGUCUGC	21983
HBB8_RT10_PBS10	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAA AGUGGCACCGAGUCGGUGCGACUCCUGAGGAGAAGUCUG	21984
HBB8_RT10_PBS9	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAA AGUGGCACCGAGUCGGUGCGACUCCUGAGGAGAAGUCU	21985
HBB8_RT10_PBS8	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAA AGUGGCACCGAGUCGGUGCGACUCCUGAGGAGAAGUC	21986
HBB8_RT9_PBS17	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAA AGUGGCACCGAGUCGGUGCACUCCUGAGGAGAAGUCUGCCGUUAC	21987
HBB8_RT9_PBS16	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAA AGUGGCACCGAGUCGGUGCACUCCUGAGGAGAAGUCUGCCGUUA	21988
HBB8_RT9_PBS15	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAA AGUGGCACCGAGUCGGUGCACUCCUGAGGAGAAGUCUGCCGUU	21989
HBB8_RT9_PBS14	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAA AGUGGCACCGAGUCGGUGCACUCCUGAGGAGAAGUCUGCCGU	21990
HBB8_RT9_PBS13	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAA AGUGGCACCGAGUCGGUGCACUCCUGAGGAGAAGUCUGCCG	21991
HBB8_RT9_PBS12	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAA AGUGGCACCGAGUCGGUGCACUCCUGAGGAGAAGUCUGCC	21992
HBB8_RT9_PBS11	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAA AGUGGCACCGAGUCGGUGCACUCCUGAGGAGAAGUCUGC	21993
HBB8_RT9_PBS10	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAA AGUGGCACCGAGUCGGUGCACUCCUGAGGAGAAGUCUG	21994

HBB8_RT9_PBS9	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCACUCCUGAGGAGAAGUCU	21995
HBB8_RT9_PBS8	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCACUCCUGAGGAGAAGUC	21996

Table C: Gene Modifying Polypeptide

Nucleic Acid Sequence	ATGAAACGGACAGCCGACGGAAGCGAGTTCGAGTCACCAAAGAAGAAGCGGAAAG TCGACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCC GTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACAC CGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCG AAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACG GAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGG ACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAG CACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAA GTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCG ACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCT GATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGC TGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTG GACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCT GATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGAAACCTGATTGCCC TGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCA AACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAG ATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATC CTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGC CTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCT CGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGA ACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTC ATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAA CAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACC AGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCAT	SEQ ID NO: 20601

	TCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCCTACT
	ACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGC
	GAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGC
	CCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGG
	TGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCA
	AAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCCGCCTTCCTGAGCGGCGAGCA
	GAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGC
	AGCTGAAAGAGGACTACTTCAAGAAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCG
	GCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTA
	TCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATC
	GTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAAC
	CTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACA
	CCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTC
	CGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCAT
	GCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGG
	TGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCC
	GCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGT
	GATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAG
	ACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGG
	GCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAG
	CTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGT
	GGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACCATATCGTGCC
	TCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACA
	AGGCCCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAA
	GAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACA
	ATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATC
	AAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGA
	CTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAG
	TGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAA
	AGTGCGCGAGATCAACAACTACCACGCCCACGACGCCTACCTGAACGCCGTCGT
	GGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCG
	ACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGG
	CAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAG
	ATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGA

	AACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTG
	CTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTT
	CAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGA
	AGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTG
	TGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAA
	AGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCG
	ACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTG
	CCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCC
	GGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTG
	TACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAA
	ACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCA
	GCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCG
	CCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCAC
	CTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCA
	TCGACCGGAAGAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCAC
	CAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGTGA
	CTCTGGAGGATCTAGCGGAGGATCCTCTGGCAGCGAGACACCAGGAACAAGCGAGT
	CAGCAACACCAGAGAGCAGTGGCGGCAGCAGCGGCGGCAGCAGCACCCTAAATATA
	GAAGATGAGTATCGGCTACATGAGACCTCAAAAGAGCCAGATGTTTCTCTAGGGTCC
	ACATGGCTGTCTGATTTTCCTCAGGCCTGGGCGGAAACCGGGGGGCATGGGACTGGC
	AGTTCGCCAAGCTCCTCTGATCATACCTCTGAAAGCAACCTCTACCCCCGTGTCCATA
	AAACAATACCCCATGTCACAAGAAGCCAGACTGGGGATCAAGCCCCACATACAGAG
	ACTGTTGGACCAGGGAATACTGGTACCCTGCCAGTCCCCCTGGAACACGCCCCTGCT
	ACCCGTTAAGAAACCAGGGACTAATGATTATAGGCCTGTCCAGGATCTGAGAGAAG
	TCAACAAGCGGGTGGAAGACATCCACCCCACCGTGCCCAACCCTTACAACCTCTTGA
	GCGGGCTCCCACCGTCCCACCAGTGGTACACTGTGCTTGATTTAAAGGATGCCTTTTT
	CTGCCTGAGACTCCACCCCACCAGTCAGCCTCTCTTCGCCTTTGAGTGGAGAGATCCA
	GAGATGGGAATCTCAGGACAATTGACCTGGACCAGACTCCCACAGGGTTTCAAAAA
	CAGTCCCACCCTGTTTAATGAGGCACTGCACAGAGACCTAGCAGACTTCCGGATCCA
	GCACCCAGACTTGATCCTGCTACAGTACGTGGATGACTTACTGCTGGCCGCCACTTCT
	GAGCTAGACTGCCAACAAGGTACTCGGGCCCTGTTACAAACCCTAGGGAACCTCGG
	GTATCGGGCCTCGGCCAAGAAAGCCCAAATTTGCCAGAAACAGGTCAAGTATCTGG
	GGTATCTTCTAAAAGAGGGTCAGAGATGGCTGACTGAGGCCAGAAAAGAGACTGTG
	ATGGGGCAGCCTACTCCGAAGACCCCTCGACAACTAAGGGAGTTCCTAGGGAAGGC

	AGGCTTCTGTCGCCTCTTCATCCCTGGGTTTGCAGAAATGGCAGCCCCCCTGTACCCT CTCACCAAACCGGGGACTCTGTTTAATTGGGGCCCAGACCAACAAAAGGCCTATCAA GAAATCAAGCAAGCTCTTCTAACTGCCCCAGCCCTGGGGTTGCCAGATTTGACTAAG CCCTTTGAACTCTTTGTCGACGAGAAGCAGGGCTACGCCAAAGGTGTCCTAACGCAA AAACTGGGACCTTGGCGTCGGCCGGTGGCCTACCTGTCCAAAAAGCTAGACCCAGTA GCAGCTGGGTGGCCCCCTTGCCTACGGATGGTAGCAGCCATTGCCGTACTGACAAAG GATGCAGGCAAGCTAACCATGGGACAGCCACTAGTCATTCTGGCCCCCCATGCAGTA GAGGCACTAGTCAAACAACCCCCCGACCGCTGGCTTTCCAACGCCCGGATGACTCAC TATCAGGCCTTGCTTTTGGACACGGACCGGGTCCAGTTCGGACCGGTGGTAGCCCTG AACCCGGCTACGCTGCTCCCACTGCCTGAGGAAGGGCTGCAACACACAACTGCCTTGAT ATCCTGGCCGAAGCCCACGGAACCCGACCCGACCTAACGGACCAGCCGCTCCCAGAC GCCGACCACACCTGGTACACGGATGGAAGCAGTCTCTTACAAGAGGGACAGCGTAA GGCGGGAGCTGCGGTGACCACCGAGACCGAGGTAATCTGGGCTAAAGCCCTGCCAG CCGGGACATCCGCTCAGCGGGCTGAACTGATAGCACTCACCCAGGCCCTAAAGATG GCAGAAGGTAAGAAGCTAAATGTTTATACTGATAGCCGTTATGCTTTTGCTACTGCCC ATATCCATGGAGAAATATACAGAAGGCGTGGGTGGCTCACATCAGAAGGCAAAGAG ATCAAAAATAAAGACGAGATCTTGGCCCTACTAAAAGCCCTCTTTCTGCCCAAAAGA CTTAGCATAATCCATTGTCCAGGACATCAAAAGGGACACAGCGCCGAGGCTAGAGG CAACCGGATGGCTGACCAAGCGGCCCGAAAGGCAGCCATCACAGAGACTCCAGACA CCTCTACCCTCCTCATAGAAAATTCATCACCCTCTGGCGGCTCAAAAAGAACCGCCGA CGGCAGCGAATTCGAGCCCAAGAAGAAGAGGAAAGTC	SEQ ID NO: 20602
Amino Acid Sequence	MKRTADGSEFESPKKKRKVDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHS IKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEES FLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRG HFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQ LPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFF DQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQ IHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITP WNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGM RKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHD LLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTG WGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGD	

	SLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNS
	RERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYD
	VDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRK
	FDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVIT
	LKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDV
	RKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDF
	ATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVA
	YSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLF
	ELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHK
	HYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYF
	DTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDSGGSSGGSSGSETPGTSESATP
	ESSGGSSGGSSTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPL
	IIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYR
	PVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAF
	EWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLA
	ATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETV
	MGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEI
	KQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW
	PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALL
	LDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYT
	DGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYT
	DSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSA
	EARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEPKKKRKV

Example 5: Quantifying activity of a gene editing polypeptide and template for rewriting the endogenous B-globin locus achieved in 293T cells and CD34+ primary human hematopoietic stem cells (HSCs)

This example demonstrates the use of a gene modifying system containing a gene modifying polypeptide and a template RNA, to convert the glutamic acid codon (GAG) at amino acid position 7 in the endogenous B-globin locus in primary human HSCs to alanine (GCA), thereby rewriting a non-pathogenic sequence into position 7. This conversion comprises a change of two base pairs (i.e., replacement of the DNA bases adenine and guanine at nucleotide positions 20 and 21 to the bases cytosine and adenine, respectively).

In this example, the template RNA contained:

(1) a gRNA spacer;
(2) a gRNA scaffold;
(3) a heterologous object sequence; and
(4) a primer binding site (PBS) sequence.

More specifically, the template RNAs comprised the following sequences from 5' to 3', wherein the first 3, and last 3 bases have 2'-O-methyl phosphorothioate chemical modifications.

FYF tgRNA11
CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAU AAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGACUUC UCUGCAGGAGUCAGGU (SEQ ID NO: 20603)

FYF tgRNA12
CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAU AAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGACUUC UCUGCAGGAGUCAGGUG (SEQ ID NO: 20604)

FYF tgRNA13
CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAU

AAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGACUUC
UCUGCAGGAGUCAGGUGCAC (SEQ ID NO: 20605)

FYF tgRNA14

CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAU
AAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAGACUU
CUCUGCAGGAGUCAGGUG (SEQ ID NO: 20606)

FYF tgRNA15

CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAU
AAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAGACUU
CUCUGCAGGAGUCAGGUGC (SEQ ID NO: 20607)

FYF tgRNA16

CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAU
AAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAGACUU
CUCUGCAGGAGUCAGGUGCA (SEQ ID NO: 20608)

FYF tgRNA17

CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAU
AAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAGACUU
CUCUGCAGGAGUCAGGUGCAC (SEQ ID NO: 20609)

FYF tgRNA18

GCAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAA
UAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAGACU
UCUCUGCAGGAGUCAGGUGCAC (SEQ ID NO: 20610)

FYF tgRNA19

CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAU
AAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGGCAGA
CUUCUCUGCAGGAGUCAGGUGC (SEQ ID NO: 20611)

FYF tgRNA20

CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAU

AAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGGCAGA CUUCUCUGCAGGAGUCAGGUGCAC (SEQ ID NO: 20612)

The gene modifying polypeptides tested comprised the sequence set out in Example 8 labeled RNAV209.

The gene modifying system comprising the gene modifying polypeptides and the template RNA described above was transfected into 293T cells and human HSCs. The gene modifying polypeptide and the template RNA were delivered by nucleofection in RNA format. Specifically, 1000 or 2000 ng of gene modifying polypeptide RNA were combined with 1000 or 2000 ng template RNA in RNA format, all at a 1 to 1 ratio. The RNA mixture was added to 200,000 293T cells or 200,000 primary human HSCs in a total of 20 µL of Lonza SF buffer (293T) or Lonza P3 buffer (HSC) and cells were nucleofected in 16-well nucleofection cassettes using program DS-150 (293T) or DZ-100 (HSC). After nucleofection, cells incubated at room temperature for 10 minutes and were transferred to 24-well plates containing 500 µL of DMEM + 10% fetal bovine serum (293T) or 500 µL of StemSpan-XF + SCF at 100 ng/mL, Flt3-L at 100 ng/mL, and TPO at 100 ng/mL (HSC) in each well and cultured at 37˚C, 5% CO_2 for 3 days prior to cell lysis and genomic DNA extraction. To analyze gene editing activity, primers flanking the target insertion site locus were used to amplify across the locus. Amplicons were analyzed via short read sequencing using an Illumina MiSeq. Replacement of the DNA bases adenine and guanine at nucleotide positions 20 and 21 to the bases cytosine and adenine, respectively, downstream of the transcriptional start site within the endogenous B-globin locus indicates successful editing.

The gene modifying systems tested achieved up to 18.5% average perfect rewrite in 293T cells and up to 7.9% perfect rewrite in primary human HSCs. As shown in FIG. 2, average perfect rewrite levels of 4% - 18% were detected in 293T cells (single nick at 2000 ng per RNA) and 0% - 2.5% in primary human HSCs (single nick at 2000 ng per RNA) when screened with template gRNAs. As shown in FIG. 3, average perfect rewrite levels of 6% - 18.5% were detected in 293T cells (single nick at 2000 ng per RNA) and 0% - 7.9% in primary human HSCs (single nick at 2000 ng per RNA) using the gRNAs shown. These results demonstrate the use of a gene modifying system to rewrite a non-pathogenic sequence into a clinically relevant codon in the endogenous B-globin locus in primary human HSCs.

Example 6: Quantifying activity of a gene editing polypeptide and template for rewriting the endogenous B-globin locus achieved in human primary fibroblasts

This example demonstrates the use of a gene modifying system containing a gene modifying polypeptide and a template RNA, to convert the glutamic acid codon (GAG) at amino acid position 7 in the endogenous B-globin locus in human primary fibroblasts to alanine (GCA). This conversion comprises a change of two base pairs (i.e., replacement of the DNA bases adenine and guanine at nucleotide positions 20 and 21 to the bases cytosine and adenine, respectively).

In this example, the template RNA contained:

(1) a gRNA spacer;
(2) a gRNA scaffold;
(3) a heterologous object sequence; and
(4) a primer binding site (PBS) sequence.

More specifically, the template RNA comprised the sequence of tgRNA14 as described in the previous example.

The gene modifying polypeptides tested comprised the sequence set out in Example 8 labeled RNAV209.

The system further comprises a gRNA sequence designed to produce a second nick, wherein the first 3, and last 3 bases have 2'-O-methyl phosphorothioate modifications and is comprised of the following sequence 5'-CCUUGAUACCAACCUGCCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUUU -3' (SEQ ID NO: 20613).

The gene modifying system comprising the gene modifying polypeptides and the template RNA described above was electroporated into human primary fibroblasts. The gene modifying polypeptide and the template RNA were delivered by electroporation in RNA format and comprised the sequences detailed above. Specifically, two doses were delivered (1000 ng and 2000 ng) wherein each gene editing component was delivered as RNA at the specified dose. For

example, for the 1000 ng dose, 1000 ng of gene modifying polypeptide RNA were combined with 1000 ng template RNA in RNA format and 1000 ng of second nick gRNA in RNA format, in a 10 µL electroporation mixture comprised of 200,000 primary human fibroblasts resuspended in Buffer R (Invitrogen). The electroporation mixture was then aspirated into a 10 µL neon electroporation tip (Invitrogen), transferred to the neon electroporation system (Invitrogen), and electroporated with one pulse at 1700 mV, for 20 mS. Cells were then transferred to one well of a 12-well plate (Corning), cultured in 1 mL of Glutamax containing DMEM supplemented with 15% fetal bovine serum, 1% non-essential amino acids, 1% sodium pyruvate, and 1% HEPES (all Gibco), and cultured for 3 days at 37˚C, 5% CO_2 prior to cell lysis and genomic DNA extraction. To analyze gene editing activity, primers flanking the target insertion site locus were used to amplify across the locus. Amplicons were analyzed via short read sequencing using an Illumina MiSeq. Replacement of the DNA bases adenine and guanine at nucleotide positions 20 and 21 to the bases cytosine and adenine, respectively, downstream of the transcriptional start site within the endogenous B-globin locus indicated successful editing.

As shown in FIG. 4, perfect rewrite levels of 3.7% and 10.6% were detected at the 1000 ng and 2000 ng doses, respectively, when the gene editing polypeptide was combined with the template guide RNA and no second nick gRNA was added. Addition of a second nick increased perfect rewriting from 3.7% to 44.5% at the 1000 ng dose and from 10.6% to 56.5% at the 2000 ng dose. In this experiment, indel levels in the range of 1.5-1.65% (single nick; 1000 ng, 2000 ng) and 7.9-5.8% (second nick; 1000 ng, 2000 ng) were observed. These results demonstrate the use of a gene modifying system to rewrite a non-pathogenic sequence into a clinically relevant codon in the endogenous B-globin locus in human primary fibroblasts. Furthermore, introduction of a second nick gRNA increased perfect rewriting by five to ten-fold, depending on dose administered.

Example 7: Comparing the activity of a gene editing polypeptide and multiple templates for rewriting different sequences into the same location within the endogenous B-globin locus in wild-type human primary fibroblasts and fibroblasts containing the sickle cell mutation.

This example demonstrates similar efficacy when installing different mutations into the same genomic loci by changing the sequences within the reverse transcriptase (RT) domain of a template guide RNA and holding the design of a gene modifying polypeptide, template RNA

primer binding side (PBS) and template guide RNA scaffold constant. In this example, two adjacent DNA bases, one of which is positioned at the site mutated in sickle cell disease within the B-globin locus, were substituted in wild type fibroblasts, converting the glutamic acid codon (GAG) at amino acid position 7 in the endogenous B-globin locus in human primary fibroblasts to alanine (GCA). In parallel, at the same amino acid position, the valine codon (GTG) present in sickle mutation containing fibroblasts was converted to a synonymous glutamic acid codon (GAA).

In this example, the template RNA contained:

(1) a gRNA spacer;
(2) a gRNA scaffold;
(3) a heterologous object sequence; and
(4) a primer binding site (PBS) sequence.

More specifically, the template RNA utilized in wild type fibroblasts comprised the sequence of tgRNA14 as described in the previous example.

The template RNA utilized in sickle fibroblasts comprised the following sequence and contained 2'-O-methyl phosphorothioate modifications at the first 3, and last 3 bases: 5'-CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAGACUUCUCUUCAGGAGUCAGGUG-3' (SEQ ID NO: 20614)

The gene modifying polypeptides tested comprised the sequence set out in Example 8 labeled RNAV209.

The system further comprised a gRNA sequence designed to produce a second nick, wherein the gRNA has a sequence of 5'-CCUUGAUACCAACCUGCCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUUU -3' (SEQ ID NO: 20615).

The same gRNA comprised of the sequence above was utilized for both wild type and sickle cell second nick conditions within this example.

The gene modifying system comprising the gene modifying polypeptides and the template RNA described above was electroporated into wild type and sickle mutation-containing human primary fibroblasts. The gene modifying polypeptide and the template RNA were delivered by electroporation in RNA format and comprised of the sequences detailed above. One dose was delivered (1000 ng) wherein each gene editing component was delivered as RNA at the specified dose. Specifically, 1000 ng of gene modifying polypeptide RNA were combined with 1000 ng template RNA in RNA format and 1000 ng of second nick gRNA in RNA format, in a 10 µL electroporation mixture comprised of 200,000 primary human fibroblasts resuspended in Buffer R (Invitrogen). The electroporation mixture was then aspirated into a 10 µL neon electroporation tip (Invitrogen), transferred to the neon electroporation system (Invitrogen), and electroporated with one pulse at 1700 mV, for 20 mS. Cells were then transferred to one well of a 12-well plate (Corning), cultured in 1 mL of Glutamax containing DMEM supplemented with 15% fetal bovine serum, 1% non-essential amino acids, 1% sodium pyruvate, and 1% HEPES (all Gibco), and cultured for 3 days at 37˚C, 5% CO_2 prior to cell lysis and genomic DNA extraction. To analyze gene editing activity, primers flanking the target insertion site locus were used to amplify across the locus. Amplicons were analyzed by Sanger sequencing followed by analysis using the TIDER algorithm. Replacement of the DNA bases adenine and guanine at nucleotide positions 20 and 21 to the bases cytosine and adenine, respectively, downstream of the transcriptional start site within the endogenous B-globin locus indicated successful editing in wild type cells. Conversely, replacement of the DNA bases thymine and guanine at nucleotide positions 20 and 21 to the base adenine, respectively, downstream of the transcriptional start site within the endogenous B-globin locus indicated successful editing in sickle mutation containing fibroblasts.

As shown in FIG. 5, perfect rewrite levels of 10.8% and 6.1% were detected in wild type and sickle fibroblasts, respectively, when the gene editing polypeptide was combined with the template guide RNA. Addition of a second nick increased perfect rewriting to 75.6% in wild type cells and to 74.6% in sickle fibroblasts. These results demonstrate the use of a gene modifying system to correct a pathogenic mutation in sickle mutation-bearing human primary fibroblasts and to install a non-pathogenic mutation into wild-type human primary fibroblasts. Furthermore, introduction of a second nick gRNA increased perfect rewriting more than 7-fold in wild type primary fibroblasts and over ten-fold in sickle primary fibroblasts.

Example 8: Quantifying activity of a gene editing polypeptide and template for rewriting the endogenous FAH locus achieved in primary mouse hepatocytes

This example demonstrates the use of a gene modifying system containing a gene modifying polypeptide and a template RNA, to convert an A nucleotide to a G nucleotide in the endogenous *Fah* locus in mouse primary hepatocytes derived from a Fah5981SB mouse. The Fah5981SB mouse model harbors a G to A point mutation in the last nucleotide of exon 8 of the *Fah* gene, leading to aberrant mRNA splicing and subsequent mRNA degradation, without the production of Fah protein and, and thus serves as a mouse model of hereditary tyrosinemia type I.

In this example, the template RNA contained:

(1) a gRNA spacer;
(2) a gRNA scaffold;
(3) a heterologous object sequence; and
(4) a primer binding site (PBS) sequence.

More specifically, the template RNA (including chemical modification pattern) comprised the following sequences:

FAH1_R14_P12_Heavy RNACS048

mG*mG*mA*rUrGrGrUrCrCrUrCrArUrGrArArCrGrArCrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrUrUrArCrCrGrCrUrCrCrArGrUrCrGrUrUrCrArUrGrArG*mG*mA*mC (SEQ ID NO: 20616)

FAH1_R15_P10_Heavy RNACS049

mG*mG*mA*rUrGrGrUrCrCrUrCrArUrGrArArCrGrArCrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAm

GmUmCmGmGmUmGmCrArUrUrArCrCrGrCrUrCrCrArGrUrCrGrUrUrCrArUrG*mA*m
G*mG (SEQ ID NO: 20617)

FAH2_R19_P11_MUT_Heavy RNACS052

mU*mC*mA*rGrArGrGrArArGrCrUrGrGrGrCrCrArCrCrGrUrUrUrUrArGrAmGmCm
UmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrG
rUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAm
GmUmCmGmGmUmGmCrUrGrGrArGrCrGrGrUrArArUrGrGrCrUrGrGrUrGrGrCrCrCrA
rGrC*mU*mU*mC (SEQ ID NO: 20618)

FAH2_R19_P13_MUT_Heavy RNACS053

mU*mC*mA*rGrArGrGrArArGrCrUrGrGrGrCrCrArCrCrGrUrUrUrUrArGrAmGmCm
UmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrG
rUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAm
GmUmCmGmGmUmGmCrUrGrGrArGrCrGrGrUrArArUrGrGrCrUrGrGrUrGrGrCrCrCrA
rGrCrUrU*mC*mC*mU (SEQ ID NO: 20619)

Additional exemplary template RNAs that could be utilized in this experiment include the following:

FAH1 RNACS050

mG*mG*mA*rUrGrGrUrCrCrUrCrArUrGrArArCrGrArCrGrUrUrUrUrArGrAmGmCmUmAm
GmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUr
CrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmG
mUmGmCrArGrGrCrArUrUrArCrCrGrCrUrCrCrArGrUrCrGrUrUrCrArUrGrArG*mG*mA*m
C (SEQ ID NO: 20620)

FAH1 RNACS051

mG*mG*mA*rUrGrGrUrCrCrUrCrArUrGrArArCrGrArCrGrUrUrUrUrArGrAmGmCmUmAm
GmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUr
CrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmG
mUmGmCrArGrGrCrArUrUrArCrCrGrCrUrCrCrArGrUrCrGrUrUrCrArUrG*mA*mG*mG
(SEQ ID NO: 20621)

In the sequences above m=2'-O-methyl ribonucleotide, r=ribose and *=phosphorothioate bond.

The gene modifying polypeptides tested comprised sequence of: RNAV209 (nCas9-RT) and RNAV214 (wtCas9-RT). Specifically, the nCas9-RT and the wtCas9-RT had the following amino acid sequences:

nCas9-RT (RNAV209):

MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLI
GALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVE
EDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHF
LIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQL
PGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYAD
LFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYK
EIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNG
SIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKS
EETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVK
YVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRF
NASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKV
MKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKE
DIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMAR
ENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMY
VDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKN
YWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMN
TKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRK
RPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKL
IARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNP
IDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYL
ASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHR
DKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRI
DLSQLGGDSGGSSGGSSGSETPGTSESATPESSGGSSGGSSTLNIEDEYRLHETSKEPDVS

LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQR
LLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGL
PPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTL
FNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAK
KAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPG
FAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQG
YAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPL
VILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEG
LQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIW
AKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS
EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPD
TSTLLIENSSPSGGSKRTADGSEFEKRTADGSEFESPKKKAKVE (SEQ ID NO: 20622)

wtCas9-RT (RNAV214):

MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLI
GALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVE
EDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHF
LIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQL
PGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYAD
LFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYK
EIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNG
SIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKS
EETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVK
YVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRF
NASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKV
MKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKE
DIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMAR
ENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMY
VDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKN
YWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMN
TKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK

KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRK
RPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKL
IARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNP
IDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYL
ASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHR
DKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRI
DLSQLGGDSGGSSGGSSGSETPGTSESATPESSGGSSGGSSTLNIEDEYRLHETSKEPDVS
LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQR
LLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGL
PPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTL
FNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAK
KAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPG
FAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQG
YAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPL
VILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEG
LQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIW
AKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS
EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPD
TSTLLIENSSPSGGSKRTADGSEFEKRTADGSEFESPKKKAKVE (SEQ ID NO: 20623)

Underlining indicates the residue that differs between the nickase and wild-type sequences.

The gene modifying system comprising the gene modifying polypeptides listed above and the template RNA described above were transfected into primary mouse hepatocytes. The gene modifying polypeptide and the template RNA were delivered by nucleofection in the RNA format. Specifically, 4 μg of gene modifying polypeptide mRNA were combined with 10 μg of chemically synthesized template RNA in 5 μL of water. The transfection mix was added to 100,000 mouse primary hepatocytes in Buffer P3 [Lonza], and cells were nucleofected using program DG-138. After nucleofection, cells were grown at 37°C, 5% CO_2 for 3 days prior to cell lysis and genomic DNA extraction. To analyze gene editing activity, primers flanking the target insertion site locus were used to amplify across the locus. Amplicons were analyzed via short

read sequencing using an Illumina MiSeq. Conversion of terminal A to G sequence in exon 8 of *fah* gene indicates successful editing.

As shown in FIG. 2, for FAH2 templates, perfect rewrite levels (conversion of A to G with no unwanted mutations detected) of 4-8% were detected with RNAV209 but not with RNAV214-040. Indel levels of 4.4 to 6.6% were observed with RNAV209. Furthermore, the amount of WT *Fah* mRNA was measured using quantitative RT-PCR using primers that bind to exons 7 and 8. As shown in FIG. 3, FAH2 templates result in an increase in the abundance of *Fah* mRNA relative to WT by up to 12% when FAH2 template is tested with RNAV209-013 mRNA. These results demonstrate the use of a gene modifying system to reverse a mutation in the *Fah* gene, resulting in partial restoration of the expression of wild-type *Fah* mRNA.

Example 9: Quantifying activity of a gene editing polypeptide and template in vivo for rewriting the endogenous FAH locus achieved in mouse liver

This example demonstrates the use of a gene modifying system containing a gene modifying polypeptide and a template RNA, to convert an A nucleotide to a G nucleotide in the Fah5981SB mouse model into the endogenous *Fah* locus in mouse liver. The Fah5981SB mouse model harbors a G to A point mutation in the last nucleotide of exon 8 of the *Fah* gene, leading to aberrant mRNA splicing and subsequent mRNA degradation, without the production of Fah protein and serves as a mouse model of hereditary tyrosinemia type I.

In this example, the template RNA contained:

(1) a gRNA spacer;
(2) a gRNA scaffold;
(3) a heterologous object sequence; and
(4) a primer binding site (PBS) sequence.

More specifically, the template RNA comprised the following sequences:

FAH1_R14_P12_Heavy RNACS048

mG*mG*mA*rUrGrGrUrCrCrUrCrArUrGrArArCrGrArCrGrUrUrUrUrArGrAmGmCm
UmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrG

rUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAm
GmUmCmGmGmUmGmCrUrUrArCrCrGrCrUrCrCrArGrUrCrGrUrUrCrArUrGrArG*mG*
mA*mC (SEQ ID NO: 20624)

FAH1_R15_P10_Heavy RNACS049

mG*mG*mA*rUrGrGrUrCrCrUrCrArUrGrArArCrGrArCrGrUrUrUrUrArGrAmGmCm
UmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrG
rUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAm
GmUmCmGmGmUmGmCrArUrUrArCrCrGrCrUrCrCrArGrUrCrGrUrUrCrArUrG*mA*m
G*mG (SEQ ID NO: 20625)

FAH2_R19_P11_MUT_Heavy RNACS052

mU*mC*mA*rGrArGrGrArArGrCrUrGrGrGrCrCrArCrCrGrUrUrUrUrArGrAmGmCm
UmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrG
rUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAm
GmUmCmGmGmUmGmCrUrGrGrArGrCrGrUrArArUrGrGrCrUrGrGrUrGrCrCrCrA
rGrC*mU*mU*mC (SEQ ID NO: 20626)

FAH2_R19_P13_MUT_Heavy RNACS053

mU*mC*mA*rGrArGrGrArArGrCrUrGrGrGrCrCrArCrCrGrUrUrUrUrArGrAmGmCm
UmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrG
rUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAm
GmUmCmGmGmUmGmCrUrGrGrArGrCrGrUrArArUrGrGrCrUrGrGrUrGrCrCrCrA
rGrCrUrU*mC*mC*mU (SEQ ID NO: 20627)

The gene modifying polypeptides tested comprised a sequence of: RNAV209 and RNAV214, the sequences of which are each provided in Example 3.

The gene modifying system comprising the gene modifying polypeptides and the template RNA described above was formulated in LNP and delivered to mice. Specifically, 2mg/kg of total RNA equivalent formulated in LNPs, combined at 1:1 (w/w) of template RNA and mRNA, were dosed intravenously in 7 to 9-week-old, mixed gender Fah5981SB mice. Six hours or 6

days post-dosing, animals were sacrificed, and their liver collected for analyses. To determine the expression distribution of the gene modifying polypeptide in the liver, 6-hr liver samples were subjected to immunohistochemistry using an anti-Cas9 antibody. Upon staining, quantification of Cas9-positive hepatocytes was determined by QuPath Markup. As shown in FIG.4, the expression of the gene modifying polypeptide was observed in 82-91% of hepatocytes.

To analyze gene editing activity, primers flanking the target insertion site locus were used to amplify across the locus in the genomic DNA of liver samples collected 6 days post-dosing. Amplicons were analyzed via short read sequencing using an Illumina MiSeq. Conversion of an A nucleotide to a G nucleotide indicates successful editing. As shown in FIG.5, perfect rewrite levels (conversion of A to G with no unwanted mutations detected) of 0.1% - 1.9% were detected across the different groups. Indel levels were in the range of 0.2% - 0.4%.

To determine the phenotypic correction caused by the gene editing activity, the restoration of wild-type FAH mRNA was determined by real-time qRT-PCR, and the restoration of Fah protein expression determined by immunohistochemistry using an anti-Fah antibody. As shown in FIG.6, wild-type mRNA restoration of 0.1% - 6%, relative to littermate heterozygous mice, was detected across the different groups. As shown in FIG. 7, Fah protein was detected in 0.1% - 7% of liver cross-sectional area across the different groups. These results demonstrate the use of a gene modifying system to reverse a mutation in the *Fah* gene in an *in vivo* mouse model for hereditary tyrosinemia type I, resulting in partial restoration of expression of wild-type *Fah* mRNA and Fah protein.

Example 10. Gene editing at the TTR locus in an in vivo mouse model

This Example demonstrates successful delivery of an mRNA and guide using Cas9-mediated gene editing using the protospacer sequence ACACAAAUACCAGUCCAGCG that targets the TTR locus using a gene modifying polypeptide and RNA in a C57Blk/6 mouse.

RNAs were prepared as follows. An mRNA encoding a gene modifying polypeptide having the sequence shown in Table 10A below was produced by in vitro transcription and the purified mRNA was dissolved in 1 mM sodium citrate, pH 6, to a final concentration of RNA of 1-2 mg/mL. Similarly, a guide RNA having a sequence shown in Table 10A below was produced

by chemical synthesis and dissolved in water or aqueous buffer, to a final concentration of RNA of 1-2 mg/mL.

Table 10A. Sequences of Example 10

Name	Nucleic acid sequence	SEQ ID NO
Cas9-RT gene modifying polypeptide	AUGCCUGCGGCUAAGCGGGUAAAAUUGGAUGGU GGGGACAAGAAGUACAGCAUCGGCCUGGACAUCG GCACCAACUCUGUGGGCUGGGCCGUGAUCACCGA CGAGUACAAGGUGCCCAGCAAGAAAUUCAAGGUG CUGGGCAACACCGACCGGCACAGCAUCAAGAAGA ACCUGAUCGGAGCCCUGCUGUUCGACAGCGGCGA AACAGCCGAGGCCACCCGGCUGAAGAGAACCGCC AGAAGAAGAUACACCAGACGGAAGAACCGGAUCU GCUAUCUGCAAGAGAUCUUCAGCAACGAGAUGGC CAAGGUGGACGACAGCUUCUUCCACAGACUGGAA GAGUCCUUCCUGGUGGAAGAGGAUAAGAAGCACG AGCGGCACCCCAUCUUCGGCAACAUCGUGGACGA GGUGGCCUACCACGAGAAGUACCCCACCAUCUAC CACCUGAGAAAGAAACUGGUGGACAGCACCGACA AGGCCGACCUGCGGCUGAUCUAUCUGGCCCUGGC CCACAUGAUCAAGUUCCGGGGCCACUUCCUGAUC GAGGGCGACCUGAACCCCGACAACAGCGACGUGG ACAAGCUGUUCAUCCAGCUGGUGCAGACCUACAA CCAGCUGUUCGAGGAAAACCCCAUCAACGCCAGC GGCGUGGACGCCAAGGCCAUCCUGUCUGCCAGAC UGAGCAAGAGCAGACGGCUGGAAAAUCUGAUCGC CCAGCUGCCCGGCGAGAAGAAGAAUGGCCUGUUC GGAAACCUGAUUGCCCUGAGCCUGGGCCUGACCC CCAACUUCAAGAGCAACUUCGACCUGGCCGAGGA UGCCAAACUGCAGCUGAGCAAGGACACCUACGAC GACGACCUGGACAACCUGCUGGCCCAGAUCGGCG ACCAGUACGCCGACCUGUUUCUGGCCGCCAAGAA CCUGUCCGACGCCAUCCUGCUGAGCGACAUCCUG AGAGUGAACACCGAGAUCACCAAGGCCCCCCUGA GCGCCUCUAUGAUCAAGAGAUACGACGAGCACCA CCAGGACCUGACCCUGCUGAAAGCUCUCGUGCGG CAGCAGCUGCCUGAGAAGUACAAAGAGAUUUUCU UCGACCAGAGCAAGAACGGCUACGCCGGCUACAU UGACGGCGGAGCCAGCCAGGAAGAGUUCUACAAG UUCAUCAAGCCCAUCCUGGAAAAGAUGGACGGCA CCGAGGAACUGCUCGUGAAGCUGAACAGAGAGGA CCUGCUGCGGAAGCAGCGGACCUUCGACAACGGC AGCAUCCCCCACCAGAUCCACCUGGGAGAGCUGC ACGCCAUUCUGCGGCGGCAGGAAGAUUUUUACCC	20628

	AUUCCUGAAGGACAACCGGGAAAAGAUCGAGAAG AUCCUGACCUUCCGCAUCCCCUACUACGUGGGCC CUCUGGCCAGGGGAAACAGCAGAUUCGCCUGGAU GACCAGAAAGAGCGAGGAAACCAUCACCCCCUGG AACUUCGAGGAAGUGGUGGACAAGGGCGCUUCCG CCCAGAGCUUCAUCGAGCGGAUGACCAACUUCGA UAAGAACCUGCCCAACGAGAAGGUGCUGCCCAAG CACAGCCUGCUGUACGAGUACUUCACCGUGUAUA ACGAGCUGACCAAAGUGAAAUACGUGACCGAGGG AAUGAGAAAGCCCGCCUUCCUGAGCGGCGAGCAG AAAAAGGCCAUCGUGGACCUGCUGUUCAAGACCA ACCGGAAAGUGACCGUGAAGCAGCUGAAAGAGGA CUACUUCAAGAAAAUCGAGUGCUUCGACUCCGUG GAAAUCUCCGGCGUGGAAGAUCGGUUCAACGCCU CCCUGGGCACAUACCACGAUCUGCUGAAAAUUAU CAAGGACAAGGACUUCCUGGACAAUGAGGAAAAC GAGGACAUUCUGGAAGAUAUCGUGCUGACCCUGA CACUGUUUGAGGACAGAGAGAUGAUCGAGGAAC GGCUGAAAACCUAUGCCCACCUGUUCGACGACAA AGUGAUGAAGCAGCUGAAGCGGCGGAGAUACACC GGCUGGGGCAGGCUGAGCCGGAAGCUGAUCAACG GCAUCCGGGACAAGCAGUCCGGCAAGACAAUCCU GGAUUUCCUGAAGUCCGACGGCUUCGCCAACAGA AACUUCAUGCAGCUGAUCCACGACGACAGCCUGA CCUUUAAAGAGGACAUCCAGAAAGCCCAGGUGUC CGGCCAGGGCGAUAGCCUGCACGAGCACAUUGCC AAUCUGGCCGGCAGCCCCGCCAUUAAGAAGGGCA UCCUGCAGACAGUGAAGGUGGUGGACGAGCUCGU GAAAGUGAUGGGCCGGCACAAGCCCGAGAACAUC GUGAUCGAAAUGGCCAGAGAGAACCAGACCACCC AGAAGGGACAGAAGAACAGCCGCGAGAGAAUGA AGCGGAUCGAAGAGGGCAUCAAAGAGCUGGGCAG CCAGAUCCUGAAAGAACACCCCGUGGAAAACACC CAGCUGCAGAACGAGAAGCUGUACCUGUACUACC UGCAGAAUGGGCGGGAUAUGUACGUGGACCAGG AACUGGACAUCAACCGGCUGUCCGACUACGAUGU GGACCAUAUCGUGCCUCAGAGCUUUCUGAAGGAC GACUCCAUCGACAACAAGGUGCUGACCAGAAGCG ACAAGAAUCGGGGCAAGAGCGACAACGUGCCCUC CGAAGAGGUCGUGAAGAAGAUGAAGAACUACUG GCGGCAGCUGCUGAACGCCAAGCUGAUUACCCAG AGAAAGUUCGACAAUCUGACCAAGGCCGAGAGAG GCGGCCUGAGCGAACUGGAUAAGGCCGGCUUCAU CAAGAGACAGCUGGUGGAAACCCGGCAGAUCACA AAGCACGUGGCACAGAUCCUGGACUCCCGGAUGA ACACUAAGUACGACGAGAAUGACAAGCUGAUCCG	

	GGAAGUGAAAGUGAUCACCCUGAAGUCCAAGCUG GUGUCCGAUUUCCGGAAGGAUUUCCAGUUUUACA AAGUGCGCGAGAUCAACAACUACCACCACGCCCA CGACGCCUACCUGAACGCCGUCGUGGGAACCGCC CUGAUCAAAAAGUACCCUAAGCUGGAAAGCGAGU UCGUGUACGGCGACUACAAGGUGUACGACGUGCG GAAGAUGAUCGCCAAGAGCGAGCAGGAAAUCGGC AAGGCUACCGCCAAGUACUUCUUCUACAGCAACA UCAUGAACUUUUUCAAGACCGAGAUUACCCUGGC CAACGGCGAGAUCCGGAAGCGGCCUCUGAUCGAG ACAAACGGCGAAACCGGGGAGAUCGUGUGGGAUA AGGGCCGGGAUUUUGCCACCGUGCGGAAAGUGCU GAGCAUGCCCCAAGUGAAUAUCGUGAAAAAGACC GAGGUGCAGACAGGCGGCUUCAGCAAAGAGUCUA UCCUGCCCAAGAGGAACAGCGAUAAGCUGAUCGC CAGAAAGAAGGACUGGGACCCUAAGAAGUACGGC GGCUUCGACAGCCCCACCGUGGCCUAUUCUGUGC UGGUGGUGGCCAAAGUGGAAAAGGGCAAGUCCA AGAAACUGAAGAGUGUGAAAGAGCUGCUGGGGA UCACCAUCAUGGAAAGAAGCAGCUUCGAGAAGAA UCCCAUCGACUUUCUGGAAGCCAAGGGCUACAAA GAAGUGAAAAAGGACCUGAUCAUCAAGCUGCCUA AGUACUCCCUGUUCGAGCUGGAAAACGGCCGGAA GAGAAUGCUGGCCUCUGCCGGCGAACUGCAGAAG GGAAACGAACUGGCCCUGCCCUCCAAAUAUGUGA ACUUCCUGUACCUGGCCAGCCACUAUGAGAAGCU GAAGGGCUCCCCCGAGGAUAAUGAGCAGAAACAG CUGUUUGUGGAACAGCACAAGCACUACCUGGACG AGAUCAUCGAGCAGAUCAGCGAGUUCUCCAAGAG AGUGAUCCUGGCCGACGCUAAUCUGGACAAAGUG CUGUCCGCCUACAACAAGCACCGGGAUAAGCCCA UCAGAGAGCAGGCCGAGAAUAUCAUCCACCUGUU UACCCUGACCAAUCUGGGAGCCCCUGCCGCCUUC AAGUACUUUGACACCACCAUCGACCGGAAGAGGU ACACCAGCACCAAAGAGGUGCUGGACGCCACCCU GAUCCACCAGAGCAUCACCGGCCUGUACGAGACA CGGAUCGACCUGUCUCAGCUGGGAGGUGACUCUG GAGGAUCUAGCGGAGGAUCCUCUGGCAGCGAGAC ACCAGGAACAAGCGAGUCAGCAACACCAGAGAGC AGUGGCGGCAGCAGCGGCGGCAGCAGCACCCUAA AUAUAGAAGAUGAGUAUCGGCUACAUGAGACCUC AAAAGAGCCAGAUGUUUCUCUAGGGUCCACAUGG CUGUCUGAUUUUCCUCAGGCCUGGGCGGAAACCG GGGGCAUGGGACUGGCAGUUCGCCAAGCUCCUCU GAUCAUACCUCUGAAAGCAACCUCUACCCCCGUG UCCAUAAAACAAUACCCCAUGUCACAAGAAGCCA	

	GACUGGGGAUCAAGCCCCACAUACAGAGACUGUU GGACCAGGGAAUACUGGUACCCUGCCAGUCCCCC UGGAACACGCCCCUGCUACCCGUUAAGAAACCAG GGACUAAUGAUUAUAGGCCUGUCCAGGAUCUGAG AGAAGUCAACAAGCGGGUGGAGGACAUCCACCCC ACCGUGCCCAACCCUUACAACCUCUUGAGCGGGC UCCCACCGUCCCACCAGUGGUACACUGUGCUUGA UUUAAAGGAUGCCUUUUUCUGCCUGAGACUCCAC CCCACCAGUCAGCCUCUCUUCGCCUUUGAGUGGA GAGAUCCAGAGAUGGGAAUCUCAGGACAAUUGAC CUGGACCAGACUCCCACAGGGUUUCAAAAACAGU CCCACCCUGUUUAAUGAGGCACUGCACAGAGACC UAGCAGACUUCCGGAUCCAGCACCCAGACUUGAU CCUGCUACAGUACGUGGAUGACUUACUGCUGGCC GCCACUUCUGAGCUAGACUGCCAACAAGGUACUC GGGCCCUGUUACAAACCCUAGGGAACCUCGGGUA UCGGGCCUCGGCCAAGAAAGCCCAAAUUUGCCAG AAACAGGUCAAGUAUCUGGGGUAUCUUCUAAAA GAGGGUCAGAGAUGGCUGACUGAGGCCAGAAAA GAGACUGUGAUGGGGCAGCCUACUCCGAAGACCC CUCGACAACUAAGGGAGUUCCUAGGGAAGGCAGG CUUCUGUCGCCUCUUCAUCCCUGGGUUUGCAGAA AUGGCAGCCCCCCUGUACCCUCUCACCAAACCGG GGACUCUGUUUAAUUGGGGCCCAGACCAACAAAA GGCCUAUCAAGAAAUCAAGCAAGCCCUUCUAACU GCCCCAGCCCUGGGGUUGCCAGAUUUGACUAAGC CCUUUGAACUCUUUGUCGACGAGAAGCAGGGCUA CGCCAAAGGUGUCCUAACGCAAAAACUGGGACCU UGGCGUCGGCCGGUGGCCUACCUGUCCAAAAAGC UAGACCCAGUAGCAGCUGGGUGGCCCCCUUGCCU ACGGAUGGUAGCAGCCAUUGCCGUACUGACAAAG GAUGCAGGCAAGCUAACCAUGGGACAGCCACUAG UCAUUCUGGCCCCCCAUGCAGUAGAGGCACUAGU CAAACAACCCCCCGACCGCUGGCUUUCCAACGCC CGGAUGACUCACUAUCAGGCCUUGCUUUUGGACA CGGACCGGGUCCAGUUCGGACCGGUGGUAGCCCU GAACCCGGCUACGCUGCUCCCACUGCCUGAGGAA GGGCUGCAACACAACUGCCUUGAUAUCCUGGCCG AAGCCCACGGAACCCGACCCGACCUAACGGACCA GCCGCUCCCAGACGCCGACCACACCUGGUACACG GAUGGAAGCAGUCUCUUACAAGAGGGACAGCGUA AGGCGGGAGCUGCGGUGACCACCGAGACCGAGGU AAUCUGGGCUAAAGCCCUGCCAGCCGGGACAUCC GCUCAGCGGGCUGAACUGAUAGCACUCACCCAGG CCCUAAAGAUGGCAGAAGGUAAGAAGCUAAAUG UUUAUACUGAUAGCCGUUAUGCUUUUGCUACUGC	

	CCAUAUCCAUGGAGAAAUAUACAGAAGGCGUGGG UGGCUCACAUCAGAAGGCAAAGAGAUCAAAAAUA AAGACGAGAUCUUGGCCCUACUAAAAGCCCUCUU UCUGCCCAAAAGACUUAGCAUAAUCCAUUGUCCA GGACAUCAAAAGGGACACAGCGCCGAGGCUAGAG GCAACCGGAUGGCUGACCAAGCGGCCCGAAAGGC AGCCAUCACAGAGACUCCAGACACCUCUACCCUC CUCAUAGAAAAUUCAUCACCCUCUGGCGGCUCAA AAAGAACCGCCGACGGCAGCGAAUUCGAGAAAAG GACGGCGGAUGGUAGCGAAUUCGAGAGCCCUAAA AAGAAGGCCAAGGUAGAGUAA	
guide RNA	mA*mC*mA*CAAAUACCAGUCCAGCGGUUUUAGA mGmCmUmAmGmAmAmAmUmAmGmCAAGUUAAA AUAAGGCUAGUCCGUUAUCAmAmCmUmUmGmAm AmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUm CmGmGmUmGmCmU*mU*mU*mU m=2′OMethyl, *=phosphorothioate linkage	20629

Lipid nanoparticle (LNP) components (ionizable lipid, helper lipid, sterol, PEG) were dissolved in 100% ethanol with the lipid component molar ratios of 47:8:43.5:1.5, respectively. RNA (guide and mRNA) was combined in a 1:1 weight ratio and diluted to a concentration of 0.05-0.2 mg/mL in sodium acetate buffer, pH 5. RNA was formulated into distinct LNPs with a lipid amine to total RNA phosphate (N:P) molar ratio of 4.0. The LNPs were formed by microfluidic or turbulent mixing of the lipid and RNA solutions. A 3:1 ratio of aqueous to organic solvent was maintained during mixing using differential flow rates. After mixing, the LNPs were diluted, collected and buffer exchanged into 50 mM Tris, 9% sucrose buffer using tangential flow filtration. Formulations were concentrated to 1.0 mg/mL or higher then filtered through 0.2 μm sterile filter. The final LNP were stored at −80˚C until further use.

The LNP formulations were delivered intravenously by bolus tail vein injection to C57Blk/6 mice that were approximately 8 weeks old at concentrations ranging from 1-0.1 mg/kg. The expression of the Cas9-RT was measured by 6 hours after injection by euthanizing animals and collecting livers during necropsy. Animals were euthanized at 5 days after injection where liver was collected upon necropsy to which the activity of gene editing of the TTR locus was assessed. Expression of the Cas9-RT gene editing polypeptide in liver was measured by Western blot where Cas9 was detected by a mouse monoclonal antibody (7A9-3A3, Cell

Signaling Technology) and GAPDH (Cell Signaling Technology) was used as a loading control. (FIG. 12). Editing of the TTR locus was quantified by Sanger sequencing followed by TIDE analysis of an amplicon of the TTR locus near the binding site of the protospacer. Editing of the TTR locus was observed, as shown in FIG. 13. TTR protein levels in serum were quantified by an ELISA using a standard curve (Aviva Biosciences). TTR protein levels in serum declined in treated animals, as shown in FIG. 14. These experiments demonstrate that the Cas9-RT polypeptide can be expressed *in vivo*, and can edit the TTR locus, resulting in a decrease in TTR protein levels in serum.

Example 11. Gene editing at the TTR locus in an in vivo cynomolgus macaque model

This Example demonstrates successful delivery of an mRNA and guide using Cas9-mediated gene editing using the protospacer sequence ACACAAAUACCAGUCCAGCG (SEQ ID NO: 20630) that targets the TTR locus using a gene modifying polypeptide and RNA in a cynomolgus model.

RNAs were prepared as follows. An mRNA encoding a gene modifying polypeptide having the sequence shown in Table 11A below was produced by in vitro transcription and the purified mRNA was dissolved in 1 mM sodium citrate, pH 6, to a final concentration of RNA of 1-2 mg/mL. Similarly, a guide RNA having a sequence shown in Table 11A below was produced by chemical synthesis and dissolved in water or aqueous buffer, to a final concentration of RNA of 1-2 mg/mL.

Table 11A. Sequences of Example 11

Name	Nucleic acid sequence	SEQ ID NO
Cas9-RT gene modifying polypeptide	AUGCCUGCGGCUAAGCGGGUAAAAUUGGAUGGUGGGGACA AGAAGUACAGCAUCGGCCUGGACAUCGGCACCAACUCUGU GGGCUGGGCCGUGAUCACCGACGAGUACAAGGUGCCCAGC AAGAAAUUCAAGGUGCUGGGCAACACCGACCGGCACAGCA UCAAGAAGAACCUGAUCGGAGCCCUGCUGUUCGACAGCGG CGAAACAGCCGAGGCCACCCGGCUGAAGAGAACCGCCAGA AGAAGAUACACCAGACGGAAGAACCGGAUCUGCUAUCUGC AAGAGAUCUUCAGCAACGAGAUGGCCAAGGUGGACGACAG CUUCUUCCACAGACUGGAAGAGUCCUUCCUGGUGGAAGAG GAUAAGAAGCACGAGCGGCACCCCAUCUUCGGCAACAUCG UGGACGAGGUGGCCUACCACGAGAAGUACCCCACCAUCUA	20631

	CCACCUGAGAAAGAAACUGGUGGACAGCACCGACAAGGCC GACCUGCGGCUGAUCUAUCUGGCCCUGGCCCACAUGAUCA AGUUCCGGGGCCACUUCCUGAUCGAGGGCGACCUGAACCC CGACAACAGCGACGUGGACAAGCUGUUCAUCCAGCUGGUG CAGACCUACAACCAGCUGUUCGAGGAAAACCCCAUCAACG CCAGCGGCGUGGACGCCAAGGCCAUCCUGUCUGCCAGACU GAGCAAGAGCAGACGGCUGGAAAAUCUGAUCGCCCAGCUG CCCGGCGAGAAGAAGAAUGGCCUGUUCGGAAACCUGAUUG CCCUGAGCCUGGGCCUGACCCCCAACUUCAAGAGCAACUUC GACCUGGCCGAGGAUGCCAAACUGCAGCUGAGCAAGGACA CCUACGACGACGACCUGGACAACCUGCUGGCCCAGAUCGG CGACCAGUACGCCGACCUGUUUCUGGCCGCCAAGAACCUG UCCGACGCCAUCCUGCUGAGCGACAUCCUGAGAGUGAACA CCGAGAUCACCAAGGCCCCCCUGAGCGCCUCUAUGAUCAA GAGAUACGACGAGCACCACCAGGACCUGACCCUGCUGAAA GCUCUCGUGCGGCAGCAGCUGCCUGAGAAGUACAAAGAGA UUUUCUUCGACCAGAGCAAGAACGGCUACGCCGGCUACAU UGACGGCGGAGCCAGCCAGGAAGAGUUCUACAAGUUCAUC AAGCCCAUCCUGGAAAAGAUGGACGGCACCGAGGAACUGC UCGUGAAGCUGAACAGAGAGGACCUGCUGCGGAAGCAGCG GACCUUCGACAACGGCAGCAUCCCCCACCAGAUCCACCUGG GAGAGCUGCACGCCAUUCUGCGGCGGCAGGAAGAUUUUUA CCCAUUCCUGAAGGACAACCGGGAAAAGAUCGAGAAGAUC CUGACCUUCCGCAUCCCCUACUACGUGGGCCCUCUGGCCAG GGGAAACAGCAGAUUCGCCUGGAUGACCAGAAAGAGCGAG GAAACCAUCACCCCCUGGAACUUCGAGGAAGUGGUGGACA AGGGCGCUUCCGCCCAGAGCUUCAUCGAGCGGAUGACCAA CUUCGAUAAGAACCUGCCCAACGAGAAGGUGCUGCCCAAG CACAGCCUGCUGUACGAGUACUUCACCGUGUAUAACGAGC UGACCAAAGUGAAAUACGUGACCGAGGGAAUGAGAAAGCC CGCCUUCCUGAGCGGCGAGCAGAAAAAGGCCAUCGUGGAC CUGCUGUUCAAGACCAACCGGAAAGUGACCGUGAAGCAGC UGAAAGAGGACUACUUCAAGAAAAUCGAGUGCUUCGACUC CGUGGAAAUCUCCGGCGUGGAAGAUCGGUUCAACGCCUCC CUGGGCACAUACCACGAUCUGCUGAAAAUUAUCAAGGACA AGGACUUCCUGGACAAUGAGGAAAACGAGGACAUUCUGGA AGAUAUCGUGCUGACCCUGACACUGUUUGAGGACAGAGAG AUGAUCGAGGAACGGCUGAAAACCUAUGCCCACCUGUUCG ACGACAAAGUGAUGAAGCAGCUGAAGCGGCGGAGAUACAC CGGCUGGGGCAGGCUGAGCCGGAAGCUGAUCAACGGCAUC CGGGACAAGCAGUCCGGCAAGACAAUCCUGGAUUUCCUGA AGUCCGACGGCUUCGCCAACAGAAACUUCAUGCAGCUGAU CCACGACGACAGCCUGACCUUUAAAGAGGACAUCCAGAAA GCCCAGGUGUCCGGCCAGGGCGAUAGCCUGCACGAGCACA UUGCCAAUCUGGCCGGCAGCCCCGCCAUUAAGAAGGGCAU CCUGCAGACAGUGAAGGUGGUGGACGAGCUCGUGAAAGUG	

	AUGGGCCGGCACAAGCCCGAGAACAUCGUGAUCGAAAUGG CCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAG CCGCGAGAGAAUGAAGCGGAUCGAAGAGGGCAUCAAAGAG CUGGGCAGCCAGAUCCUGAAAGAACACCCCGUGGAAAACA CCCAGCUGCAGAACGAGAAGCUGUACCUGUACUACCUGCA GAAUGGGCGGGAUAUGUACGUGGACCAGGAACUGGACAUC AACCGGCUGUCCGACUACGAUGUGGACCAUAUCGUGCCUC AGAGCUUUCUGAAGGACGACUCCAUCGACAACAAGGUGCU GACCAGAAGCGACAAGAAUCGGGGCAAGAGCGACAACGUG CCCUCCGAAGAGGUCGUGAAGAAGAUGAAGAACUACUGGC GGCAGCUGCUGAACGCCAAGCUGAUUACCCAGAGAAAGUU CGACAAUCUGACCAAGGCCGAGAGAGGCGGCCUGAGCGAA CUGGAUAAGGCCGGCUUCAUCAAGAGACAGCUGGUGGAAA CCCGGCAGAUCACAAAGCACGUGGCACAGAUCCUGGACUC CCGGAUGAACACUAAGUACGACGAGAAUGACAAGCUGAUC CGGGAAGUGAAAGUGAUCACCCUGAAGUCCAAGCUGGUGU CCGAUUUCCGGAAGGAUUUCCAGUUUUACAAAGUGCGCGA GAUCAACAACUACCACCACGCCCACGACGCCUACCUGAACG CCGUCGUGGGAACCGCCCUGAUCAAAAAGUACCCUAAGCU GGAAAGCGAGUUCGUGUACGGCGACUACAAGGUGUACGAC GUGCGGAAGAUGAUCGCCAAGAGCGAGCAGGAAAUCGGCA AGGCUACCGCCAAGUACUUCUUCUACAGCAACAUCAUGAA CUUUUUCAAGACCGAGAUUACCCUGGCCAACGGCGAGAUC CGGAAGCGGCCUCUGAUCGAGACAAACGGCGAAACCGGGG AGAUCGUGUGGGAUAAGGGCCGGGAUUUUGCCACCGUGCG GAAAGUGCUGAGCAUGCCCCAAGUGAAUAUCGUGAAAAAG ACCGAGGUGCAGACAGGCGGCUUCAGCAAAGAGUCUAUCC UGCCCAAGAGGAACAGCGAUAAGCUGAUCGCCAGAAAGAA GGACUGGGACCCUAAGAAGUACGGCGGCUUCGACAGCCCC ACCGUGGCCUAUUCUGUGCUGGUGGUGGCCAAAGUGGAAA AGGGCAAGUCCAAGAAACUGAAGAGUGUGAAAGAGCUGCU GGGGAUCACCAUCAUGGAAAGAAGCAGCUUCGAGAAGAAU CCCAUCGACUUUCUGGAAGCCAAGGGCUACAAAGAAGUGA AAAAGGACCUGAUCAUCAAGCUGCCUAAGUACUCCCUGUU CGAGCUGGAAAACGGCCGGAAGAGAAUGCUGGCCUCUGCC GGCGAACUGCAGAAGGGAAACGAACUGGCCCUGCCCUCCA AAUAUGUGAACUUCCUGUACCUGGCCAGCCACUAUGAGAA GCUGAAGGGCUCCCCCGAGGAUAAUGAGCAGAAACAGCUG UUUGUGGAACAGCACAAGCACUACCUGGACGAGAUCAUCG AGCAGAUCAGCGAGUUCUCCAAGAGAGUGAUCCUGGCCGA CGCUAAUCUGGACAAAGUGCUGUCCGCCUACAACAAGCAC CGGGAUAAGCCCAUCAGAGAGCAGGCCGAGAAUAUCAUCC ACCUGUUUACCCUGACCAAUCUGGGAGCCCCUGCCGCCUUC AAGUACUUUGACACCACCAUCGACCGGAAGAGGUACACCA GCACCAAAGAGGUGCUGGACGCCACCCUGAUCCACCAGAG CAUCACCGGCCUGUACGAGACACGGAUCGACCUGUCUCAG	

	CUGGGAGGUGACUCUGGAGGAUCUAGCGGAGGAUCCUCUG GCAGCGAGACACCAGGAACAAGCGAGUCAGCAACACCAGA GAGCAGUGGCGGCAGCAGCGGCGGCAGCAGCACCCUAAAU AUAGAAGAUGAGUAUCGGCUACAUGAGACCUCAAAAGAGC CAGAUGUUUCUCUAGGGUCCACAUGGCUGUCUGAUUUUCC UCAGGCCUGGGCGGAAACCGGGGGCAUGGGACUGGCAGUU CGCCAAGCUCCUCUGAUCAUACCUCUGAAAGCAACCUCUA CCCCCGUGUCCAUAAAACAAUACCCCAUGUCACAAGAAGC CAGACUGGGGAUCAAGCCCCACAUACAGAGACUGUUGGAC CAGGGAAUACUGGUACCCUGCCAGUCCCCCUGGAACACGC CCCUGCUACCCGUUAAGAAACCAGGGACUAAUGAUUAUAG GCCUGUCCAGGAUCUGAGAGAAGUCAACAAGCGGGUGGAG GACAUCCACCCCACCGUGCCCAACCCUUACAACCUCUUGAG CGGGCUCCCACCGUCCCACCAGUGGUACACUGUGCUUGAU UUAAAGGAUGCCUUUUUCUGCCUGAGACUCCACCCCACCA GUCAGCCUCUCUUCGCCUUUGAGUGGAGAGAUCCAGAGAU GGGAAUCUCAGGACAAUUGACCUGGACCAGACUCCCACAG GGUUUCAAAAACAGUCCCACCCUGUUUAAUGAGGCACUGC ACAGAGACCUAGCAGACUUCCGGAUCCAGCACCCAGACUU GAUCCUGCUACAGUACGUGGAUGACUUACUGCUGGCCGCC ACUUCUGAGCUAGACUGCCAACAAGGUACUCGGGCCCUGU UACAAACCCUAGGGAACCUCGGGUAUCGGGCCUCGGCCAA GAAAGCCCAAAUUUGCCAGAAACAGGUCAAGUAUCUGGGG UAUCUUCUAAAAGAGGGUCAGAGAUGGCUGACUGAGGCCA GAAAAGAGACUGUGAUGGGGCAGCCUACUCCGAAGACCCC UCGACAACUAAGGGAGUUCCUAGGGAAGGCAGGCUUCUGU CGCCUCUUCAUCCCUGGGUUUGCAGAAAUGGCAGCCCCCC UGUACCCUCUCACCAAACCGGGGACUCUGUUUAAUUGGGG CCCAGACCAACAAAAGGCCUAUCAAGAAAUCAAGCAAGCC CUUCUAACUGCCCCAGCCCUGGGGUUGCCAGAUUUGACUA AGCCCUUUGAACUCUUUGUCGACGAGAAGCAGGGCUACGC CAAAGGUGUCCUAACGCAAAAACUGGGACCUUGGCGUCGG CCGGUGGCCUACCUGUCCAAAAAGCUAGACCCAGUAGCAG CUGGGUGGCCCCCUUGCCUACGGAUGGUAGCAGCCAUUGC CGUACUGACAAAGGAUGCAGGCAAGCUAACCAUGGGACAG CCACUAGUCAUUCUGGCCCCCCAUGCAGUAGAGGCACUAG UCAAACAACCCCCCGACCGCUGGCUUUCCAACGCCCGGAUG ACUCACUAUCAGGCCUUGCUUUUGGACACGGACCGGGUCC AGUUCGGACCGGUGGUAGCCCUGAACCCGGCUACGCUGCU CCCACUGCCUGAGGAAGGGCUGCAACACAACUGCCUUGAU AUCCUGGCCGAAGCCCACGGAACCCGACCCGACCUAACGGA CCAGCCGCUCCCAGACGCCGACCACACCUGGUACACGGAUG GAAGCAGUCUCUUACAAGAGGGACAGCGUAAGGCGGGAGC UGCGGUGACCACCGAGACCGAGGUAAUCUGGGCUAAAGCC CUGCCAGCCGGGACAUCCGCUCAGCGGGCUGAACUGAUAG CACUCACCCAGGCCCUAAAGAUGGCAGAAGGUAAGAAGCU	

	AAAUGUUUAUACUGAUAGCCGUUAUGCUUUUGCUACUGCC CAUAUCCAUGGAGAAAUAUACAGAAGGCGUGGGUGGCUCA CAUCAGAAGGCAAAGAGAUCAAAAAUAAAGACGAGAUCUU GGCCCUACUAAAAGCCCUCUUUCUGCCCAAAAGACUUAGC AUAAUCCAUUGUCCAGGACAUCAAAAGGGACACAGCGCCG AGGCUAGAGGCAACCGGAUGGCUGACCAAGCGGCCCGAAA GGCAGCCAUCACAGAGACUCCAGACACCUCUACCCUCCUCA UAGAAAAUUCAUCACCCUCUGGCGGCUCAAAAAGAACCGC CGACGGCAGCGAAUUCGAGAAAAGGACGGCGGAUGGUAGC GAAUUCGAGAGCCCUAAAAAGAAGGCCAAGGUAGAGUAA	
guide RNA	mA*mC*mA*CAAAUACCAGUCCAGCGGUUUUAGAmGmCmU mAmGmAmAmAmUmAmGmCAAGUUAAAAUAAGGCUAGUCC GUUAUCAmAmCmUmUmGmAmAmAmAmGmUmGmGmCm AmCmCmGmAmGmUmCmGmGmUmGmCmU*mU*mU*mU m=2′OMethyl, *=phosphorothioate linkage	20632

Lipid nanoparticle (LNP) components (ionizable lipid, helper lipid, sterol, PEG) were dissolved in 100% ethanol with the lipid component molar ratios of 47:8:43.5:1.5, respectively. RNA (guide and mRNA) was combined in a 1:1 weight ratio and diluted to a concentration of 0.05-0.2 mg/mL in sodium acetate buffer, pH 5. RNA was formulated into distinct LNPs with a lipid amine to total RNA phosphate (N:P) molar ratio of 4.0. The LNPs were formed by microfluidic or turbulent mixing of the lipid and RNA solutions. A 3:1 ratio of aqueous to organic solvent was maintained during mixing using differential flow rates. After mixing, the LNPs were diluted, collected and buffer exchanged into 50 mM Tris, 9% sucrose buffer using tangential flow filtration. Formulations were concentrated to 1.0 mg/mL or higher then filtered through 0.2 μm sterile filter. The final LNP were stored at −80˚C until further use. The LNP formulations were delivered intravenously by infusion over the course of 1 hour at 2 mg/kg where the volume of the infusion was 5 ml/kg. Cynomolgus macaques from mainland Asia were given dexamethasone 2 mg/kg bolus via intramuscular injection 1.5-2 h prior to intravenous infusion using a syringe pump. Animals were monitored after infusion and the expression of the Cas9-RT was measured by laparoscopic biopsies taken from the liver 8-12 h, 24 h, and 48 h after infusion. Animals were euthanized 14 days after infusion and liver was harvested by dividing the organ up into 8 different segments to which the activity of gene editing of the TTR locus was

assessed. Expression of the Cas9-RT gene editing polypeptide in liver was quantified by capillary electrophoresis western blot using the ProteinSimple Jess system (bio-techne) where Cas9 was detected by a mouse monoclonal antibody (7A9-3A3, Cell Signaling Technology).

Relative expression of the Cas9-RT gene editing polypeptide was measured by an area under curve analysis, as shown in FIG. 15. Editing of the TTR locus was quantified by amplicon-sequencing of the TTR locus near the binding site of the protospacer. Editing of the TTR locus was observed, as shown in FIG. 16. These experiments demonstrate that the Cas9-RT polypeptide can be expressed *in vivo* in a non-human primate model and can edit the TTR locus.

Example 12: Quantifying activity of a gene modifying polypeptide and template RNA for editing the endogenous B-globin locus achieved in CD34+ primary human hematopoietic stem cells (HSCs)

This example demonstrates the use of a gene modifying system containing an exemplary gene modifying polypeptide and a template RNA, to convert the glutamic acid codon (GAG) at amino acid position 7 in the endogenous B-globin locus in primary human HSCs to alanine (GCG), thereby demonstrating targeting the sequence position associated with sickle cell disease (SCD) and editing of the sequence to encode a non-pathogenic amino acid at position 7. The "C" residue installed by this process is referred to as the "Makassar" variant and is a non-pathogenic sequence variant that occurs in the human population. This conversion comprises the change of one base pair (i.e., replacement of the DNA base adenine at nucleotide positions 20 to the base cytosine in SEQ ID NO: 20633).

ATGGTGCATCTGACTCCTGA
GGAGAAGTCTGCCGTTACTGCCCTGTGGGGCAAGGTGAACGTGGATGAAGTTGGTGGTGAGGCCCTGGGC
AGGCTGCTGGTGGTCTACCCTTGGACCCAGAGGTTCTTTGAGTCCTTTGGGGATCTGTCCACTCCTGATG
CTGTTATGGGCAACCCTAAGGTGAAGGCTCATGGCAAGAAAGTGCTCGGTGCCTTTAGTGATGGCCTGGC
TCACCTGGACAACCTCAAGGGCACCTTTGCCACACTGAGTGAGCTGCACTGTGACAAGCTGCACGTGGAT
CCTGAGAACTTCAGGCTCCTGGGCAACGTGCTGGTCTGTGTGCTGGCCCATCACTTTGGCAAAGAATTCA
CCCCACCAGTGCAGGCTGCCTATCAGAAAGTGGTGGCTGGTGTGGCTAATGCCCTGGCCCACAAGTATCA
CTAAGCTCGCTTTCTTGCTGTCCAATTTCTATTAAAGGTTCCTTTGTTCCCTAA (SEQ ID NO: 20633)

In this example, the template RNAs contained:

(1) a gRNA spacer;

(2) a gRNA scaffold;

(3) a heterologous object sequence; and

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

The exemplary template RNAs comprised the following sequences from 5' to 3' wherein the first 3, and last 3 bases have 2'-O-methyl phosphorothioate chemical modifications as indicated. In the sequences below, m=2'-O-methyl ribonucleotide, r=ribose, and *=phosphorothioate bond.

tg34
mG*mU*mA*rArCrGrGrCrArGrArCrUrUrCrUrCrCrUrCrGrUrUrUrUrArGrArGrCrUrArGrArArArUrArGrCrArA
rGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCr
GrArGrUrCrGrGrUrGrCrArCrCrUrGrArCrUrCrCrUrGrCrGrGrArGrArArGrUrCrU*mG*mC (SEQ ID NO: 20634)

tg35
mG*mU*mA*rArCrGrGrCrArGrArCrUrUrCrUrCrCrUrCrGrUrUrUrUrArGrArGrCrUrArGrArArArUrArGrCrArA
rGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCr
GrArGrUrCrGrGrUrGrCrArCrCrUrGrArCrUrCrCrUrGrCrGrGrArGrArArGrUrCrU*mG*mC*mC (SEQ ID NO: 20635)

tg36
mG*mU*mA*rArCrGrGrCrArGrArCrUrUrCrUrCrCrUrCrGrUrUrUrUrArGrArGrCrUrArGrArArArUrArGrCrArA
rGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCr
GrArGrUrCrGrGrUrGrCrGrCrArCrCrUrGrArCrUrCrCrUrGrCrGrGrArGrArArGrUrC*mU*mG*mC (SEQ ID NO: 20636)

Unmodified versions of these sequences are shown in Table BB below. In some embodiments, the sequences used in this table can be used without chemical modifications.

Table BB. tg34, tg35, and tg36 without nucleotide modifications.

Name	Sequence	SEQ ID NO
tg34	GUAACGGCAGACUUCUCCUCGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCACCUGACUCCUGCGGAGAAGUCUGC	21767
tg35	GUAACGGCAGACUUCUCCUCGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCACCUGACUCCUGCGGAGAAGUCUGCC	21768
tg36	GUAACGGCAGACUUCUCCUCGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGCACCUGACUCCUGCGGAGAAGUCUGC	21769

The gene modifying polypeptide tested comprised the sequence set out in Example 8 labeled RNAV209.

The gene modifying system comprising the gene modifying polypeptides and the template RNA described above was transfected into human HSCs. The gene modifying polypeptide and the template RNA were delivered by nucleofection in RNA format. Specifically, 2000 ng of mRNA encoding the gene modifying polypeptide were combined with 2000 ng template RNA. The RNA mixture was added to 200,000 primary human HSCs in a total of 20 μL of Lonza P3 buffer and HSC were nucleofected in 16-well nucleofection cassettes using program DZ-100. After nucleofection, cells were incubated at room temperature for 10 minutes and were transferred to 24-well plates containing 500 μL of StemSpan-XF + SCF at 100 ng/mL, Flt3-L at 100 ng/mL, and TPO at 100 ng/mL in each well and cultured at 37˚C, 5% CO_2 for 3 days prior to cell lysis and genomic DNA extraction. To analyze gene editing activity, primers flanking the target insertion site locus were used to amplify across the locus. Amplicons were analyzed via short read sequencing using an Illumina MiSeq. Replacement of the DNA base adenine at nucleotide position 20 to the base cytosine downstream of the transcriptional start site within the endogenous B-globin locus indicated successful editing.

As shown in **FIG. 17**, average perfect rewrite levels, corresponding to replacement of the C nucleotide with an A at the SCD codon, of 1.3% - 1.8% were detected in primary human HSCs when the primary human HSCs were treated with the exemplary template gRNAs and mRNA encoding the exemplary gene modifying polypeptide. These results demonstrate the use of a gene modifying system to edit a non-pathogenic sequence into a clinically relevant codon in the endogenous B-globin locus in primary human HSCs. The results further demonstrate that several exemplary template RNAs can be used to achieve the desired editing.

Example 13: Comparing the activity of different second strand-targeting gRNA in combination with a gene modifying polypeptide and template RNAs for editing the endogenous B-globin locus in CD34+ primary human hematopoietic stem cells (HSCs).

This example demonstrates the use of exemplary gene modifying systems containing a gene modifying polypeptide, a template RNA, and one of several different exemplary second strand-targeting gRNAs to convert the glutamic acid codon (GAG) at amino acid position 7 in the endogenous B-globin locus in primary human HSCs to alanine (GCA or GCG), thereby demonstrating targeting the sequence position associated with sickle cell disease (SCD) and editing of the sequence to encode a non-pathogenic amino acid at position 7. This conversion comprises a change of two base pairs for exemplary template RNAs comprising the exemplary HBB5 spacer (i.e., replacement of the DNA bases adenine and guanine at nucleotide positions 20 and 21 to the bases cytosine and adenine, respectively) and the change of one base pair for exemplary template RNAs comprising the exemplary HBB8 spacer (i.e., replacement of the DNA base adenine at nucleotide positions 20 to the base cytosine).

In this example, the template RNA contained:

(1) a gRNA spacer;

(2) a gRNA scaffold;

(3) a heterologous object sequence; and

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

The template RNAs comprised the nucleic acid sequence set out in Example 5 labeled FYF tgRNA14 for the exemplary HBB5 template RNA or tg34 for the exemplary HBB8 template RNA, respectively.

The gene modifying polypeptide comprised the amino acid sequence set out in Example 8 labeled RNAV209.

The second strand-targeting gRNA sequences, designed to produce a second nick, comprised the sequences listed in Table X1.

Table X1: Exemplary Second Strand-Targeting gRNAs

Name	RNA sequence	SEQ ID NO
HBB5_216rv	mC*mU*mU*rGrCrCrCrCrArCrArGrGrGrCrArGrUrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCmU*mU*mU*mU	20817
HBB5_24rv	mU*mG*mC*rArGrGrArGrUrCrArGrGrUrGrCrArCrCrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCmU*mU*mU*mU	20818
HBB5_34rv	mC*mA*mG*rArCrUrUrCrUrCrUrGrCrArGrGrArGrUrCrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCmU*mU*mU*mU	20819
HBB5_34rv_hs1	mC*mA*mG*rArCrUrUrCrUrCrUrGrCrCrGrGrArGrUrCrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCmU*mU*mU*mU	20820
HBB5_41rv	mG*mU*mA*rArCrGrGrCrArGrArCrUrUrCrUrCrUrGrCrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCmU*mU*mU*mU	20821
HBB5_122rv	mA*mA*mG*rCrArArArUrGrUrArArGrGrCrArArUrArGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCmU*mU*mU*mU	20822
HBB5_92rv	mC*mU*mG*rArCrUrUrUrUrArUrGrCrCrCrArGrCrCrCrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCmU*mU*mU*mU	20823
HBB5_g27	mC*mC*mU*rUrGrArUrArCrCrArArCrCrUrGrCrCrCrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCmU*mU*mU*mU	20824
HBB5_g37	mC*mA*mC*rGrUrUrCrArCrCrUrUrGrCrCrCrCrArCrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCmU*mU*mU*mU	20825
HBB5_g38	mC*mC*mA*rCrGrUrUrCrArCrCrUrUrGrCrCrCrCrArCrGrUrUrUrUrArGrArGrCrUrArGrArArArUrArGrCrArArGrUrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCmU*mU*mU*rU	20826
HBB5_g39	mA*mC*mC*rUrUrGrArUrArCrCrArArCrCrUrGrCrCrCrGrUrUrUrUrArGrArGrCrUrArGrArArArUrArGrCrArArGrUrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCmU*mU*mU*rU	20827
HBB5_g40	mU*mC*mC*rArCrArUrGrCrCrCrArGrUrUrUrCrUrArUrGrUrUrUrUrArGrArGrCrUrArGrArArArUrArGrCrArArGrUrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCmU*mU*mU*rU	20828

HBB8_gRNA1	mC*mA*mG*rGrGrCrUrGrGrGrCrArUrArArArArGrUrCrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmGmUmUmGmCmAmGmUmUmCmGmAmUmUmCmGmUmCmUmU*mU*mU*mU	20829
HBB8_gRNA2	mA*mG*mG*rGrCrUrGrGrGrCrArUrArArArArGrUrCrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmGmUmUmGmCmAmGmUmUmCmGmAmUmUmCmGmUmCmUmU*mU*mU*mU	20830
HBB8_gRNA3	mG*mC*mA*rArCrCrUrCrArArArCrArGrArCrCrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmGmUmUmGmCmAmGmUmUmCmGmAmUmUmCmGmUmCmUmU*mU*mU*mU	20831
HBB8_gRNA4	mG*mG*mA*rGrGrGrCrArGrGrArGrCrCrArGrGrGrCrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmGmUmUmGmCmAmGmUmUmCmGmAmUmUmCmGmUmCmUmU*mU*mU*mU	20832
HBB8_231fw	mG*mU*mC*rUrGrCrCrGrUrUrArCrCrUrGrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmGmUmUmGmCmAmGmUmUmCmGmAmUmUmCmGmUmCmUmU*mU*mU*mU	20833
HBB8_237fw	mC*mG*mU*rUrArCrUrGrCrCrCrUrGrUrGrGrGrCrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmGmUmUmGmCmAmGmUmUmCmGmAmUmUmCmGmUmCmUmU*mU*mU*mU	20834
HBB8_246fw	mC*mC*mU*rGrUrGrGrGrGrCrArArGrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmGmUmUmGmCmAmGmUmUmCmGmAmUmUmCmGmUmCmUmU*mU*mU*mU	20835
HBB8_256fw	mA*mA*mG*rGrUrGrArArArCrGrUrGrGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmGmUmUmGmCmAmGmUmUmCmGmAmUmUmCmGmUmCmUmU*mU*mU*mU	20836
HBB8_270fw	mU*mG*mA*rArGrUrUrGrGrUrGrArArGrGrCrCrCrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmGmUmUmGmCmAmGmUmUmCmGmAmUmUmCmGmUmCmUmU*mU*mU*mU	20837
HBB8_279fw	mU*mG*mG*rUrGrArArGrGrCrCrCrUrGrGrGrCrArGrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmGmUmUmGmCmAmGmUmUmCmGmAmUmUmCmGmUmCmUmU*mU*mU*mU	20838
HBB8_299fw	mU*mG*mG*rUrArUrCrArArArGrArCrCrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmGmUmUmGmCmAmGmUmUmCmGmAmUmUmCmGmUmCmUmU*mU*mU*mU	20839
HBB8_306fw	mA*mA*mG*rGrUrUrArCrCrArArGrArCrCrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmGmUmUmGmCmAmGmUmUmCmGmAmUmUmCmGmUmCmUmU*mU*mU*mU	20840

Table X1A shows the sequences of X1 without modifications. In some embodiments, the sequences used in this table can be used without chemical modifications.

Table X1A: Table X1 Sequences without Modifications

Name	RNA sequence	SEQ ID NO
HBB5_216rv	CUUGCCCCACAGGGCAGUAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUUU	21770
HBB5_24rv	UGCAGGAGUCAGGUGCACCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUUU	21771
HBB5_34rv	CAGACUUCUCUGCAGGAGUCGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUUU	21772
HBB5_34rv_hs1	CAGACUUCUCUGCCGGAGUCGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUUU	21773
HBB5_41rv	GUAACGGCAGACUUCUCUGCGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUUU	21774
HBB5_122rv	AAGCAAAUGUAAGCAAUAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUUU	21775
HBB5_92rv	CUGACUUUUAUGCCCAGCCCGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUUU	21776
HBB5_g27	CCUUGAUACCAACCUGCCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUUU	21777
HBB5_g37	CACGUUCACCUUGCCCCACAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUUU	21778
HBB5_g38	CCACGUUCACCUUGCCCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUUU	21779
HBB5_g39	ACCUUGAUACCAACCUGCCCGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUUU	21780
HBB5_g40	UCCACAUGCCCAGUUUCUAUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUUU	21781
HBB8_gRNA1	CAGGGCUGGGCAUAAAAGUCGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUUU	21782

HBB8_gRNA2	AGGGCUGGGGCAUAAAAGUCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUUU	21783
HBB8_gRNA3	GCAACCUCAAACAGACACCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUUU	21784
HBB8_gRNA4	GGAGGGCAGGAGCCAGGGCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUUU	21785
HBB8_231fw	GUCUGCCGUUACUGCCCUGUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUUU	21786
HBB8_237fw	CGUUACUGCCCUGUGGGGCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUUU	21787
HBB8_246fw	CCUGUGGGGCAAGGUGAACGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUUU	21788
HBB8_256fw	AAGGUGAACGUGGAUGAAGUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUUU	21789
HBB8_270fw	UGAAGUUGGUGGUGAGGCCCGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUUU	21790
HBB8_279fw	UGGUGAGGCCCUGGGCAGGUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUUU	21791
HBB8_299fw	UGGUAUCAAGGUUACAAGACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUUU	21792
HBB8_306fw	AAGGUUACAAGACAGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUUU	21793

The gene modifying system comprising the gene modifying polypeptides and the template RNA described above was transfected into human HSCs. The gene modifying polypeptide and the template RNA were delivered by nucleofection in RNA format. Specifically, 3000 ng of mRNA encoding the gene modifying polypeptide were combined with 2000 ng template RNA and 2000 ng (for systems comprising HBB5 template RNA) or 3000 ng (for systems comprising HBB8 template RNA) of second strand-targeting gRNA. The RNA mixture was added to 200,000 primary human HSCs in a total of 20 µL of Lonza P3 buffer and HSC were nucleofected in 16-well nucleofection cassettes using program DZ-100. After nucleofection, cells incubated at room temperature for 10 minutes and were transferred to 24-well plates containing 500 µL of StemSpan-XF + SCF at 100 ng/mL, Flt3-L at 100 ng/mL, and TPO at 100 ng/mL in each well and cultured at 37˚C, 5% CO_2 for 3 days prior to cell lysis and genomic DNA extraction. To analyze gene editing activity, primers flanking the target insertion site locus were used to amplify across the locus. Amplicons were analyzed via short read sequencing using an Illumina MiSeq. Replacement of the DNA bases adenine and guanine at nucleotide positions 20 and 21 to the bases cytosine and adenine (HBB5 template RNA) or replacement of the DNA bases adenine at nucleotide positions 20 to the base cytosine (HBB8 template RNA) downstream of the transcriptional start site within the endogenous B-globin locus indicated successful editing.

As shown in FIG. 18A, average perfect rewrite levels, corresponding to replacement of adenine and guanine at nucleotide positions 20 and 21 to the bases cytosine and adenine (respectively) at the SCD codon, of 4.5% - 21.3% were detected in primary human HSCs when the HSCs were treated with exemplary gene modifying systems comprising exemplary HBB5 template RNA tg14 and various second strand-targeting gRNAs. As shown in FIG. 18B, average perfect rewrite levels, corresponding to replacement of adenine at nucleotide positions 20 to the base cytosine at the SCD codon, of 2.9% - 24.6% were detected in primary human HSCs when the HSCs were treated with exemplary gene modifying systems comprising exemplary HBB8 template gRNA tg34 and various second strand-targeting gRNAs.

These results demonstrate that use of a second strand-targeting gRNA increases the editing activity of exemplary gene modifying systems targeting a clinically relevant codon in the endogenous B-globin locus in primary human HSCs. The results further demonstrate that adjusting the positioning of a second strand-targeting gRNA (e.g., relative to the sequence targeted by a spacer of an exemplary template RNA) increases the enhancement to editing

activity, e.g., to more than 9-fold higher than perfect rewriting in the absence of second strand-targeting gRNA.

Example 14: Characterizing configurations of template RNAs including silent substitutions for editing the endogenous B-globin locus in CD34+ primary human hematopoietic stem cells (HSCs).

This example demonstrates the use of a gene modifying system containing an exemplary gene modifying polypeptide and various template RNAs comprising different silent substitutions, to convert the glutamic acid codon at amino acid position 7 in the endogenous B-globin locus in primary human HSCs to alanine, thereby demonstrating targeting the sequence position associated with sickle cell disease (SCD) and editing of the sequence to encode a non-pathogenic sequence into position 7. This conversion comprises a change of two base pairs for exemplary HBB5 template RNAs (i.e., replacement of the DNA bases adenine and guanine at nucleotide positions 20 and 21 to the bases cytosine and adenine) plus the inclusion of additional relevant silent substitutions (which alter the nucleic acid sequence of the DNA but not the protein sequence through the usage of different synonymous codons).

In this example, the template RNA contained:

(1) a gRNA spacer;

(2) a gRNA scaffold;

(3) a heterologous object sequence; and

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

More specifically, the exemplary template RNAs comprised the following sequences from 5' to 3', wherein the first 3, and last 3 bases have 2'-O-methyl phosphorothioate chemical modifications. In the sequences below, m=2'-O-methyl ribonucleotide, r=ribose, and *=phosphorothioate bond. Different combinations of substitutions and RT/PBS length were included (Table X2).

Table X2: Exemplary Silent Substitution-Containing Template RNAs.

Name	Sequence	SEQ ID NO	RT length	PBS length	Substitution
tg14_h	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArCrUrCrCrUrGrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArGrArCrUrUrCrUrCrUrGrCrArGrGrArGrUrCrArGrG*mG*mU*mG	20841	14	10	none
tg14_hs1	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArCrUrCrCrUrGrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArGrArCrUrUrCrUrCrUrGrCrCrGrGrArGrUrCrArGrG*mG*mU*mG	20842	14	10	sub1
tg14_hs2	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArCrUrCrCrUrGrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArGrArCrUrUrCrUrCrUrGrCrCrGrGrArGrUrCrArGrG*mG*mU*mG	20843	14	10	sub2
tg14_hs3	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArCrUrCrCrUrGrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArGrArCrUrUrCrUrCrUrGrCrUrGrGrArGrUrCrArGrG*mG*mU*mG	20844	14	10	sub3
tg14_hs4	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArCrUrCrCrUrGrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArGrArUrUrUrCrUrCrUrGrCrArGrGrArGrUrCrArGrG*mG*mU*mG	20845	14	10	sub4
tg14_hs5	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArCrUrCrCrUrGrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArGrArCrUrUrCrUrCrUrGrCrArGrGrArGrUrCrArGrG*mG*mU*mG	20846	14	10	sub5
tg14_hs6	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArCrUrCrCrUrGrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArGrArCrUrUrCrUrCrUrGrCrCrGrGrArGrUrCrArGrG*mG*mU*mG	20847	14	10	sub6
tg14_hs7	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArCrUrCrCrUrGrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArGrArCrUrUrCrUrCrUrGrCrArGrGrArGrUrCrArGrG*mG*mU*mG	20848	14	10	sub7

	mGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArGrArCrUrUrUrUrCrUrGrCrGrGrArGrUrCrArG*mG*mU*mG				
tg14_hs8	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArCrUrCrCrUrGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmUmA mGmCrArArGrUrUrArArArArUrArArArGrGrCrUrArArUrCrCrGrUrUrArArUrCrAmAmCmUmUmGmAmAmAmA mGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArGrArCrUrUrUrUrCrUrGrCrCrGrGrArGrUrCrArG*mG*mU*mG	20849	14	10	sub 8
tg14_hs9	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArCrUrCrCrUrGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmUmA mGmCrArArGrUrUrArArArArUrArArArGrGrCrUrArArUrCrCrGrUrUrArArUrCrAmAmCmUmUmGmAmAmAmA mGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArGrArUrUrUrUrCrUrGrCrCrGrGrArGrUrCrArG*mG*mU*mG	20850	14	10	sub 9
tg14_hs10	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArCrUrCrCrUrGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmUmA mGmCrArArGrUrUrArArArArUrArArArGrGrCrUrArArUrCrCrGrUrUrArArUrCrAmAmCmUmUmGmAmAmAmA mGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArGrArUrUrUrCrUrGrCrCrGrGrArGrUrCrArG*mG*mU*mG	20851	14	10	sub 10
tg14_hs11	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArCrUrCrCrUrGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmUmA mGmCrArArGrUrUrArArArArUrArArArGrGrCrUrArArUrCrCrGrUrUrArArUrCrAmAmCmUmUmGmAmAmAmA mGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArGrArUrUrUrCrUrGrCrCrGrGrArGrUrCrArG*mG*mU*mG	20852	14	10	sub 11
tg14_hs12	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArCrUrCrCrUrGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmUmA mGmCrArArGrUrUrArArArArUrArArArGrGrCrUrArArUrCrCrGrUrUrArArUrCrAmAmCmUmUmGmAmAmAmA mGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArGrArUrUrUrCrUrGrCrCrGrGrArGrUrCrArG*mG*mU*mG	20853	14	10	sub 12
tg14_hs13	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArCrUrCrCrUrGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmUmA mGmCrArArGrUrUrArArArArUrArArArGrGrCrUrArArUrCrCrGrUrUrArArUrCrAmAmCmUmUmGmAmAmAmA mGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArGrArUrUrUrCrUrGrCrCrGrGrArGrUrCrArG*mG*mU*mG	20854	14	10	sub 13
tg14_hs14	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArCrUrCrCrUrGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmUmA mGmCrArArGrUrUrArArArArUrArArArGrGrCrUrArArUrCrCrGrUrUrArArUrCrAmAmCmUmUmGmAmAmAmA mGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArGrArUrUrUrCrUrGrCrCrGrGrArGrUrCrArG*mG*mU*mG	20855	14	10	sub 14
tg14_hs15	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArCrUrCrCrUrGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmUmA mGmCrArArGrUrUrArArArArUrArArArGrGrCrUrArArUrCrCrGrUrUrArArUrCrAmAmCmUmUmGmAmAmAmA mGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArGrArUrUrUrCrUrGrCrCrGrGrArGrUrCrArG*mG*mU*mG	20856	14	10	sub 15
tg19_h	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArCrUrCrCrUrGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmUmA mGmCrArArGrUrUrArArArArUrArArArGrGrCrUrArArUrCrCrGrUrUrArArUrCrAmAmCmUmUmGmAmAmAmA	20857	17	11	none

	mGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrGrGrCrArGrArCrUrUrCrUrGrCrArGrGrAr GrUrCrArGrG*mU*mG*mC				
tg19_hs1	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmUmA mGmCrArArGrUrUrArArArArUrArArGrGrCrUrArArUrCrAmAmCmUmUmGmAmAmAmA mGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrGrGrCrArGrArCrUrUrCrUrGrCrGrGrAr GrUrCrArGrG*mU*mG*mC	20858	17	11	sub 1
tg19_hs2	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmUmA mGmCrArArGrUrUrArArArArUrArArGrGrCrUrArArUrCrAmAmCmUmUmGmAmAmAmA mGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrGrGrCrArGrArCrUrUrCrUrGrCrGrGrAr GrUrCrArGrG*mU*mG*mC	20859	17	11	sub 2
tg19_hs3	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmUmA mGmCrArArGrUrUrArArArArUrArArGrGrCrUrArArUrCrAmAmCmUmUmGmAmAmAmA mGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrGrGrCrArGrArCrUrUrCrUrGrCrGrGrAr GrUrCrArGrG*mU*mG*mC	20860	17	11	sub 3
tg19_hs4	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmUmA mGmCrArArGrUrUrArArArArUrArArGrGrCrUrArArUrCrAmAmCmUmUmGmAmAmAmA mGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrGrGrCrArGrArCrUrUrCrUrGrCrGrGrAr GrUrCrArGrG*mU*mG*mC	20861	17	11	sub 4
tg19_hs5	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmUmA mGmCrArArGrUrUrArArArArUrArArGrGrCrUrArArUrCrAmAmCmUmUmGmAmAmAmA mGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrGrGrCrArGrArCrUrUrCrUrGrCrGrGrAr GrUrCrArGrG*mU*mG*mC	20862	17	11	sub 5
tg19_hs6	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmUmA mGmCrArArGrUrUrArArArArUrArArGrGrCrUrArArUrCrAmAmCmUmUmGmAmAmAmA mGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrGrGrCrArGrArCrUrUrCrUrGrCrGrGrAr GrUrCrArGrG*mU*mG*mC	20863	17	11	sub 6
tg19_hs7	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmUmA mGmCrArArGrUrUrArArArArUrArArGrGrCrUrArArUrCrAmAmCmUmUmGmAmAmAmA mGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrGrGrCrArGrArCrUrUrCrUrGrCrGrGrAr GrUrCrArGrG*mU*mG*mC	20864	17	11	sub 7
tg19_hs8	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmUmA mGmCrArArGrUrUrArArArArUrArArGrGrCrUrArArUrCrAmAmCmUmUmGmAmAmAmA mGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrGrGrCrArGrArCrUrUrCrUrGrCrGrGrAr GrUrCrArGrG*mU*mG*mC	20865	17	11	sub 8
tg19_hs9	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmUmA mGmCrArArGrUrUrArArArArUrArArGrGrCrUrArArUrCrAmAmCmUmUmGmAmAmAmA	20866	17	11	sub 9

	mGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrGrGrCrArGrArUrUrUrCrUrCrCrGrGrAr GrUrCrArGrG*mU*mG*mC				
tg19_hs10	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmUmA mGmCrArArGrUrUrArArArArUrArArGrGrCrUrArArUrCrCrGrUrUrArArUrCrAmAmCmUmUmGmAmAmAmA mGmUmGmGmCmAmAmCmCmGmAmGmUmCmGmGmCrGrCrArGrArUrUrUrCrUrCrCrGrGrAr GrUrCrArGrG*mU*mG*mC	20867	17	11	sub 10
tg19_hs11	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmUmA mGmCrArArGrUrUrArArArArUrArArGrGrCrUrArArUrCrCrGrUrUrArArUrCrAmAmCmUmUmGmAmAmAmA mGmUmGmGmCmAmAmCmCmGmAmGmUmCmGmGmCrGrCrArGrArUrUrUrCrUrCrCrGrGrAr GrUrCrArGrG*mU*mG*mC	20868	17	11	sub 11
tg19_hs12	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmUmA mGmCrArArGrUrUrArArArArUrArArGrGrCrUrArArUrCrCrGrUrUrArArUrCrAmAmCmUmUmGmAmAmAmA mGmUmGmGmCmAmAmCmCmGmAmGmUmCmGmGmCrGrCrArGrArUrUrUrCrUrCrCrGrGrAr GrUrCrArGrG*mU*mG*mC	20869	17	11	sub 12
tg19_hs13	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmUmA mGmCrArArGrUrUrArArArArUrArArGrGrCrUrArArUrCrCrGrUrUrArArUrCrAmAmCmUmUmGmAmAmAmA mGmUmGmGmCmAmAmCmCmGmAmGmUmCmGmGmCrGrCrArGrArUrUrUrCrUrCrCrGrGrAr GrUrCrArGrG*mU*mG*mC	20870	17	11	sub 13
tg19_hs14	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmUmA mGmCrArArGrUrUrArArArArUrArArGrGrCrUrArArUrCrCrGrUrUrArArUrCrAmAmCmUmUmGmAmAmAmA mGmUmGmGmCmAmAmCmCmGmAmGmUmCmGmGmCrGrCrArGrArUrUrUrCrUrCrCrGrGrAr GrUrCrArGrG*mU*mG*mC	20871	17	11	sub 14
tg19_hs15	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmUmA mGmCrArArGrUrUrArArArArUrArArGrGrCrUrArArUrCrCrGrUrUrArArUrCrAmAmCmUmUmGmAmAmAmA mGmUmGmGmCmAmAmCmCmGmAmGmUmCmGmGmCrGrCrArGrArUrUrUrCrUrCrCrGrGrAr GrUrCrArGrG*mU*mG*mC	20872	17	11	sub 15
tg41_h	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmUmA mGmCrArArGrUrUrArArArArUrArArGrGrCrUrArArUrCrAmAmCmUmUmGmAmAmAmA mGmUmGmGmCmAmAmCmCmGmAmGmUmCmArCrGrGrCrArGrArCrUrUrCrUrCrArGr GrArGrUrCrArGrG*mU*mG*mC	20873	19	11	non e
tg41_hs1	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmUmA mGmCrArArGrUrUrArArArArUrArArGrGrCrUrArArUrCrAmAmCmUmUmGmAmAmAmA mGmUmGmGmCmAmAmCmCmGmAmGmUmCmArCrGrGrCrArGrArCrUrUrCrUrCrArGr GrArGrUrCrArGrG*mU*mG*mC	20874	19	11	sub 1
tg41_hs2	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmUmA mGmCrArArGrUrUrArArArArUrArArGrGrCrUrArArUrCrAmAmCmUmUmGmAmAmAmA	20875	19	11	sub 2

	mGmUmGmGmCmAmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrGrGrCrArGrArCrUrUrCrUrGrCrGrGr GrArGrUrCrArGrG*mU*mG*mC				
tg41_hs3	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmUmA mGmCrArArGrUrUrArArArArUrArArGrGrCrUrArArUrCrAmAmCmUmUmGmAmAmAmA mGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrGrGrCrArGrArCrUrUrCrUrGrCrGrGr GrArGrUrCrArGrG*mU*mG*mC	20876	19	11	sub 3
tg41_hs4	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmUmA mGmCrArArGrUrUrArArArArUrArArGrGrCrUrArArUrCrAmAmCmUmUmGmAmAmAmA mGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrGrGrCrArGrArUrUrCrUrGrCrArGr GrArGrUrCrArGrG*mU*mG*mC	20877	19	11	sub 4
tg41_hs5	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmUmA mGmCrArArGrUrUrArArArArUrArArGrGrCrUrArArUrCrAmAmCmUmUmGmAmAmAmA mGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrGrGrCrArGrArUrUrCrUrGrCrArGr GrArGrUrCrArGrG*mU*mG*mC	20878	19	11	sub 5
tg41_hs6	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmUmA mGmCrArArGrUrUrArArArArUrArArGrGrCrUrArArUrCrAmAmCmUmUmGmAmAmAmA mGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrGrGrCrArGrArCrUrUrUrUrGrCrCrGr GrArGrUrCrArGrG*mU*mG*mC	20879	19	11	sub 6
tg41_hs7	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmUmA mGmCrArArGrUrUrArArArArUrArArGrGrCrUrArArUrCrAmAmCmUmUmGmAmAmAmA mGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrGrGrCrArGrArCrUrUrUrUrGrCrGrGr GrArGrUrCrArGrG*mU*mG*mC	20880	19	11	sub 7
tg41_hs8	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmUmA mGmCrArArGrUrUrArArArArUrArArGrGrCrUrArArUrCrAmAmCmUmUmGmAmAmAmA mGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrGrGrCrArGrArCrUrUrUrUrGrCrGrGr GrArGrUrCrArGrG*mU*mG*mC	20881	19	11	sub 8
tg41_hs9	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmUmA mGmCrArArGrUrUrArArArArUrArArGrGrCrUrArArUrCrAmAmCmUmUmGmAmAmAmA mGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrGrGrCrArGrArUrUrCrUrGrCrCrGr GrArGrUrCrArGrG*mU*mG*mC	20882	19	11	sub 9
tg41_hs10	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmUmA mGmCrArArGrUrUrArArArArUrArArGrGrCrUrArArUrCrAmAmCmUmUmGmAmAmAmA mGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrGrGrCrArGrArUrUrCrUrGrCrGrGr GrArGrUrCrArGrG*mU*mG*mC	20883	19	11	sub 10
tg41_hs11	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmUmA mGmCrArArGrUrUrArArArArUrArArGrGrCrUrArArUrCrAmAmCmUmUmGmAmAmAmA	20884	19	11	sub 11

	mGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrGrGrCrArGrArUrUrUrCrUrGrCrUrGr GrArGrUrCrArGrG*mU*mG*mC				
tg41_hs12	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmUmA mGmCrArArGrUrUrArArArArUrArArGrGrCrUrArArUrCrCrGrUrUrArArUrCrAmAmCmUmUmGmAmAmAmA mGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrGrGrCrArGrArUrUrUrUrCrUrGrCrArGr GrArGrUrCrArGrG*mU*mG*mC	20885	19	11	sub 12
tg41_hs13	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmUmA mGmCrArArGrUrUrArArArArUrArArGrGrCrUrArArUrCrCrGrUrUrArArUrCrAmAmCmUmUmGmAmAmAmA mGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrGrGrCrArGrArUrUrUrUrCrUrGrCrCrGr GrArGrUrCrArGrG*mU*mG*mC	20886	19	11	sub 13
tg41_hs14	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmUmA mGmCrArArGrUrUrArArArArUrArArGrGrCrUrArArUrCrCrGrUrUrArArUrCrAmAmCmUmUmGmAmAmAmA mGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrGrGrCrArGrArUrUrUrUrCrUrGrCrCrGr GrArGrUrCrArGrG*mU*mG*mC	20887	19	11	sub 14
tg41_hs15	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmUmA mGmCrArArGrUrUrArArArArUrArArGrGrCrUrArArUrCrCrGrUrUrArArUrCrAmAmCmUmUmGmAmAmAmA mGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrGrGrCrArGrArUrUrUrUrCrUrGrCrUrGr GrArGrUrCrArGrG*mU*mG*mC	20888	19	11	sub 15
tg42_h	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmUmA mGmCrArArGrUrUrArArArArUrArArGrGrCrUrArArUrCrCrGrUrUrArArUrCrAmAmCmUmUmGmAmAmAmA mGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArArArCrGrGrCrArGrArCrUrUrCrUrGrGrCr ArGrGrArGrUrCrArGrG*mU*mG*mC	20889	21	11	none
tg42_hs1	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmUmA mGmCrArArGrUrUrArArArArUrArArGrGrCrUrArArUrCrAmAmCmUmUmGmAmAmAmA mGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArArArCrGrGrCrArGrArCrUrUrCrUrGrGrCr CrGrGrArGrUrCrArGrG*mU*mG*mC	20890	21	11	sub 1
tg42_hs2	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmUmA mGmCrArArGrUrUrArArArArUrArArGrGrCrUrArArUrCrAmAmCmUmUmGmAmAmAmA mGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArArArCrGrGrCrArGrArCrUrUrCrUrGrGrCr GrGrGrArGrUrCrArGrG*mU*mG*mC	20891	21	11	sub 2
tg42_hs3	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmUmA mGmCrArArGrUrUrArArArArUrArArGrGrCrUrArArUrCrAmAmCmUmUmGmAmAmAmA mGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArArArCrGrGrCrArGrArCrUrUrCrUrGrGrCr UrGrGrArGrUrCrArGrG*mU*mG*mC	20892	21	11	sub 3
tg42_hs4	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmUmA mGmCrArArGrUrUrArArArArUrArArGrGrCrUrArArUrCrAmAmCmUmUmGmAmAmAmA	20893	21	11	sub 4

	mGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrUrArArCrGrGrCrArGrArUrUrCrUrCrUrGrCr ArGrGrArGrUrCrArGrG*mU*mG*mC				
tg42_hs5	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmUmA mGmCrArArGrUrUrArArArArUrArArGrGrCrUrArArUrCrArAmAmCmUmUmGmAmAmAmA mGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrUrArArCrGrGrCrArGrArUrUrCrUrCrUrGrCr ArGrGrArGrUrCrArGrG*mU*mG*mC	20894	21	11	sub 5
tg42_hs6	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmUmA mGmCrArArGrUrUrArArArArUrArArGrGrCrUrArArUrCrArAmAmCmUmUmGmAmAmAmA mGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrUrArArCrGrGrCrArGrArUrUrCrUrCrUrGrCr CrGrGrArGrUrCrArGrG*mU*mG*mC	20895	21	11	sub 6
tg42_hs7	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmUmA mGmCrArArGrUrUrArArArArUrArArGrGrCrUrArArUrCrArAmAmCmUmUmGmAmAmAmA mGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrUrArArCrGrGrCrArGrArUrUrCrUrCrUrGrCr GrGrGrArGrUrCrArGrG*mU*mG*mC	20896	21	11	sub 7
tg42_hs8	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmUmA mGmCrArArGrUrUrArArArArUrArArGrGrCrUrArArUrCrArAmAmCmUmUmGmAmAmAmA mGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrUrArArCrGrGrCrArGrArUrUrCrUrCrUrGrCr UrGrGrArGrUrCrArGrG*mU*mG*mC	20897	21	11	sub 8
tg42_hs9	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmUmA mGmCrArArGrUrUrArArArArUrArArGrGrCrUrArArUrCrArAmAmCmUmUmGmAmAmAmA mGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrUrArArCrGrGrCrArGrArUrUrCrUrCrUrGrCr CrGrGrArGrUrCrArGrG*mU*mG*mC	20898	21	11	sub 9
tg42_hs10	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmUmA mGmCrArArGrUrUrArArArArUrArArGrGrCrUrArArUrCrArAmAmCmUmUmGmAmAmAmA mGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrUrArArCrGrGrCrArGrArUrUrCrUrCrUrGrCr GrGrGrArGrUrCrArGrG*mU*mG*mC	20899	21	11	sub 10
tg42_hs11	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmUmA mGmCrArArGrUrUrArArArArUrArArGrGrCrUrArArUrCrArAmAmCmUmUmGmAmAmAmA mGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrUrArArCrGrGrCrArGrArUrUrCrUrCrUrGrCr UrGrGrArGrUrCrArGrG*mU*mG*mC	20900	21	11	sub 11
tg42_hs12	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmUmA mGmCrArArGrUrUrArArArArUrArArGrGrCrUrArArUrCrArAmAmCmUmUmGmAmAmAmA mGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrUrArArCrGrGrCrArGrArUrUrCrUrCrUrGrCr ArGrGrArGrUrCrArGrG*mU*mG*mC	20901	21	11	sub 12
tg42_hs13	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmUmA mGmCrArArGrUrUrArArArArUrArArGrGrCrUrArArUrCrArAmAmCmUmUmGmAmAmAmA	20902	21	11	sub 13

	mGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrUrArArCrGrGrCrArGrArUrUrUrUrCrUrGrCr CrGrGrArGrUrCrArGrG*mU*mG*mC				
tg42_hs14	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmUmA mGmCrArArGrUrUrArArArArUrArArGrGrCrUrArArUrCrArAmAmCmUmUmGmAmAmAmA mGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrUrArArCrGrGrCrArGrArUrUrUrUrCrUrGrCr GrGrGrArGrUrCrArGrG*mU*mG*mC	20903	21	11	sub 14
tg42_hs15	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmUmA mGmCrArArGrUrUrArArArArUrArArGrGrCrUrArArUrCrArAmAmCmUmUmGmAmAmAmA mGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrUrArArCrGrGrCrArGrArUrUrUrUrCrUrGrCr UrGrGrArGrUrCrArGrG*mU*mG*mC	20904	21	11	sub 15
tg43_h	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmUmA mGmCrArArGrUrUrArArArArUrArArGrGrCrUrArArUrCrArAmAmCmUmUmGmAmAmAmA mGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArArCrGrGrCrArGrArCrUrUrCrUrGrCr GrCrArGrGrArGrUrCrArGrG*mU*mG*mC	20905	23	11	non e
tg43_hs1	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmUmA mGmCrArArGrUrUrArArArArUrArArGrGrCrUrArArUrCrArAmAmCmUmUmGmAmAmAmA mGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArArCrGrGrCrArGrArCrUrUrCrUrGrCrUr GrCrCrGrGrArGrUrCrArGrG*mU*mG*mC	20906	23	11	sub 1
tg43_hs2	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmUmA mGmCrArArGrUrUrArArArArUrArArGrGrCrUrArArUrCrArAmAmCmUmUmGmAmAmAmA mGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArArCrGrGrCrArGrArCrUrUrCrUrGrCrUr GrCrCrGrGrArGrUrCrArGrG*mU*mG*mC	20907	23	11	sub 2
tg43_hs3	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmUmA mGmCrArArGrUrUrArArArArUrArArGrGrCrUrArArUrCrArAmAmCmUmUmGmAmAmAmA mGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArArCrGrGrCrArGrArCrUrUrCrUrGrCrUr GrCrUrGrGrArGrUrCrArGrG*mU*mG*mC	20908	23	11	sub 3
tg43_hs4	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmUmA mGmCrArArGrUrUrArArArArUrArArGrGrCrUrArArUrCrArAmAmCmUmUmGmAmAmAmA mGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArArCrGrGrCrArGrArArUrUrCrUrGrCrUr GrCrArGrGrArGrUrCrArGrG*mU*mG*mC	20909	23	11	sub 4
tg43_hs5	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmUmA mGmCrArArGrUrUrArArArArUrArArGrGrCrUrArArUrCrArAmAmCmUmUmGmAmAmAmA mGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArArCrGrGrCrArGrArArUrUrCrUrGrCrUr GrCrArGrGrArGrUrCrArGrG*mU*mG*mC	20910	23	11	sub 5
tg43_hs6	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmUmA mGmCrArArGrUrUrArArArArUrArArGrGrCrUrArArUrCrArAmAmCmUmUmGmAmAmAmA	20911	23	11	sub 6

	mGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArGrUrArArCrGrGrCrArGrArCrUrUrUrCrUr GrCrCrGrGrArArGrUrCrArArGrG*mU*mG*mC				
tg43_hs7	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArGrUrUrUrUrArGrArAmGmCmUmAmGmAmAmUmA mGmCrArArGrUrUrArArArArUrArArArGrGrCrUrArArUrCrCrGrUrUrArArUrCrAmAmCmUmUmGmAmAmAmA mGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArGrUrArArCrGrGrCrArGrArCrUrUrUrCrUr GrCrGrGrGrArArGrUrCrArArGrG*mU*mG*mC	20912	23	11	sub 7
tg43_hs8	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArGrUrUrUrUrArGrArAmGmCmUmAmGmAmAmUmA mGmCrArArGrUrUrArArArArUrArArArGrGrCrUrArArUrCrCrGrUrUrArArUrCrAmAmCmUmUmGmAmAmAmA mGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArGrUrArArCrGrGrCrArGrArCrUrUrUrCrUr GrCrUrGrGrArArGrUrCrArArGrG*mU*mG*mC	20913	23	11	sub 8
tg43_hs9	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArGrUrUrUrUrArGrArAmGmCmUmAmGmAmAmUmA mGmCrArArGrUrUrArArArArUrArArArGrGrCrUrArArUrCrCrGrUrUrArArUrCrAmAmCmUmUmGmAmAmAmA mGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArGrUrArArCrGrGrCrArGrArCrUrUrUrCrUr GrCrCrGrGrArArGrUrCrArArGrG*mU*mG*mC	20914	23	11	sub 9
tg43_hs10	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArGrUrUrUrUrArGrArAmGmCmUmAmGmAmAmUmA mGmCrArArGrUrUrArArArArUrArArArGrGrCrUrArArUrCrCrGrUrUrArArUrCrAmAmCmUmUmGmAmAmAmA mGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArGrUrArArCrGrGrCrArGrArCrUrUrUrCrUr GrCrGrGrGrArArGrUrCrArArGrG*mU*mG*mC	20915	23	11	sub 10
tg43_hs11	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArGrUrUrUrUrArGrArAmGmCmUmAmGmAmAmUmA mGmCrArArGrUrUrArArArArUrArArArGrGrCrUrArArUrCrCrGrUrUrArArUrCrAmAmCmUmUmGmAmAmAmA mGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArGrUrArArCrGrGrCrArGrArCrUrUrUrCrUr GrCrUrGrGrArArGrUrCrArArGrG*mU*mG*mC	20916	23	11	sub 11
tg43_hs12	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArGrUrUrUrUrArGrArAmGmCmUmAmGmAmAmUmA mGmCrArArGrUrUrArArArArUrArArArGrGrCrUrArArUrCrCrGrUrUrArArUrCrAmAmCmUmUmGmAmAmAmA mGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArGrUrArArCrGrGrCrArGrArCrUrUrUrCrUr GrCrArGrGrArArGrUrCrArArGrG*mU*mG*mC	20917	23	11	sub 12
tg43_hs13	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArGrUrUrUrUrArGrArAmGmCmUmAmGmAmAmUmA mGmCrArArGrUrUrArArArArUrArArArGrGrCrUrArArUrCrCrGrUrUrArArUrCrAmAmCmUmUmGmAmAmAmA mGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArGrUrArArCrGrGrCrArGrArCrUrUrUrCrUr GrCrCrGrGrArArGrUrCrArArGrG*mU*mG*mC	20918	23	11	sub 13
tg43_hs14	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArGrUrUrUrUrArGrArAmGmCmUmAmGmAmAmUmA mGmCrArArGrUrUrArArArArUrArArArGrGrCrUrArArUrCrCrGrUrUrArArUrCrAmAmCmUmUmGmAmAmAmA mGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArGrUrArArCrGrGrCrArGrArCrUrUrUrCrUr GrCrGrGrGrArArGrUrCrArArGrG*mU*mG*mC	20919	23	11	sub 14
tg43_hs15	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArGrUrUrUrUrArGrArAmGmCmUmAmGmAmAmUmA mGmCrArArGrUrUrArArArArUrArArArGrGrCrUrArArUrCrCrGrUrUrArArUrCrAmAmCmUmUmGmAmAmAmA	20920	23	11	sub 15

	mGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArGrUrArArCrGrGrCrArGrArUrUrUrUrUrCrUrGrCrUrGrGrArGrUrCrArGrG*mU*mG*mC				
tg43_hs16	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArCrUrCrCrUrGrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArGrUrArArCrGrGrCrUrGrArUrUrUrUrUrCrUrGrCrCrGrGrArGrUrCrArGrG*mU*mG*mC	20921	23	11	sub 16
tg43_hs17	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArCrUrCrCrUrGrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArGrUrArArCrGrGrCrCrGrArUrUrUrUrUrCrUrGrCrCrGrGrArGrUrCrArGrG*mU*mG*mC	20922	23	11	sub 17

Table X2A shows the sequences of X2 without modifications. In some embodiments, the sequences used in this table can be used without chemical modifications.

Table X2A: Table X2 Sequences without Modifications

Name	Sequence	SEQ ID NO
tg14_h	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAGACUUCUCUGCAGGAGUCAGGUG	21794
tg14_hs1	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAGACUUCUCUGCCGGAGUCAGGUG	21795
tg14_hs2	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAGACUUCUCUGCGGGAGUCAGGUG	21796
tg14_hs3	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAGACUUCUCUGCUGGAGUCAGGUG	21797
tg14_hs4	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAGAUUUCUCUGCAGGAGUCAGGUG	21798
tg14_hs5	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAGACUUUUCUGCAGGAGUCAGGUG	21799
tg14_hs6	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAGACUUUUCUGCCGGAGUCAGGUG	21800
tg14_hs7	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAGACUUUUCUGCGGGAGUCAGGUG	21801

tg14_hs8	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAGACUUUUCUGCUGGAGUCAGGUG	21802
tg14_hs9	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAGAUUUUCUCUGCCGGAGUCAGGUG	21803
tg14_hs10	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAGAUUUUCUCUGCGGGAGUCAGGUG	21804
tg14_hs11	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAGAUUUUCUCUGCUGGAGUCAGGUG	21805
tg14_hs12	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAGAUUUUUUCUGCAGGAGUCAGGUG	21806
tg14_hs13	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAGAUUUUUUCUGCCGGAGUCAGGUG	21807
tg14_hs14	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAGAUUUUUUCUGCGGGAGUCAGGUG	21808
tg14_hs15	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAGAUUUUUUCUGCUGGAGUCAGGUG	21809
tg19_h	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGGCAGACUUCUCUCUGCAGGAGUCAGGUGC	21810
tg19_hs1	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGGCAGACUUCUCUCUGCCGGAGUCAGGUGC	21811
tg19_hs2	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGGCAGACUUCUCUCUGCGGGAGUCAGGUGC	21812
tg19_hs3	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGGCAGACUUCUCUCUGCUGGAGUCAGGUGC	21813
tg19_hs4	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGGCAGAUUUUCUCUGCAGGAGUCAGGUGC	21814
tg19_hs5	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGGCAGACUUUUUCUGCAGGAGUCAGGUGC	21815
tg19_hs6	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGGCAGACUUUUUCUGCCGGAGUCAGGUGC	21816
tg19_hs7	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGCAGACUUUUUCUGCGGGAGUCAGGUGC	21817
tg19_hs8	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGGCAGAUUUUUUCUGCUGGAGUCAGGUGC	21818
tg19_hs9	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGGCAGAUUUUUUCUGCCGGAGUCAGGUGC	21819

tg19_hs10	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGG UGCGGCAGAUUUUCUCUGCGGGAGUCAGGUGC	21820
tg19_hs11	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGG UGCGGCAGAUUUUCUCUGCUGGAGUCAGGUGC	21821
tg19_hs12	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGG UGCGGCAGAUUUUUCUGCAGGAGUCAGGUGC	21822
tg19_hs13	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGG UGCGGCAGAUUUUUCUGCCGGAGUCAGGUGC	21823
tg19_hs14	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGG UGCGGCAGAUUUUUCUGCGGGAGUCAGGUGC	21824
tg19_hs15	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGG UGCCGGCAGAUUUUUCUGCCGGAGUCAGGUGC	21825
tg41_h	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGG UGCACGGCAGACUUCUCCUGCAGGAGUCAGGUGC	21826
tg41_hs1	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGG UGCACGGCAGACUUCUCCUGCCGGAGUCAGGUGC	21827
tg41_hs2	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGG UGCACGGCAGACUUCUCUGCGGGAGUCAGGUGC	21828
tg41_hs3	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGG UGCACGGCAGACUUCUCCUGCUGGAGUCAGGUGC	21829
tg41_hs4	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGG UGCACGGCAGAUUUCUCCUGCAGGAGUCAGGUGC	21830
tg41_hs5	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGG UGCACGGCAGACUUUUCUGCAGGAGUCAGGUGC	21831
tg41_hs6	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGG UGCACGGCAGACUUUUCUGCCGGAGUCAGGUGC	21832
tg41_hs7	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGG UGCACGGCAGACUUUUCUGCGGGAGUCAGGUGC	21833
tg41_hs8	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGG UGCACGGCAGACUUUUCUGCUGGAGUCAGGUGC	21834
tg41_hs9	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGG UGCACGGCAGAUUUCUCUGCCGGAGUCAGGUGC	21835
tg41_hs10	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGG UGCACGGCAGAUUUCUCUGCGGGAGUCAGGUGC	21836
tg41_hs11	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGG UGCACGGCAGAUUUCUCUGCUGGAGUCAGGUGC	21837

tg41_hs12	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGG UGCACGGCAGAUUUUUCUGCAGGAGUCAGGUGC	21838
tg41_hs13	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGG UGCACGGCAGAUUUUUCUGCCGGAGUCAGGUGC	21839
tg41_hs14	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGG UGCACGGCAGAUUUUUCUGCGGGAGUCAGGUGC	21840
tg41_hs15	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGG UGCACGGCAGAUUUUUCUGCUGGAGUCAGGUGC	21841
tg42_h	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGG UGCUAACGGCAGACUUCUCUGCAGGAGUCAGGUGC	21842
tg42_hs1	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGG UGCUAACGGCAGACUUCUCUGCCGGAGUCAGGUGC	21843
tg42_hs2	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGG UGCUAACGGCAGACUUCUCUGCGGGAGUCAGGUGC	21844
tg42_hs3	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGG UGCUAACGGCAGACUUCUCUGCUGGAGUCAGGUGC	21845
tg42_hs4	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGG UGCUAACGGCAGAUUUUCUCUGCAGGAGUCAGGUGC	21846
tg42_hs5	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGG UGCUAACGGCAGACUUUUCUGCAGGAGUCAGGUGC	21847
tg42_hs6	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGG UGCUAACGGCAGACUUUUCUGCCGGAGUCAGGUGC	21848
tg42_hs7	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGG UGCUAACGGCAGACUUUUCUGCGGGAGUCAGGUGC	21849
tg42_hs8	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGG UGCUAACGGCAGACUUUUCUGCUGGAGUCAGGUGC	21850
tg42_hs9	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGG UGCUAACGGCAGAUUUUCUCUGCCGGAGUCAGGUGC	21851
tg42_hs10	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGG UGCUAACGGCAGAUUUUCUCUGCGGGAGUCAGGUGC	21852
tg42_hs11	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGG UGCUAACGGCAGAUUUUCUCUGCUGGAGUCAGGUGC	21853
tg42_hs12	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGG UGCUAACGGCAGAUUUUUCUGCAGGAGUCAGGUGC	21854
tg42_hs13	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGG UGCUAACGGCAGAUUUUUCUGCCGGAGUCAGGUGC	21855

tg42_hs14	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGG UGCUAACGGCAGAUUUUUCUGCGGGAGUCAGGUGC	21856
tg42_hs15	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGG UGCUAACGGCAGAUUUUUCUGCUGGAGUCAGGUGC	21857
tg43_h	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGG UGCAGUAACGGCAGACUUCUCUGCAGGAGUCAGGUGC	21858
tg43_hs1	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGG UGCAGUAACGGCAGACUUCUCUGCCGGAGUCAGGUGC	21859
tg43_hs2	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGG UGCAGUAACGGCAGACUUCUCUGCGGGAGUCAGGUGC	21860
tg43_hs3	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGG UGCAGUAACGGCAGACUUCUCUGCUGGAGUCAGGUGC	21861
tg43_hs4	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGG UGCAGUAACGGCAGAUUUCUCUGCAGGAGUCAGGUGC	21862
tg43_hs5	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGG UGCAGUAACGGCAGACUUUUCUGCAGGAGUCAGGUGC	21863
tg43_hs6	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGG UGCAGUAACGGCAGACUUUUCUGCCGGAGUCAGGUGC	21864
tg43_hs7	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGG UGCAGUAACGGCAGACUUUUCUGCGGGAGUCAGGUGC	21865
tg43_hs8	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGG UGCAGUAACGGCAGACUUUUCUGCUGGAGUCAGGUGC	21866
tg43_hs9	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGG UGCAGUAACGGCAGAUUUCUCUGCCGGAGUCAGGUGC	21867
tg43_hs10	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGG UGCAGUAACGGCAGAUUUCUCUGCGGGAGUCAGGUGC	21868
tg43_hs11	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGG UGCAGUAACGGCAGAUUUCUCUGCUGGAGUCAGGUGC	21869
tg43_hs12	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGG UGCAGUAACGGCAGAUUUUUCUGCAGGAGUCAGGUGC	21870
tg43_hs13	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGG UGCAGUAACGGCAGAUUUUUCUGCCGGAGUCAGGUGC	21871
tg43_hs14	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGG UGCAGUAACGGCAGAUUUUUCUGCGGGAGUCAGGUGC	21872
tg43_hs15	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGG UGCAGUAACGGCAGAUUUUUCUGCUGGAGUCAGGUGC	21873

tg43_hs16	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGG UGCAGUAACGGCUGAUUUUUCUGCCGGAGUCAGGUGC	21874
tg43_hs17	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGG UGCAGUAACGGCCGAUUUUUCUGCCGGAGUCAGGUGC	21875

Select corresponding template RNA sequences not comprising silent substitutions are given in Example 5 (e.g., FYF tgRNA14 is a corresponding template RNA sequence to tg14h, FYF tgRNA19 is a corresponding template RNA sequence to tg19h, etc.).

The gene modifying polypeptide used comprised the sequence set out in Example 8 labeled RNAV209.

The gene modifying system comprising the gene modifying polypeptides and the template RNA described above was transfected into human HSCs. The gene modifying polypeptide and the template RNA were delivered by nucleofection in RNA format. Specifically, 3000 ng of mRNA encoding the gene modifying polypeptide were combined with 2000 ng template RNA. The RNA mixture was added to 200,000 primary human HSCs in a total of 20 µL of Lonza P3 buffer and HSC were nucleofected in 16-well nucleofection cassettes using program DZ-100. After nucleofection, cells incubated at room temperature for 10 minutes and were transferred to 24-well plates containing 500 µL of StemSpan-XF + SCF at 100 ng/mL, Flt3-L at 100 ng/mL, and TPO at 100 ng/mL in each well and cultured at 37˚C, 5% CO_2 for 3 days prior to cell lysis and genomic DNA extraction. To analyze gene editing activity, primers flanking the target insertion site locus were used to amplify across the locus. Amplicons were analyzed via short read sequencing using an Illumina MiSeq. Replacement of the DNA bases adenine and guanine at nucleotide positions 20 and 21 to the bases cytosine and adenine (HBB5 template RNA) plus the inclusion of the expected silent substitutions downstream of the transcriptional start site within the endogenous B-globin locus indicated successful editing.

As shown in FIG. 19A, average perfect rewrite levels of 0.2% - 7.3%, corresponding to replacement of adenine and guanine at nucleotide positions 20 and 21 to the bases cytosine and adenine (respectively) at the SCD codon, were detected in primary human HSCs when the HSCs were treated with exemplary gene modifying systems comprising exemplary HBB5 template RNAs containing various silent substitutions. The results show that in some cases a silent substitution or substitutions can increase editing activity across several different template RNAs, e.g., exemplary silent substitution(s) hs1. In particular, replacement of the codon encoding the 6th amino acid, counting the initial methionine, of the HBB gene (the proline) to either CCC or CCG resulted in increased editing.

These results demonstrate that introducing silent substitutions within an exemplary template RNA increases editing activity of a gene modifying system comprising said template RNAs up to 5-fold when targeting a clinically relevant codon in the endogenous B-globin locus in primary human HSCs. The results further demonstrate that adjusting the identity or identities of the silent substitution(s) can increase the enhancement to editing activity.

Example 15: Characterizing configurations of template RNAs including silent substitutions for editing the endogenous B-globin locus in CD34+ primary human hematopoietic stem cells (HSCs).

This example demonstrates the use of a gene modifying system containing an exemplary gene modifying polypeptide and various template RNAs comprising different silent substitutions, to convert the glutamic acid codon at amino acid position 7 in the endogenous B-globin locus in primary human HSCs to alanine, thereby demonstrating targeting the sequence position associated with sickle cell disease (SCD) and editing of the sequence to encode a non-pathogenic sequence into position 7. This conversion comprises a change of one base pair for exemplary HBB8 template RNAs (i.e., replacement of the DNA base adenine at nucleotide positions 20 to the base cytosine) plus the inclusion of additional relevant silent substitutions (which alter the nucleic acid sequence of the DNA but not the protein sequence through the usage of different synonymous codons).

In this example, the template RNA contained:

(1) a gRNA spacer;

(2) a gRNA scaffold;

(3) a heterologous object sequence; and

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

More specifically, the exemplary template RNAs comprised the following sequences from 5' to 3', wherein the first 3, and last 3 bases have 2'-O-methyl phosphorothioate chemical modifications. In the sequences below, m=2'-O-methyl ribonucleotide, r=ribose, and *=phosphorothioate bond. Different combinations of substitutions and RT/PBS length were included (Table X3).

Table X3: Exemplary Silent Substitution-Containing Template RNAs

Name	Sequence	SEQ ID NO	RT length	PBS length	Substitution
tg34	mG*mU*mA*rArCrGrGrCrArGrArCrUrUrCrUrCrCrUrCrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrCrUrGrArCrUrCrCrUrGrCrGrGrArGrArArGrUrC*mU*mG*mC	20923	14	11	none
tg34_HBB8hs	mG*mU*mA*rArCrGrGrCrArGrArCrUrUrCrUrCrCrUrCrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrCrUrGrArCrUrCrCrUrGrCrGrGrArGrArArGrUrC*mU*mG*mC	20924	14	11	sub
tg34_HBB8hs1	mG*mU*mA*rArCrGrGrCrArGrArCrUrUrCrUrCrCrUrCrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrCrUrGrArCrUrCrCrUrGrCrGrGrArGrArArGrUrC*mU*mG*mC	20925	14	11	Sub 1
tg34_HBB8hs2	mG*mU*mA*rArCrGrGrCrArGrArCrUrUrCrUrCrCrUrCrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrCrUrGrArCrUrCrCrUrGrCrGrGrArGrArArGrUrC*mU*mG*mC	20926	14	11	Sub 2
tg34_HBB8hs3	mG*mU*mA*rArCrGrGrCrArGrArCrUrUrCrUrCrCrUrCrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrCrUrGrArCrUrCrCrUrGrCrGrGrArGrArArGrUrC*mU*mG*mC	20927	14	11	Sub 3
tgRNA34_HBB8hs4	mG*mU*mA*rArCrGrGrCrArGrArCrUrUrCrUrCrCrUrCrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrCrUrGrArCrUrCrCrUrGrCrGrGrArGrArArGrUrC*mU*mG*mC	20928	14	11	Sub 4
tg34_HBB8hs5	mG*mU*mA*rArCrGrGrCrArGrArCrUrUrCrUrCrCrUrCrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrCrUrGrArCrUrCrCrUrGrCrGrGrArGrArArGrUrC*mU*mG*mC	20929	14	11	Sub 5
tg34_HBB8hs6	mG*mU*mA*rArCrGrGrCrArGrArCrUrUrCrUrCrCrUrCrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmG	20930	14	11	Sub 6

	mUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrCrUrGrArCrUrCrCrGrCrArGrArArGrUrC *mU*mG*mC				
tg34_HBB8hs7	mG*mU*mA*rArCrGrGrCrArGrArCrUrUrCrCrUrCrGrUrUrUrArGrArGmGmCmUmAmGmAmAmUmAm GmCrArArGrUrUrArArArArUrArArArGrGrCrUrArArGrUrCrCrGrUrArUrCrAmAmCmUmUmGmAmAmAmAmG mUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrCrUrGrArCrUrCrCrGrCrArGrArArGrUrC *mU*mG*mC	20931	14	11	Sub 7
tg34_HBB8hs8	mG*mU*mA*rArCrGrGrCrArGrArCrUrUrCrCrUrCrGrUrUrUrArGrArGmGmCmUmAmGmAmAmUmAm GmCrArArGrUrUrArArArArUrArArArGrGrCrUrArArGrUrCrCrGrUrArUrCrAmAmCmUmUmGmAmAmAmAmG mUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrCrUrGrArCrUrCrCrGrCrArGrArArGrUrC *mU*mG*mC	20932	14	11	Sub 8
tg34_HBB8hs9	mG*mU*mA*rArCrGrGrCrArGrArCrUrUrCrCrUrCrGrUrUrUrArGrArGmGmCmUmAmGmAmAmUmAm GmCrArArGrUrUrArArArArUrArArArGrGrCrUrArArGrUrCrCrGrUrArUrCrAmAmCmUmUmGmAmAmAmAmG mUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrCrUrGrArCrUrCrCrGrCrArGrArArGrUrC *mU*mG*mC	20933	14	11	Sub 9
tg34_HBB8hs10	mG*mU*mA*rArCrGrGrCrArGrArCrUrUrCrCrUrCrGrUrUrUrArGrArGmGmCmUmAmGmAmAmUmAm GmCrArArGrUrUrArArArArUrArArArGrGrCrUrArArGrUrCrCrGrUrArUrCrAmAmCmUmUmGmAmAmAmAmG mUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrCrUrGrArCrUrCrCrGrCrArGrArArGrUrC *mU*mG*mC	20934	14	11	sub 10
tg34_HBB8hs11	mG*mU*mA*rArCrGrGrCrArGrArCrUrUrCrCrUrCrGrUrUrUrArGrArGmGmCmUmAmGmAmAmUmAm GmCrArArGrUrUrArArArArUrArArArGrGrCrUrArArGrUrCrCrGrUrArUrCrAmAmCmUmUmGmAmAmAmAmG mUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrCrUrGrArCrUrCrCrGrCrArGrArArGrUrC *mU*mG*mC	20935	14	11	sub 11
tg34_HBB8hs12	mG*mU*mA*rArCrGrGrCrArGrArCrUrUrCrCrUrCrGrUrUrUrArGrArGmGmCmUmAmGmAmAmUmAm GmCrArArGrUrUrArArArArUrArArArGrGrCrUrArArGrUrCrCrGrUrArUrCrAmAmCmUmUmGmAmAmAmAmG mUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrCrUrGrArCrUrCrCrGrCrArGrArArGrUrC *mU*mG*mC	20936	14	11	sub 12
tg34_HBB8hs13	mG*mU*mA*rArCrGrGrCrArGrArCrUrUrCrCrUrCrGrUrUrUrArGrArGmGmCmUmAmGmAmAmUmAm GmCrArArGrUrUrArArArArUrArArArGrGrCrUrArArGrUrCrCrGrUrArUrCrAmAmCmUmUmGmAmAmAmAmG mUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrCrUrGrArCrUrCrCrGrCrArGrArArGrUrC *mU*mG*mC	20937	14	11	sub 13
tg34_HBB8hs14	mG*mU*mA*rArCrGrGrCrArGrArCrUrUrCrCrUrCrGrUrUrUrArGrArGmGmCmUmAmGmAmAmUmAm GmCrArArGrUrUrArArArArUrArArArGrGrCrUrArArGrUrCrCrGrUrArUrCrAmAmCmUmUmGmAmAmAmAmG mUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrCrUrGrArCrUrCrCrGrCrArGrArArGrUrC *mU*mG*mC	20938	14	11	sub 14

Table X3A shows the sequences of X3 without modifications. In some embodiments, the sequences used in this table can be used without chemical modifications.

Table X3A: Table X3 Sequences without Modifications

Name	Sequence	SEQ ID NO
tg34	GUAACGGCAGACUUCUCCUCGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCACCUGACUCCUGCGGAGAAGUCUGC	21876
tg34_HBB8hs	GUAACGGCAGACUUCUCCUCGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCACCUGACUCCGGCCGAGAAGUCUGC	21877
tg34_HBB8hs 1	GUAACGGCAGACUUCUCCUCGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCACCUGACUCCUGCAGAGAAGUCUGC	21878
tg34_HBB8hs 2	GUAACGGCAGACUUCUCCUCGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCACCUGACUCCUGCUGAGAAGUCUGC	21879
tg34_HBB8hs 3	GUAACGGCAGACUUCUCCUCGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCACCUGACUCCUGCCGAGAAGUCUGC	21880
tgRNA34_HBB8hs4	GUAACGGCAGACUUCUCCUCGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCACCUGACUCCCGCAGAGAAGUCUGC	21881
tg34_HBB8hs 5	GUAACGGCAGACUUCUCCUCGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCACCUGACUCCAGCAGAGAAGUCUGC	21882
tg34_HBB8hs 6	GUAACGGCAGACUUCUCCUCGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCACCUGACUCCGGCAGAGAAGUCUGC	21883
tg34_HBB8hs 7	GUAACGGCAGACUUCUCCUCGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCACCUGACUCCCGCUGAGAAGUCUGC	21884
tg34_HBB8hs 8	GUAACGGCAGACUUCUCCUCGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCACCUGACUCCAGCUGAGAAGUCUGC	21885
tg34_HBB8hs 9	GUAACGGCAGACUUCUCCUCGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCACCUGACUCCGGCUGAGAAGUCUGC	21886
tg34_HBB8hs 10	GUAACGGCAGACUUCUCCUCGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCACCUGACUCCCGCCGAGAAGUCUGC	21887
tg34_HBB8hs 11	GUAACGGCAGACUUCUCCUCGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCACCUGACUCCAGCCGAGAAGUCUGC	21888
tg34_HBB8hs 12	GUAACGGCAGACUUCUCCUCGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCACCUGACUCCGGCGGAGAAGUCUGC	21889
tg34_HBB8hs 13	GUAACGGCAGACUUCUCCUCGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCACCUGACUCCCGCGGAGAAGUCUGC	21890

tg34_HBB8hs 14	GUAACGGCAGACUUCUCCUCGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGU CGGUGCACCUGACUCCAGCGGAGAAGUCUGC	21891

The gene modifying polypeptides used comprised the sequence set out in Example 8 labeled RNAV209.

The gene modifying system comprising the gene modifying polypeptides and the template RNA described above was transfected into human HSCs. The gene modifying polypeptide and the template RNA were delivered by nucleofection in RNA format. Specifically, 3000 ng of mRNA encoding the gene modifying polypeptide were combined with 3000 ng template RNA. The RNA mixture was added to 200,000 primary human HSCs in a total of 20 µL of Lonza P3 buffer and HSC were nucleofected in 16-well nucleofection cassettes using program DZ-100. After nucleofection, cells incubated at room temperature for 10 minutes and were transferred to 24-well plates containing 500 µL of StemSpan-XF + SCF at 100 ng/mL, Flt3-L at 100 ng/mL, and TPO at 100 ng/mL in each well and cultured at 37°C, 5% CO_2 for 3 days prior to cell lysis and genomic DNA extraction. To analyze gene editing activity, primers flanking the target insertion site locus were used to amplify across the locus. Amplicons were analyzed via short read sequencing using an Illumina MiSeq. Replacement of the DNA bases adenine at nucleotide positions 20 to the base cytosine (HBB8 template RNA) plus the inclusion of the expected silent substitutions downstream of the transcriptional start site within the endogenous B-globin locus indicated successful editing.

As shown in FIG. 19B, average perfect rewrite levels of 0.1% - 13.1%, corresponding to replacement of adenine and guanine at nucleotide positions 20 and 21 to the bases cytosine and adenine (respectively) at the SCD codon, were detected in primary human HSCs when the HSCs were treated with exemplary gene modifying systems comprising exemplary HBB8 template RNAs containing various silent substitutions. These results further demonstrate that introducing silent substitutions within an exemplary template gRNA increases editing activity of a gene modifying system comprising said template RNAs more than 9-fold when targeting a clinically relevant codon in the endogenous B-globin locus in primary human HSCs. The results further demonstrate that adjusting the identity or identities of the silent substitution(s) can increase the enhancement to editing activity.

Example 16: Evaluating the effect of second strand-targeting gRNA and silent substitution on activity of a gene modifying polypeptide and template RNA for editing the endogenous B-globin locus achieved in CD34+ primary human hematopoietic stem cells (HSCs).

This example demonstrates the use of a gene modifying system containing or not containing a variety of second strand-targeting gRNAs, an exemplary gene modifying polypeptide, and a template RNA, to convert the glutamic acid codon at amino acid position 7 in the endogenous B-globin locus in primary human HSCs to alanine, thereby rewriting a non-pathogenic sequence into position 7. This conversion comprises a change of 2 base pairs for exemplary HBB5 template RNAs (i.e., replacement of the DNA bases thymidine, adenine and guanine at nucleotide positions 18, 20 and 21 to the bases guanine, cytosine and adenine). For exemplary HBB8 template RNAs, the conversion comprises the change of the DNA bases thymidine and adenine at nucleotide positions 18 and 20 to the bases cytosine and cytosine (e.g., using template RNA tg34_HBB8_hs13) or replacement of DNA bases thymidine, adenine and guanine at nucleotide positions 18, 20, 21 to the bases cytosine, cytosine and cytosine, respectively (e.g., using tg34_HBB8_hs10). This Example demonstrates the editing using systems comprising a variety of second strand-targeting gRNAs with: an exemplary HBB5 template RNA comprising a silent substitution (FIG. 20A), or either of two exemplary HBB8 template RNAs each comprising a different silent substitution (FIG. 20B).

In this example, the template RNA contained:

(1) a gRNA spacer;

(2) a gRNA scaffold;

(3) a heterologous object sequence; and

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

More specifically, the template RNAs comprised the sequences set out in Example 14 labeled tg14_hs1 or Example 15 labeled tg34_HBB8hs10 and tg34_HBB8hs13.

The system further comprised a second strand-targeting gRNA comprising a sequence in Table X1.

The gene modifying polypeptides tested comprised the sequence set out in Example 8 labeled RNAV209.

The gene modifying system comprising the gene modifying polypeptides and the template RNA described above was transfected into human HSCs. The gene modifying polypeptide and the template RNA were delivered by nucleofection in RNA format. Specifically, 3000 ng of mRNA encoding the gene modifying polypeptide were combined with 3000 ng template RNA with or without 2000 ng of second strand-targeting gRNA. The RNA mixture was added to 200,000 primary human HSCs in a total of 20 µL of Lonza P3 buffer and HSC were nucleofected in 16-well nucleofection cassettes using program DZ-100. After nucleofection, cells incubated at room temperature for 10 minutes and were transferred to 24-well plates containing 500 µL of StemSpan-XF + SCF at 100 ng/mL, Flt3-L at 100 ng/mL, and TPO at 100 ng/mL in each well and cultured at 37°C, 5% CO_2 for 3 days prior to cell lysis and genomic DNA extraction. To analyze gene editing activity, primers flanking the target insertion site locus were used to amplify across the locus. Amplicons were analyzed via short read sequencing using an Illumina MiSeq. Replacement of the DNA bases thymidine, adenine and guanine at nucleotide positions 18, 20 and 21 to the bases guanine, cytosine and adenine indicates successful editing for HBB5 spacer. Replacement thymidine and adenine at nucleotide positions 18 and 20 to the bases cytosine and cytosine (tg34_HBB8_hs13) or replacement of DNA bases thymidine, adenine and guanine at nucleotide positions 18, 20, 21 to the bases cytosine, cytosine and cytosine, respectively (tg34_HBB8_hs10) indicated successful editing for HBB8 spacer.

FIG. 20A shows a graph of editing % in HSCs treated with gene modifying systems comprising the exemplary HBB5 template RNA tg14_hs1 (comprising an exemplary silent substitution) with or without various second strand-targeting gRNAs. The results demonstrate the additive effect of second strand-targeting gRNAs with template gRNAs for HBB5 template RNAs containing silent substitutions for rewriting of a non-pathogenic sequence into a clinically relevant codon in the endogenous B-globin locus.

FIG. 20B shows a graph of editing % in HSCs treated with gene modifying systems comprising either of two exemplary HBB8 template RNAs, tg34_hs13 or tg34_hs10 (each comprising a different exemplary silent substitution) with or without various second strand-targeting gRNAs. The results further demonstrate the additive effect of second strand-targeting

gRNAs with template gRNAs for HBB8 template RNAs containing silent substitutions for rewriting of a non-pathogenic sequence into a clinically relevant codon in the endogenous B-globin locus.

Example 17: Evaluating the effect of second strand-targeting gRNA and silent substitution on activity of a gene modifying polypeptide and template RNA for editing the endogenous B-globin locus achieved in CD34+ primary human hematopoietic stem cells (HSCs).

This example demonstrates the use of a gene modifying system containing or not containing a second strand-targeting gRNA, an exemplary gene modifying polypeptide and various template RNAs (some comprising a silent substitution), to convert the glutamic acid codon at amino acid position 7 in the endogenous B-globin locus in primary human HSCs to alanine, thereby demonstrating targeting the sequence position associated with sickle cell disease (SCD) and editing of the sequence to encode a non-pathogenic sequence into position 7. This conversion comprises a change of 2 base pairs for exemplary HBB5 template RNAs (i.e., replacement of the DNA bases adenine and guanine at nucleotide positions 20 and 21 to the bases cytosine and adenine) plus or minus the additional replacement of thymidine to guanine at nucleotide position 18 (silent substitution).

In this example, the template RNA contained:

(1) a gRNA spacer;

(2) a gRNA scaffold;

(3) a heterologous object sequence; and

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

More specifically, the template RNAs comprised the sequences the sequence set out in Example 14 labeled tg14h, tg14_hs1, tg19h or tg19_hs1.

The system further comprised a gRNA sequence designed to produce a second nick, wherein the gRNA has the sequence labeled HBB5_g37 in Table X1.

The gene modifying polypeptides tested comprised the sequence set out in Example 8 labeled RNAV209.

The gene modifying system comprising the gene modifying polypeptides and the template RNA described above was transfected into human HSCs. The gene modifying polypeptide and the template RNA were delivered by nucleofection in RNA format. Specifically, 3000 ng of mRNA encoding the gene modifying polypeptide were combined with 2000 ng template RNA with or without 2000 ng of second strand-targeting gRNA. The RNA mixture was added to 200,000 primary human HSCs in a total of 20 µL of Lonza P3 buffer and cells were nucleofected in 16-well nucleofection cassettes using program DZ-100. After nucleofection, cells incubated at room temperature for 10 minutes and were transferred to 24-well plates containing 500 µL of StemSpan-XF + SCF at 100 ng/mL, Flt3-L at 100 ng/mL, and TPO at 100 ng/mL and cultured at 37˚C, 5% CO_2 for 3 days prior to cell lysis and genomic DNA extraction. To analyze gene editing activity, primers flanking the target insertion site locus were used to amplify across the locus. Amplicons were analyzed via short read sequencing using an Illumina MiSeq. Replacement of the DNA bases adenine and guanine at nucleotide positions 20 and 21 to the bases cytosine and adenine (tg14h or tg19h) or replacement of DNA bases thymidine, adenine and guanine at nucleotide positions 18, 20, 21 to the bases guanine, cytosine, adenine, respectively (tg14_hs1 or tg19_hs1), downstream of the transcriptional start site within the endogenous B-globin locus indicated successful editing.

As shown in FIG. 20C, average perfect rewrite levels of 1.8% and 3.4%, corresponding to replacement of adenine and guanine at nucleotide positions 20 and 21 to the bases cytosine and adenine (respectively) at the SCD codon, were detected in human HSCs when the HSCs were treated with exemplary gene modifying systems comprising exemplary HBB5 template RNAs tg14h or tg19h and no second strand-targeting gRNA was added. Inclusion of the hs1 silent substitution in the template gRNA (tg14_hs1 or tg19_hs1) increased perfect rewriting to 9.1% and 6.3%.

Addition of a second strand-targeting gRNA increased average perfect rewriting to 17.1% for tg14h and 30.2% for tg14_hs1. Similarly, addition of a second strand-targeting gRNA resulted in average perfect rewriting to 20.2% for tg19h and 32.2% for tg19_hs1.

These results demonstrate that silent substitutions and second strand-targeting gRNAs can individually increase editing activity of gene modifying systems, and further show the additive effect of the second strand-targeting gRNA and silent substitutions within an exemplary HBB5 template RNA. The results show a cumulative increase in editing activity of more than 20-fold

when using both a silent substitution and second strand-targeting gRNA in primary human HSCs to write a non-pathogenic sequence into a clinically relevant codon in the endogenous B-globin locus.

Example 18: Evaluating impact of a gene modifying systems editing the endogenous B-globin locus on stemness markers in CD34+ primary human hematopoietic stem cells (HSCs).

This example demonstrates that editing using a gene modifying system containing an exemplary gene modifying polypeptide and a template RNA with or without a second strand-targeting gRNA to convert the glutamic acid codon at amino acid position 7 in the endogenous B-globin locus in primary human HSCs to alanine does not significantly affect the levels of stem cell markers and proportions of cell marker-characterized sub-populations.

In this example, the template RNA contained:

(1) a gRNA spacer;

(2) a gRNA scaffold;

(3) a heterologous object sequence; and

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

More specifically, the template RNA comprised the nucleic acid sequences set out in Example 5 labeled FYF tgRNA14.

The system further comprised a second strand-targeting gRNA sequence designed to produce a second nick, wherein the gRNA has the sequence labeled HBB5_g37 in Table X1.

The gene modifying polypeptides tested comprised the amino acid sequence set out in Example 8 labeled RNAV209.

The gene modifying system comprising the gene modifying polypeptides and the template RNA described above was transfected into human HSCs. The gene modifying polypeptide and the template RNA were delivered by nucleofection in RNA format. Specifically, 3000 ng of mRNA encoding the gene modifying polypeptide were combined with 2000 ng template RNA with or without 2000 ng of second strand-targeting gRNA. The RNA mixture was added to 200,000

primary human HSCs in a total of 20 µL of Lonza P3 buffer and cells were nucleofected in 16-well nucleofection cassettes using program DZ-100. After nucleofection, cells incubated at room temperature for 10 minutes and were transferred to 24-well plates containing 500 µL of StemSpan-XF + SCF at 100 ng/mL, Flt3-L at 100 ng/mL, and TPO at 100 ng/mL and cultured at 37°C, 5% CO_2 for 3 days prior to cell lysis and genomic DNA extraction. To analyze gene editing activity, primers flanking the target insertion site locus were used to amplify across the locus. Amplicons were analyzed via short read sequencing using an Illumina MiSeq. Replacement of the DNA bases adenine and guanine at nucleotide positions 20 and 21 to the bases cytosine and adenine, respectively, downstream of the transcriptional start site within the endogenous B-globin locus indicated successful editing. To analyze cell surface markers representative of different HSCs subpopulations, cells were stained with fluorescently labeled anti human CD90, CD133, CD34 antibodies and analyzed by flow cytometry 3 days after nucleofection.

As shown in FIG. 21A, editing activity levels of 6.3% and 34.4%, corresponding to replacement of adenine and guanine at nucleotide positions 20 and 21 to the bases cytosine and adenine (respectively) at the SCD codon, were detected in the human HSCs when the HSCs were treated with exemplary gene editing polypeptide combined with template guide RNA tg14 without or with a second strand-targeting gRNA, respectively. Analysis of the distribution of hematopoietic subpopulations (CD34+ CD133+ CD90+, a combination of markers enriched in HSC with long term reconstitution potential; CD34+ CD133+ CD90-, a combination of markers enriched in early progenitors; CD34+ CD133-, a combination of markers enriched in committed progenitors; CD34-, the absence of which is enriched in differentiated cells) revealed no skewing of subpopulation proportions when comparing samples treated with exemplary gene modifying systems (with or without the addition of a second strand-targeting gRNA) to a mock treated control (FIG. 21B).

These results demonstrate that editing that introduces a non-pathogenic sequence into a clinically relevant codon in the endogenous B-globin locus does not affect the phenotype of primary human HSC, and specifically does not affect markers indicative of differentiation potential in HSCs.

Example 19: Evaluating editing of long-term reconstitution capable HSC subpopulations using a gene modifying polypeptide and template RNA for editing the endogenous B-globin locus achieved.

This example demonstrates that editing using a gene modifying system containing an exemplary gene modifying polypeptide and a template RNA and a second strand-targeting gRNA to convert the glutamic acid codon (GAG) at amino acid position 7 in the endogenous B-globin locus in primary human HSCs to alanine (GCA or GCG) effectively targets HSC subpopulations associated with long term reconstitution as well as other subpopulations, thereby rewriting a non-pathogenic sequence into position 7 into stem cells having longevity and differentiation potential. This conversion comprises a change of two base pairs for exemplary HBB5 template RNAs (i.e., replacement of the DNA bases adenine and guanine at nucleotide positions 20 and 21 to the bases cytosine and adenine, respectively) and the change of one base pair for exemplary HBB8 template RNAs (i.e., replacement of the DNA bases adenine at nucleotide positions 20 to the base cytosine).

In this example, the template RNA contained:

(1) a gRNA spacer;

(2) a gRNA scaffold;

(3) a heterologous object sequence; and

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

The template RNAs comprised the sequence set out in Example 5 labeled FYF tgRNA14 for HBB5 template RNA or tgRNA34 for HBB8 template RNA, respectively.

The gene modifying polypeptides tested comprised the sequence set out in Example 8 labeled RNAV209.

The system further comprised a second strand-targeting gRNA comprising the sequence listed in Table X1 as HBB5_g37 and HBB8_256fw.

The gene modifying system comprising the gene modifying polypeptides and the template RNA described above was transfected into human HSCs. The gene modifying polypeptide and the template RNA were delivered by nucleofection in RNA format. Specifically, 3000 ng of mRNA encoding the gene modifying polypeptide were combined with 2000 ng template RNA with or

without 2000 ng of second strand-targeting gRNA. The RNA mixture was added to 200,000 primary human HSCs in a total of 20 µL of Lonza P3 buffer and cells were nucleofected in 16-well nucleofection cassettes using program DZ-100. After nucleofection, cells incubated at room temperature for 10 minutes and were transferred to 24-well plates containing 500 µL of StemSpan-XF + SCF at 100 ng/mL, Flt3-L at 100 ng/mL, and TPO at 100 ng/mL and cultured at 37°C, 5% CO_2. 3 days after nucleofection, cells were stained with fluorescently labeled anti human CD90, CD133, CD34 antibodies and CD34+ CD133+ CD90+ and CD34+ CD133+ CD90- fraction were FACS-sorted and subjected to cell lysis and genomic DNA extraction. To analyze gene editing activity, primers flanking the target insertion site locus were used to amplify across the locus. Amplicons were analyzed via short read sequencing using an Illumina MiSeq. Replacement of the DNA bases adenine and guanine at nucleotide positions 20 and 21 to the bases cytosine and adenine (HBB5 template RNA) or replacement of the DNA bases adenine at nucleotide positions 20 to the base cytosine (HBB8 template RNA) downstream of the transcriptional start site within the endogenous B-globin locus indicated successful editing.

As shown in FIG. 22A, editing activity levels of 19.3% and 29.8% were detected in the CD34+ CD133+ CD90+ HSC subpopulation after treatment with gene modifying systems comprising HBB5 template RNA or HBB8 template RNA, respectively. CD34+ CD133+ CD90+ cells are enriched in HSCs with long term reconstitution potential. Editing activity levels of 23.73% and 31.5% were detected in all the rest of the HSC population (not CD34+ CD133+ CD90+) treated with the same exemplary gene modifying systems comprising HBB5 template RNAs and HBB8 template RNAs, respectively. The experiment was repeated using the exemplary HBB5 template RNA tg14_hs1 (Table X1) and a second strand-targeting gRNA (FIG. 22B), and the results showed editing activity of 56% in the CD34+ CD133+90+ HSC-enriched fraction and 52.9% in the CD34+ 90- progenitors enriched fraction. This result showed that the addition of silent substitutions to a template RNA (compare tg14_hs1 in FIG. 22B to FYF tgRNA14 in FIG. 22A) significantly increases the editing activity of a gene modifying system when used in long-term primary human HSCs.

These results demonstrate that the editing activity of exemplary gene modifying systems can write a non-pathogenic sequence into a clinically relevant codon in the endogenous B-globin locus in phenotypically long-term primary human HSCs. The results further demonstrate that the editing activity levels in the phenotypically long-term primary human HSCs were comparable to

the levels achieved in the rest of the HSC population. The results further demonstrate a high level of editing (greater than 50%) in long-term and progenitor HSCs.

Example 20: Evaluating the impact on differentiation ability of using a gene editing polypeptide and template RNA for rewriting the endogenous B-globin locus of CD34+ primary human hematopoietic stem cells (HSCs).

This example demonstrates that editing using a gene modifying system containing an exemplary gene modifying polypeptide and a template RNA with or without a second strand-targeting gRNA to convert the glutamic acid codon (GAG) at amino acid position 7 in the endogenous B-globin locus in primary human HSCs to alanine (GCA or GCG) (thereby rewriting a non-pathogenic sequence into position 7) does not significantly alter the differentiation ability of human HSCs. This conversion comprises a change of two base pairs for exemplary HBB5 template RNA (i.e., replacement of the DNA bases adenine and guanine at nucleotide positions 20 and 21 to the bases cytosine and adenine, respectively).

In this example, the template RNA contained:

(1) a gRNA spacer;

(2) a gRNA scaffold;

(3) a heterologous object sequence; and

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

The template RNAs comprised the sequence set out in Example 5 labeled FYF tgRNA14 for HBB5 template RNA.

The gene modifying polypeptides tested comprised the sequence set out in Example 8 labeled RNAV209.

The system further comprised a second strand-targeting gRNA comprising the sequence listed in Table X1 as HBB5_g27.

The gene modifying system comprising the gene modifying polypeptides and the template RNA described above was transfected into human HSCs. The gene modifying polypeptide and the template RNA were delivered by nucleofection in RNA format. Specifically, 3000 ng of mRNA encoding the gene modifying polypeptide RNA were combined with 2000 ng template RNA with or without 2000 ng of second strand-targeting gRNA. The RNA mixture was added to 200,000 primary human HSCs in a total of 20 µL of Lonza P3 buffer and cells were nucleofected in 16-well nucleofection cassettes using program DZ-100. After nucleofection, cells incubated at room temperature for 10 minutes and were transferred to 24-well plates containing 500 µL of StemSpan-XF + SCF at 100 ng/mL, Flt3-L at 100 ng/mL, and TPO at 100 ng/mL and cultured at 37˚C, 5% CO_2. 2 days after nucleofection, cells were cultured in semi-solid Methcult media for colony forming assay.

To analyze gene editing activity, primers flanking the target insertion site locus were used to amplify across the locus. Amplicons were analyzed via short read sequencing using an Illumina MiSeq. Replacement of the DNA bases adenine and guanine at nucleotide positions 20 and 21 to the bases cytosine and adenine (HBB5 template RNA) downstream of the transcriptional start site within the endogenous B-globin locus indicated successful editing.

As shown in FIG. 23A, total colony CFU numbers after treating HSCs obtained from 3 different donors with exemplary gene modifying system with or without second strand-targeting gRNA were comparable to total colony CFU numbers when the HSCs received mock treatment. These results demonstrate that treatment with the exemplary gene modifying systems did not significantly decrease the viability of treated HSCs. As shown in FIG. 23B, the numbers of CFU-E, BFU-E, CFU-M, CFU-GM, and CFU-G produced from CD34+ cells transfected with exemplary gene modifying systems after 14 days of clonal growth in methylcellulose were comparable to the corresponding CFU numbers when the CD34+ cells that received mock treatment. FIG. 23C shows a graph of the percent enucleated CD235+ cells after HSCs treated with exemplary gene modifying systems began in vitro differentiation. The results show that HSCs treated with exemplary gene modifying systems produced similar percentages of red blood cell-like cells at a similar rate as mock treated HSCs.

These results show that editing a non-pathogenic sequence into a clinically relevant codon in the endogenous B-globin locus using exemplary gene modifying systems described herein does not have a significant effect on the differentiation ability of human HSCs.

Example 21: Screening configurations of template RNAs that correct the SCD mutation in Human CD34+ cell with SCD mutation

This example describes the use of an exemplary gene modifying system containing a gene modifying polypeptide and template RNAs comprising varied lengths of heterologous object sequences and PBS sequences to identify favorable configurations for correction of the SCD mutation. In this example, a template RNA contains:

(1) a gRNA spacer;

(2) a gRNA scaffold;

(3) a heterologous object sequence; and

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

The template RNAs were designed to contain 8 – 17 nucleotide PBS sequences and 9 – 20 nucleotide heterologous object sequences (Table X4). Template RNAs with two different gRNA exemplary spacer sequences, HBB5 and HBB8, were used to target SCD mutation in CD34+ SCD human cells. The heterologous object sequences and PBS sequences were designed to correct the SCD mutation by replacing a "T" nucleotide with an "A" nucleotide (Wildtype) or with a "C" (Makassar installation) at the mutation site using a gene modifying system described herein. Template RNAs were also designed to produce either or both of 1) PAM-kill mutations or 2) one or more silent substitutions.

Table X4: **Exemplary Template RNAs Designed to Convert SCD mutation to Wildtype or Makassar.**

Name	Sequence	SEQ ID NO	RT length	PBS length	WT/Makassar
tg14_hs1	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArCrUrCrCrUrGrGrUrUrU rUrArGrGrAmGmCmUmAmGmAmAmAmUmAmGmGmCrArArArGrUrUr ArArArArArUrArArArGrGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCm UmUmGmAmAmAmAmAmAmGmUmGmGmCmAmAmCmCmGmAmG mUmCmGmGmUmGmCrArGrGrArCrUrUrCrUrUrCrUrGrCrCrGrGrAr GrUrCrArG*mG*mU*mG	20939	14	10	Makassar
tg14_hs1-SCD-wt	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArCrUrCrCrUrGrGrUrUrU rUrArGrGrAmGmCmUmAmGmAmAmAmUmAmGmGmCrArArArGrUrUr ArArArArArUrArArArGrGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCm UmUmGmAmAmAmAmAmAmGmUmGmGmCmAmAmCmCmGmAmG mUmCmGmGmUmGmCrArGrGrArCrUrUrCrUrUrCrUrGrCrCrGrGrAr GrUrCrArG*mG*mU*mG	20940	14	10	WT
tgRNA34_HBB8h-	mG*mU*mA*rArCrGrGrCrArGrArCrUrUrCrUrCrArCrGrUrUrU rUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArArGrUrUr ArArArArArUrArArArGrGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCm UmUmGmAmAmAmAmAmAmGmUmGmGmCmAmAmCmCmGmAmG	20941	14	11	Makassar

SCD-M	mUmCmGmGmUmGmCrArCrCrUrGrArCrUrUrCrCrUrGrCrGrGrAr GrArArGrUrC*mU*mG*mC	20942	14	11	WT
tgRNA34_HBB 8h-SCD-wt	mG*mU*mA*rArCrGrGrCrArGrArCrUrUrUrCrUrCrArCrGrUrUrUrU rUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArArGrUrUr ArArArArUrArArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCm UmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmG mUmCmGmGmUmGmCrArCrCrUrGrArCrUrUrCrCrUrGrArArGrGrAr GrArArGrUrC*mU*mG*mC	20943	14	11	Makassar
tgRNA34_HBB 8hs4-MK	mG*mU*mA*rArCrGrGrCrArGrArCrUrUrUrCrUrCrArCrGrUrUrUrU rUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArArGrUrUr ArArArArUrArArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCm UmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmG mUmCmGmGmUmGmCrArCrCrUrGrArCrUrUrCrCrUrGrArArGrGrAr GrArArGrUrC*mU*mG*mC	20944	14	11	WT
tgRNA34_HBB 8hs4-WT	mG*mU*mA*rArCrGrGrCrArGrArCrUrUrUrCrUrCrArCrGrUrUrUrU rUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArArGrUrUr ArArArArUrArArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCm UmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmG mUmCmGmGmUmGmCrArCrCrUrGrArCrUrUrCrCrUrGrArArGrGrAr GrArArGrUrC*mU*mG*mC	20945	14	11	Makassar
tgRNA34_	mG*mU*mA*rArCrGrGrCrArGrArCrUrUrUrCrUrCrArCrGrUrUrUrU rUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArArGrUrUr				

HBB 8hs7-MK	ArArArArUrArArGrGrCrUrArGrUrUrCrCrGrUrUrArUrCrAmAmCm UmUmGmAmAmAmAmAmGmUmGmGmCmAmAmCmCmGmAmG mUmCmGmGmUmGmCrArCrCrUrGrArCrUrCrCrCrGrCrUrGrArGrArGrUrC*mU*mG*mC	20946	14	11	WT
tgRNA34_HBB 8hs7-WT	mG*mU*mA*rArCrGrGrCrArGrArCrUrUrCrUrCrCrArCrGrUrUrU rUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUr ArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCm UmUmGmAmAmAmAmAmGmUmGmGmCmAmAmCmCmGmAmG mUmCmGmGmUmGmCrArCrCrUrGrArCrUrCrCrCrGrCrUrGrArGrArGrUrC*mU*mG*mC	20947	14	11	Makassar
tgRNA34_HBB 8hs10-MK	mG*mU*mA*rArCrGrGrCrArGrArCrUrUrCrUrCrCrArCrGrUrUrU rUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUr ArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCm UmUmGmAmAmAmAmAmGmUmGmGmCmAmAmCmCmGmAmG mUmCmGmGmUmGmCrArCrCrUrGrArCrUrCrCrCrGrCrUrGrArGrArGrUrC*mU*mG*mC	20948	14	11	WT
tgRNA34_HBB 8hs10-WT	mG*mU*mA*rArCrGrGrCrArGrArCrUrUrCrUrCrCrArCrGrUrUrU rUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUr ArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCm UmUmGmAmAmAmAmAmGmUmGmGmCmAmAmCmCmGmAmG mUmCmGmGmUmGmCrArCrCrUrGrArCrUrCrCrCrGrCrUrGrArGrArGrUrC*mU*mG*mC				

tgRNA34_HBB8hs13-MK	mG*mU*mA*rArCrGrGrCrArGrArCrUrUrUrCrUrCrArCrGrUrUrU rUrArGrArmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUr ArArArArUrArArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCm UmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmG mUmCmGmGmUmGmCrArCrCrUrGrArCrUrCrCrCrGrCrGrGrAr GrArArGrUrC*mU*mG*mC	20949	14	11	Makassar
tgRNA34_HBB8hs13-WT	mG*mU*mA*rArCrGrGrCrArGrArCrUrUrUrCrUrCrArCrGrUrUrU rUrArGrArmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUr ArArArArUrArArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCm UmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmG mUmCmGmGmUmGmCrArCrCrUrGrArCrUrCrCrCrGrArGrGrAr GrArArGrUrC*mU*mG*mC	20950	14	11	WT
tg14_PAM1-SCD-wt	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArCrUrCrCrUrGrGrUrUrU rUrArGrArmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUr ArArArArUrArArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCm UmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmG mUmCmGmGmUmGmCrArGrArCrUrUrCrUrCrArGrGrCrCrGrGrAr GrUrCrArG*mG*mU*mG	20951	14	10	WT
tg14_PAM1-C_hs1-	mC*mA*mU*rGrGrUrGrCrArCrCrUrGrArCrUrCrCrUrGrGrUrUrU rUrArGrArmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUr ArArArArUrArArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCm UmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmG	20952	14	10	WT

SCD-wt	mUmCmGmGmUmGmCrArGrArCrUrUrCrUrCrGrGrCrCrGrGrAr GrUrCrArG*mG*mU*mG				

Table X4A shows the sequences of X4 without modifications. In some embodiments, the sequences used in this table can be used without chemical modifications.

Table X4A: Table X4 Sequences without Modifications

Name	Sequence	SEQ ID NO
tg14_hs1	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCA ACUUGAAAAAGUGGCACCGAGUCGGUGCAGACUUCUCUGCCGGAGUCAGGUG	21892
tg14_hs1-SCD-wt	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCA ACUUGAAAAAGUGGCACCGAGUCGGUGCAGACUUCUCUUCCGGAGUCAGGUG	21893
tgRNA34_HBB8h-SCD-M	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCA ACUUGAAAAAGUGGCACCGAGUCGGUGCACCUGACUCCUGCGGAGAAGUCUGC	21894
tgRNA34_HBB8h-SCD-wt	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCA ACUUGAAAAAGUGGCACCGAGUCGGUGCACCUGACUCCUGAGGAGAAGUCUGC	21895
tgRNA34_HBB8hs4-MK	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCA ACUUGAAAAAGUGGCACCGAGUCGGUGCACCUGACUCCCGCAGAGAAGUCUGC	21896
tgRNA34_HBB8hs4-WT	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCA ACUUGAAAAAGUGGCACCGAGUCGGUGCACCUGACUCCCGAAGAGAAGUCUGC	21897
tgRNA34_HBB8hs7-MK	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCA ACUUGAAAAAGUGGCACCGAGUCGGUGCACCUGACUCCCGCUGAGAAGUCUGC	21898
tgRNA34_HBB8hs7-WT	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCA ACUUGAAAAAGUGGCACCGAGUCGGUGCACCUGACUCCCGAUGAGAAGUCUGC	21899
tgRNA34_HBB8hs10-MK	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCA ACUUGAAAAAGUGGCACCGAGUCGGUGCACCUGACUCCCGCCGAGAAGUCUGC	21900

tgRNA34_HBB8hs10-WT	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAAGUGGCACCGAGUCGGUGCACCUGACUCCCGACGAGAAGUCUGC	21901
tgRNA34_HBB8hs13-MK	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAAGUGGCACCGAGUCGGUGCACCUGACUCCCGCGGAGAAGUCUGC	21902
tgRNA34_HBB8hs13-WT	GUAACGGCAGACUUCUCCACGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAAGUGGCACCGAGUCGGUGCACCUGACUCCCGAGGAGAAGUCUGC	21903
tg14_PAMT_hs1-SCD-wt	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAAGUGGCACCGAGUCGGUGCAGACUUCUCUCAGCCGGAGUCAGGUG	21904
tg14_PAMC_hs1-SCD-wt	CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAAGUGGCACCGAGUCGGUGCAGACUUCUCUCGGCCGGAGUCAGGUG	21905

Exemplary gene modifying systems comprising mRNA encoding the gene modifying polypeptide and a template RNA from Table X4 with or without second strand-targeting gRNA (e.g., from Table X1) are used to transfect human HSCs harboring the SCD mutation. The gene modifying system is used to correct the SCD mutation by replacing a "T" nucleotide with an "A" (wildtype) or "C" (Makassar) nucleotide at the mutation site in the endogenous B-globin locus in primary human HSCs. Amplicon sequencing will be used to show editing at the mutation site in the endogenous B-globin locus in primary human HSCs.

The results will show that exemplary gene modifying systems have editing activity when correcting the SCD mutation in the endogenous B-globin locus in primary human HSCs.

Herein, when an RNA sequence (e.g., a template RNA sequence) is said to comprise a particular sequence (e.g., a sequence of Table A or Table B or a portion thereof) that comprises thymine (T), it is of course understood that the RNA sequence may (and frequently does) comprise uracil (U) in place of T. For instance, the RNA sequence may comprise U at every position shown as T in the sequence in Table A or B. More specifically, the present disclosure provides an RNA sequence according to every template sequence shown in Table A and B, wherein the RNA sequence has a U in place of each T in the sequence of Table A and B.

It should be understood that for all numerical bounds describing some parameter in this application, such as "about," "at least," "less than," and "more than," the description also necessarily encompasses any range bounded by the recited values. Accordingly, for example, the description "at least 1, 2, 3, 4, or 5" also describes, inter alia, the ranges 1-2, 1-3, 1-4, 1-5, 2-3, 2-4, 2-5, 3-4, 3-5, and 4-5, et cetera.

For all patents, applications, or other reference cited herein, such as non-patent literature and reference sequence information, it should be understood that they are incorporated by reference in their entirety for all purposes as well as for the proposition that is recited. Where any conflict exists between a document incorporated by reference and the present application, this application will control. All information associated with reference gene sequences disclosed in this application, such as GeneIDs or accession numbers (typically referencing NCBI accession numbers), including, for example, genomic loci, genomic sequences, functional annotations, allelic variants, and reference mRNA (including, e.g., exon boundaries or response elements) and

protein sequences (such as conserved domain structures), as well as chemical references (e.g., PubChem compound, PubChem substance, or PubChem Bioassay entries, including the annotations therein, such as structures and assays, et cetera), are hereby incorporated by reference in their entirety.

Headings used in this application are for convenience only and do not affect the interpretation of this application.

CLAIMS

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

(i) a gRNA spacer that is complementary to a first portion of the human HBB gene, wherein the gRNA spacer has a sequence comprising the core nucleotides of a gRNA spacer sequence of Table 1, and optionally comprises one or more consecutive nucleotides starting with the 3' end of the flanking nucleotides of the gRNA spacer, or wherein the gRNA spacer has a sequence of a spacer chosen from Table A, Table AA, Table B, Table B1, Tables 5A-5D, Table X4, or Table X4A;

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

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

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

2. The template RNA of claim 1, wherein the heterologous object sequence comprises the core nucleotides of an RT template sequence from Table 3, and optionally comprises one or more consecutive nucleotides starting with the 3' end of the flanking nucleotides of the RT template sequence, or wherein the heterologous object sequence comprises a sequence of an RT template sequence from Table A, Table AA, Table B, Table B1, Tables 5A-5D, Table X4, or Table X4A.

3. The template RNA of claim 1, wherein the heterologous object sequence comprises the core nucleotides of the RT template sequence of Table 3 that corresponds to the gRNA spacer sequence, and optionally comprises one or more consecutive nucleotides starting with the 3' end of the flanking nucleotides of the RT template sequence, or wherein the heterologous object sequence comprises a sequence of an RT template sequence from Table A, Table AA, Table B, Table B1, Tables 5A-5D, Table X4, or Table X4A that corresponds to the gRNA spacer sequence.

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

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

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

(iii) a heterologous object sequence comprising a mutation region to introduce a mutation into a second portion of the human HBB gene, wherein the heterologous object sequence comprises the core nucleotides of an RT template sequence of Table 3, and optionally comprises one or more consecutive nucleotides starting with the 3' end of the flanking nucleotides of the RT template sequence, or wherein the heterologous object sequence comprises an RT template sequence of Table A, Table AA, Table B, Table B1, Tables 5A-5D, Table X4, or Table X4A; and

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

5. The template RNA of claim 4, wherein the gRNA spacer comprises the core nucleotides of a gRNA spacer sequence of Table 1, and optionally comprises one or more consecutive nucleotides starting with the 3' end of the flanking nucleotides of the gRNA spacer sequence, or wherein the gRNA spacer comprises a gRNA spacer sequence of Table A, Table AA, Table B, Table B1, Tables 5A-5D, Table X4, or Table X4A.

6. The template RNA of any one of claims 1-5, wherein the gRNA spacer comprises CATGGTGCATCTGACTCCTG (SEQ ID NO: 21668) or CATGGTGCACCTGACTCCTG (SEQ ID NO: 19249).

7. The template RNA of any one of claims 1-5, wherein the gRNA spacer comprises GTAACGGCAGACTTCTCCAC (SEQ ID NO: 19971).

8. The template RNA of claim 4, wherein the heterologous object sequence comprises the core nucleotides of the gRNA spacer sequence of Table 1 that corresponds to the RT template sequence, and optionally comprises one or more consecutive nucleotides starting with the 3' end of the flanking nucleotides of the gRNA spacer sequence, or wherein the heterologous object sequence comprises the nucleotides of the gRNA spacer sequence of , Table A, Table AA, Table B, Table B1, Tables 5A-5D, Table X4, or Table X4A that corresponds to the RT template sequence.

9. The template RNA according to any one of claims 1-8, wherein the PBS sequence has a sequence comprising the core nucleotides of the PBS sequence from the same row of Table 3 as the RT template sequence, and optionally comprises one or more consecutive nucleotides starting with the 5' end of the flanking nucleotides of the PBS sequence.

10. The template RNA according any one of claims 1-8, wherein the PBS sequence has a sequence comprising the core nucleotides of a PBS sequence of Table 3 that corresponds to the RT template sequence, the gRNA spacer sequence, or both, and optionally comprises one or more consecutive nucleotides starting with the 5' end of the flanking nucleotides of the PBS sequence, or wherein the PBS sequence has a sequence comprising the core nucleotides of a PBS sequence of Table A, Table AA, Table B, Table B1, Tables 5A-5D, Table X4, or Table X4A that corresponds to the RT template sequence, the gRNA spacer sequence, or both.

11. The template RNA according to any one of claims 1-10, wherein the gRNA scaffold comprises a sequence of a gRNA scaffold of Table 12, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto.

12. The template RNA according to any one of claims 1-10, wherein the gRNA scaffold comprises a sequence of a gRNA scaffold of Table 12 that corresponds to the RT template sequence, the gRNA spacer sequence, or both, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto.

13. The template RNA according to any one of claims 1-12, wherein the mutation is a V6E mutation (e.g., to correct a pathogenic E6V mutation) of the HBB gene.

14. The template RNA of any one of claims 1-13, wherein the pre-edit sequence comprises between about 1 nucleotide to about 35 nucleotides (e.g., comprises about 1-5, 5-10, 10-15, 15-20, 20-25, 25-30, or 30-35 nucleotides) in length.

15. The template RNA of any one of claims 1-14, wherein the mutation region comprises a single nucleotide.

16. The template RNA of any one of claims 1-14, wherein the mutation region is at least two nucleotides in length.

17. The template RNA of any one of claims 1-14 or 16, wherein the mutation region is up to 32 (e.g., up to 5, 10, 15, 20, 25, 30, or 32) nucleotides in length and comprises one, two, or three sequence differences relative to a second portion of the human HBB gene.

18. The template RNA of any one of claims 1-14, 16, or 17, wherein the mutation region comprises two sequences differences relative to a second portion of the human HBB gene.

19. The template RNA of any one of claims 1-14 or 16-18, wherein the mutation region comprises a first region (e.g., a first nucleotide) designed to correct a pathogenic mutation in the HBB gene and a second region (e.g., a second nucleotide) designed to inactivate a PAM sequence (e.g., a "PAM-kill" mutation exemplified in Table A, AA, B or B1).

20. The template RNA of any of claims 1-19, wherein the heterologous object sequence has a sequence of the RT template sequence from the same row as Table A or B as the gRNA spacer sequence, or a sequence having 1, 2, or 3 substitutions thereto, wherein optionally the bolded T shown in the RT template sequence of Table A is replaced with a G (e.g., a sequence without a PAM-kill mutation), or wherein further optionally the bolded C shown in the RT template of Table B is replaced with a T or U (e.g., a sequence without a SNP that is present in HEK293T cells but absent in the hg38 human reference genome).

21. The template RNA of any one of claims 1-20, wherein the mutation region comprises less than 80%, 70%, 60%, 50%, 40%, or 30% identity to the corresponding portion of the human HBB gene.

22. The template RNA of any one of claims 1-21, wherein the template RNA comprises one or more silent mutations (e.g., silent substitutions), e.g., as exemplified in Table 7A, X4, or X4A.

23. The template RNA of embodiment 22, wherein the one or more silent mutaitons comprises a silent substitution at the codon encoding the 6th amino acid , counting the initial methionine, of the HBB gene (proline), e.g., to CCC or CCG.

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

25. The template RNA of any one of claims 1-24, which comprises one or more chemically modified nucleotides.

26. A gene modifying system comprising:

a template RNA of any of claims 1-25, and

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

27. The gene modifying system of claim 26, wherein the gene modifying polypeptide comprises:

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

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

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

28. The gene modifying system of claim 27, wherein the RT domain comprises:

(a) an RT domain of Table 6; or

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

29. The gene modifying system of claim 27 or 28, wherein the Cas domain comprises a Cas domain of Table 7 or Table 8.

30. The gene modifying system of claim 27 or 28, wherein the Cas domain:

(a) is a Cas9 domain;

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

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

31. The gene modifying system of claim 30, wherein the Cas9 domain binds a PAM sequence listed in Table 7 or Table 12.

32. The gene modifying system of claim 31, wherein a second portion of the human HBB gene overlaps with a PAM recognized by the Cas domain, e.g., wherein the second portion of the human HBB gene is within the PAM or wherein the PAM is within the second portion of the human HBB gene).

33. The gene modifying system of any one of claims 26-32, wherein the gRNA spacer is a gRNA spacer according to Table 1, and the Cas domain comprises a Cas domain listed in the same row of Table 1, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto.

34. The gene modifying system of any one of claims 26-32, wherein the template RNA comprises a sequence of a template RNA sequence of Table 3, Table A, Table AA, Table B, Table B1, Tables 5A-5D, Table X4, or Table X4A or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto.

35. The gene modifying system of any one of claims 26-32, wherein:

(a) the template RNA comprises a sequence of a template RNA sequence of Table 3, Table A, Table AA, Table B, Table B1, Tables 5A-5D, Table X4, or Table X4A;

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

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

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

36. The gene modifying system of any of claims 26-35, which produces a first nick in a first strand of the human HBB gene.

37. The gene modifying system of claim 36, which further comprises a second strand-targeting gRNA that directs a second nick to the second strand of the human HBB gene.

38. The gene modifying system of claim 37, wherein the second strand-targeting gRNA comprises:

(i) a sequence comprising the core nucleotides of a left gRNA spacer sequence or a right gRNA spacer sequence from Table 2, and optionally comprises one or more consecutive nucleotides starting with the 3' end of the flanking nucleotides of the left gRNA spacer sequence or right gRNA spacer sequence; or

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

39. The gene modifying system of claim 37, wherein the second strand-targeting gRNA comprises a sequence comprising the core nucleotides of a left gRNA spacer sequence or a right gRNA spacer sequence from Table 2 that corresponds to the gRNA spacer sequence of (i), and optionally comprises one or more consecutive nucleotides starting with the 3' end of the flanking nucleotides of the left gRNA spacer sequence or right gRNA spacer sequence.

40. The gene modifying system of claim 37, wherein the second strand-targeting gRNA comprises:

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

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

41. The gene modifying system of claim 37, wherein the second strand-targeting gRNA comprises a sequence comprising the core nucleotides of the second nick gRNA sequence from Table 4 that corresponds to the gRNA spacer sequence of (i), or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto, and optionally comprises one or more consecutive nucleotides starting with the 3' end of the flanking nucleotides of the second nick gRNA sequence.

42. The gene modifying system of any one of claims 37-41, wherein the second strand-targeting gRNA has a "PAM-in orientation" with the template RNA of the gene modifying system, e.g., as exemplified in Table 4, 6A, X4, or X4A.

43. The gene modifying system of any one of claims 37-42, the second strand-targeting gRNA targets a sequence overlapping the target mutation of the template RNA.

44. The gene modifying system of claim 43, wherein second strand-targeting gRNA comprises:

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

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

(iii) a sequence (e.g., a spacer sequence) complementary to the Makassar sequence at the sickle cell locus;

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

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

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

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

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

48. The template RNA or gene modifying system of any one of the preceding claims, wherein the mutation region comprises 1, 2, or 3 nucleotide positions of sequence difference relative to the corresponding portion of the human HBB gene.

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

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

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

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

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

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

55. The gene modifying system of claim 54, wherein the linker comprises a sequence of a linker of Table 10 (e.g., of any of SEQ ID NOS: 5217, 5106, 5190, and 5218).

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

57. The gene modifying system of claim 56, wherein the gene modifying polypeptide comprises a first NLS and a second NLS.

58. The gene modifying system of claim 56 or 57, wherein the NLS comprises a sequence of a NLS of Table 11 (e.g., of any of SEQ ID NOs: 5245, 5290, 5323, 5330, 5349, 5350, 5351, and 4001).

59. A template RNA comprising a sequence of a template RNA of Table 4, Table A, Table AA, Table B, Table B1, Table 5A-5D, Table X4, or Table X4A, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto.

60. A template RNA comprising a sequence of a template RNA of Table 4, Table A, Table AA, Table B, Table B1, Table 5A-5D, Table X4, or Table X4A.

61. A gene modifying system comprising:

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

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

62. A gene modifying system comprising:

(iii) a template RNA comprising a sequence of a template RNA of Table 4; and

(iv) a second-nick gRNA sequence from the same row of Table 4 as (i).

63. A DNA encoding the template RNA of any one of claims 1-25, 46-52, 59, or 60, or the gene modifying system of any one of claims 26-58, 60, or 61.

64. A pharmaceutical composition, comprising the system of any one of claims 26-58, 60, or 61, or one or more nucleic acids encoding the same, and a pharmaceutically acceptable excipient or carrier.

65. The pharmaceutical composition of claim 64, wherein the pharmaceutically acceptable excipient or carrier is selected from the group consisting of a plasmid vector, a viral vector, a vesicle, and a lipid nanoparticle.

66. The pharmaceutical composition of claim 65, wherein the viral vector is an adeno-associated virus.

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

68. A method of making the template RNA of any one of claims 1-25, 46-52, 59, or 60, the method comprising synthesizing the template RNA by *in vitro* transcription (e.g., solid state synthesis) or by introducing a DNA encoding the template RNA into a host cell under conditions that allow for production of the template RNA.

69. A method for modifying a target site in the human HBB gene in a cell, the method comprising contacting the cell with the gene modifying system of any one of claims 26-58, 60, or 61, or DNA encoding the same, thereby modifying the target site in the human HBB gene in a cell.

70. A method for treating a subject having a disease or condition associated with a mutation in the human HBB gene, the method comprising administering to the subject the gene modifying system of any one of claims 26-58, 60, or 61, or DNA encoding the same, thereby treating the subject having a disease or condition associated with a mutation in the human HBB gene.

71. The method of claim 69 or 70, wherein the disease or condition is sickle cell disease (SCD).

72. The method of any one of claims 69-71, wherein the subject has a E6V mutation.

73. A method for treating a subject having SCD the method comprising administering to the subject the gene modifying system of any one of claims 26-58, 60, or 61, or DNA encoding the same, thereby treating the subject having SCD.

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

75. The gene modifying system or method of any one of the preceding claims, wherein the pathogenic mutation is a E6V mutation, and wherein the correction comprises an amino acid substitution of V6E

76. The gene modifying system or method of any one of the preceding claims, wherein introduction of the system into a target cell results in a mutation that causes the restoration of the function of the HBB gene.

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

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

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

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

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

82. The method of any one of the preceding claims, wherein the subject is a human.

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

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

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

FIG. 1

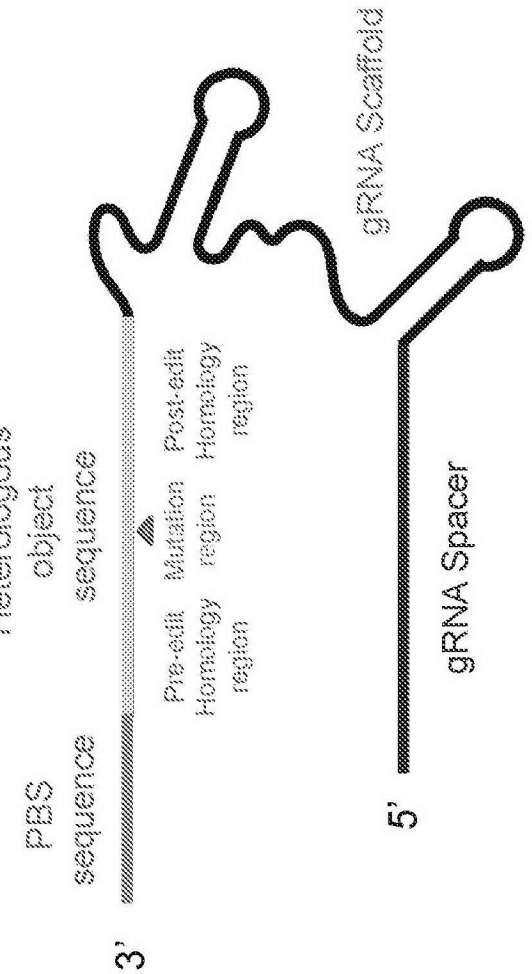

Gene modifying polypeptide
Linker
RT domain
Cas Nickase domain
Template RNA
Heterologous object sequence
PBS sequence
Pre-edit Homology region
Mutation region
Post-edit Homology region
3'
5'
gRNA Spacer
gRNA Scaffold

FIG. 2

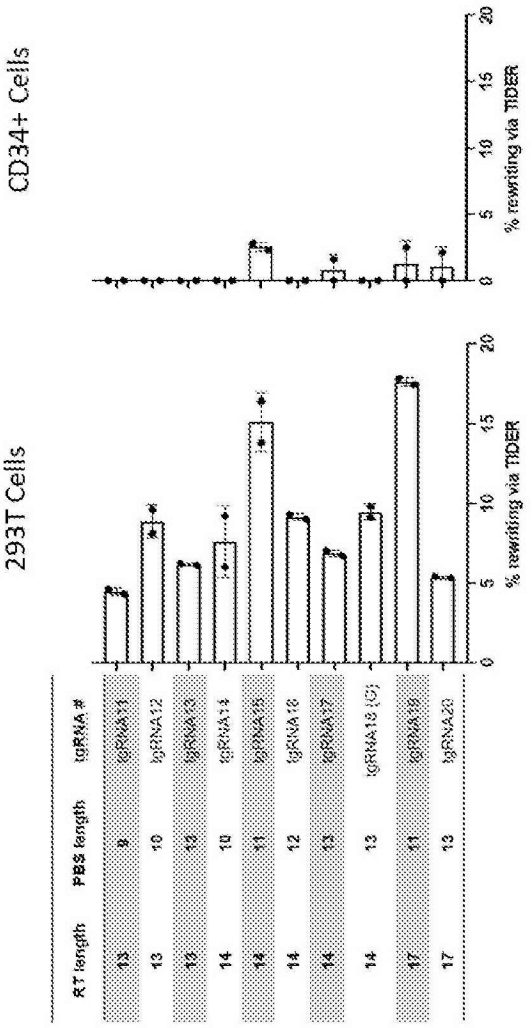
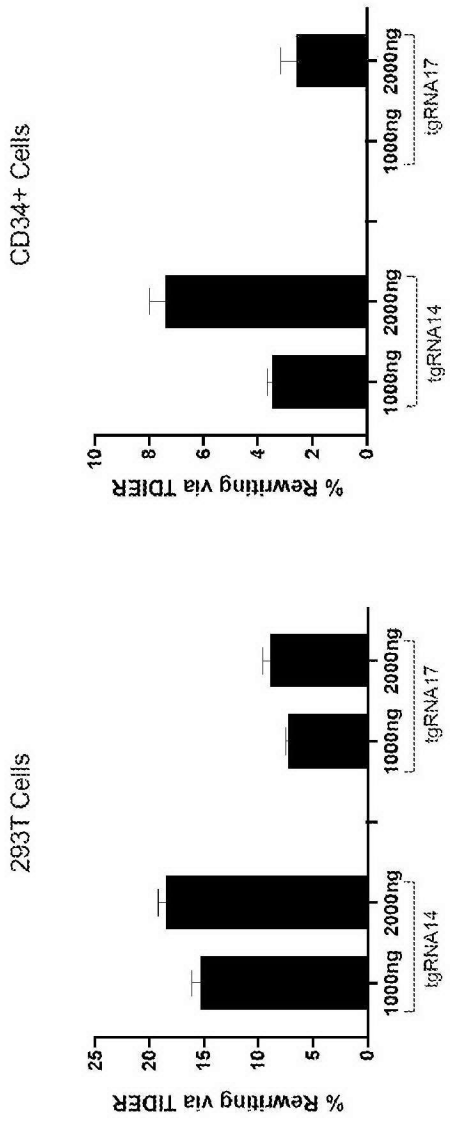

293T Cells
CD34+ Cells
% rewriting via TIDER
RT length
PBS length
tgRNA #
tgRNA11
tgRNA12
tgRNA13
tgRNA14
tgRNA15
tgRNA16
tgRNA17
tgRNA18 (G)
tgRNA19
tgRNA20

FIG. 3


293T Cells
% Rewriting via TIDER
0
5
10
15
20
25
1000ng 2000ng
tgRNA14
1000ng 2000ng
tgRNA17
CD34+ Cells
% Rewriting via TIDER
0
2
4
6
8
10
1000ng 2000ng
tgRNA14
1000ng 2000ng
tgRNA17

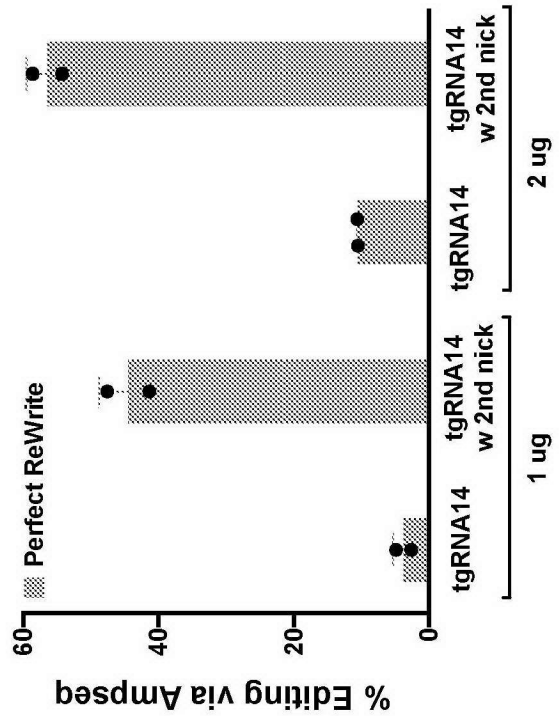

% Editing via Ampseq
60
40
20
0
Perfect ReWrite
tgRNA14
tgRNA14 w 2nd nick
tgRNA14
tgRNA14 w 2nd nick
1 ug
2 ug

FIG. 4

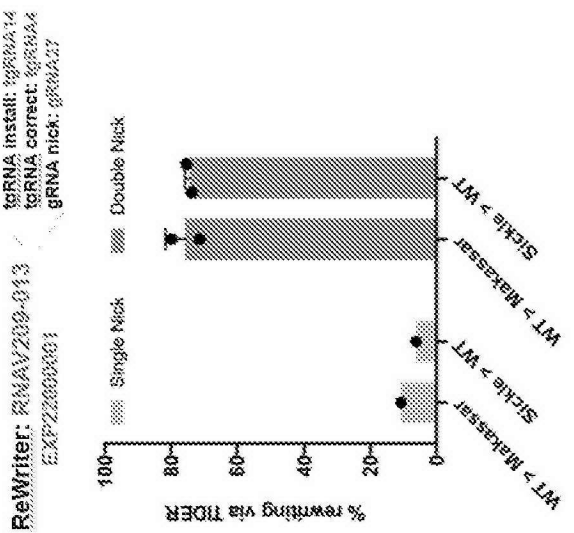

ReWriter: RMAV2.0-013
EXP2.0-0001
tgRNA install: tgRNA14
tgRNA correct: tgRNA4
gRNA nick: gRNA17
Single Nick
Double Nick
% rewriting via TIDER
100
80
60
40
20
0
WT > Makassar
Sickle > WT
WT > Makassar
Sickle > WT

FIG. 5

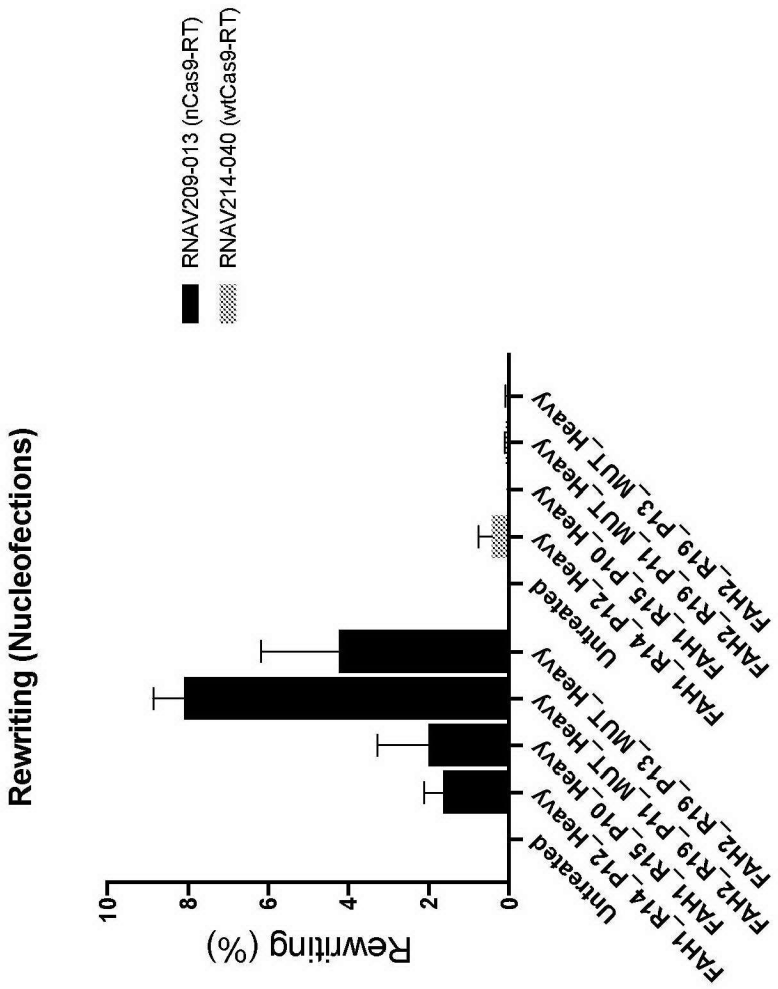

Rewriting (Nucleofections)
RNAV209-013 (nCas9-RT)
RNAV214-040 (wtCas9-RT)
Rewriting (%)
10
8
6
4
2
0
Untreated
FAH1_R14_P12_Heavy
FAH1_R15_P10_Heavy
FAH2_R19_P11_MUT_Heavy
FAH2_R19_P13_MUT_Heavy
Untreated
FAH1_R14_P12_Heavy
FAH1_R15_P10_Heavy
FAH2_R19_P11_MUT_Heavy
FAH2_R19_P13_MUT_Heavy

FIG. 6

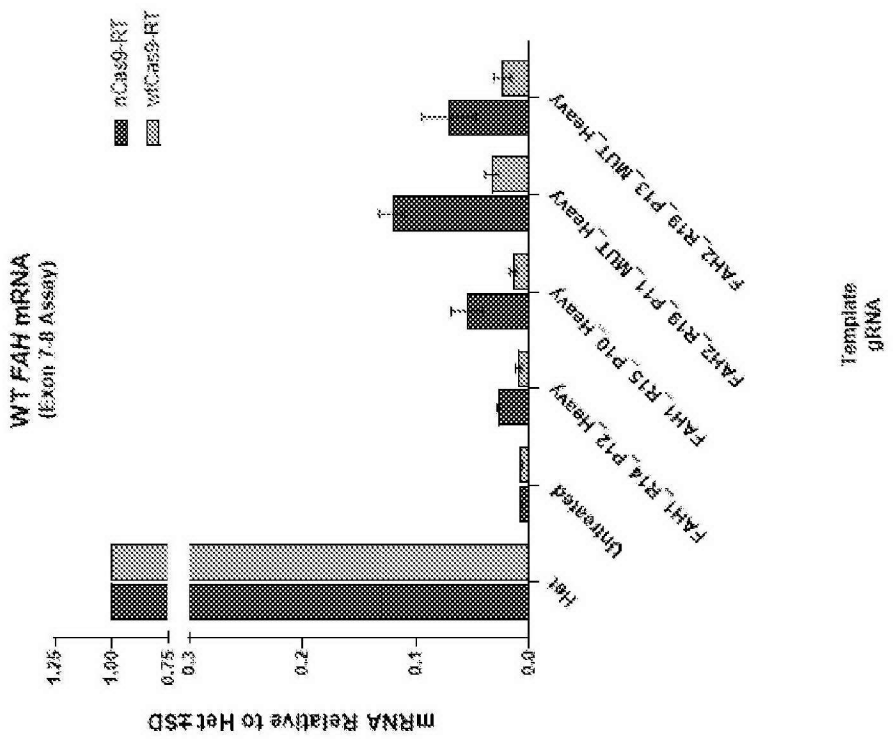
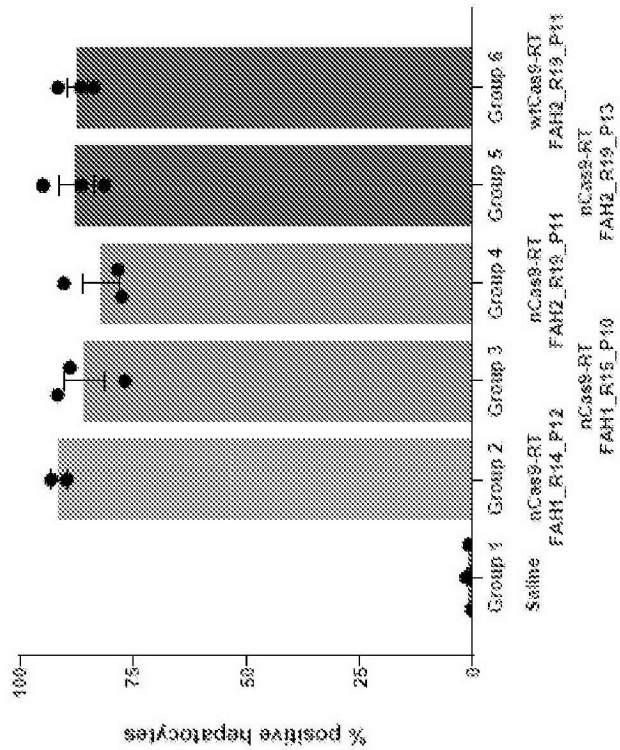

WT FAH mRNA
(Exon 7-8 Assay)
nCas9-RT
vdCas9-RT
mRNA Relative to Het±SD
1.25
1.00
0.75
0.3
0.2
0.1
0.0
Het
Untreated
FAH_R14_P12_Heavy
FAH_R15_P10_Heavy
FAH2_R19_P11_MUT_Heavy
FAH2_R19_P13_MUT_Heavy
Template
gRNA

FIG. 7

FIG. 8


Cas9 IHC
(6h post dosing)
% positive hepatocytes
100
75
50
25
0
Group 1
Group 2
Group 3
Group 4
Group 5
Group 6
Saline
nCas9-RT
FAH_R14_P12
nCas9-RT
FAH1_R15_P10
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FAH2_R19_P11

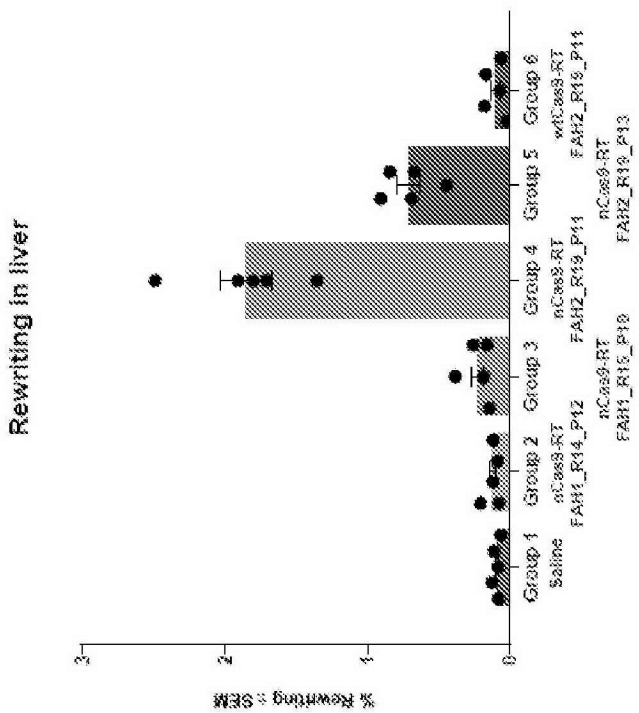

Rewriting in liver
% Rewriting ± SEM
0
2
4
Group 1
Saline
Group 2
nCas9-RT
FAH1_R14_P12
Group 3
nCas9-RT
FAH1_R15_P10
Group 4
nCas9-RT
FAH2_R19_P11
Group 5
nCas9-RT
FAH2_R19_P13
Group 6
nCas9-RT
FAH2_R19_P11

FIG. 9

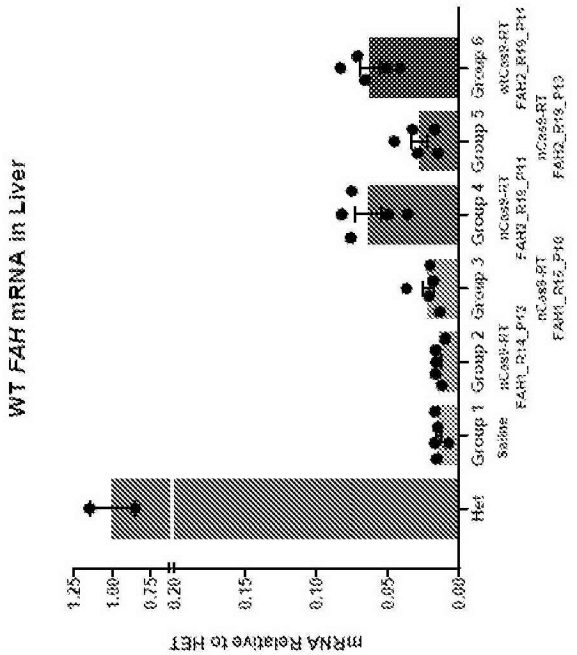

WT FAH mRNA in Liver
mRNA Relative to HET
1.25
1.00
0.75
0.20
0.15
0.10
0.05
0.00
Het
Group 1
Saline
Group 2
mCas9-RT
FAH_R14_P13
Group 3
mCas9-RT
FAH_R15_P16
Group 4
mCas9-RT
FAH_R15_P13
Group 5
mCas9-RT
FAH2_R15_P13
Group 6
mCas9-RT
FAH2_R15_P13

FIG. 10

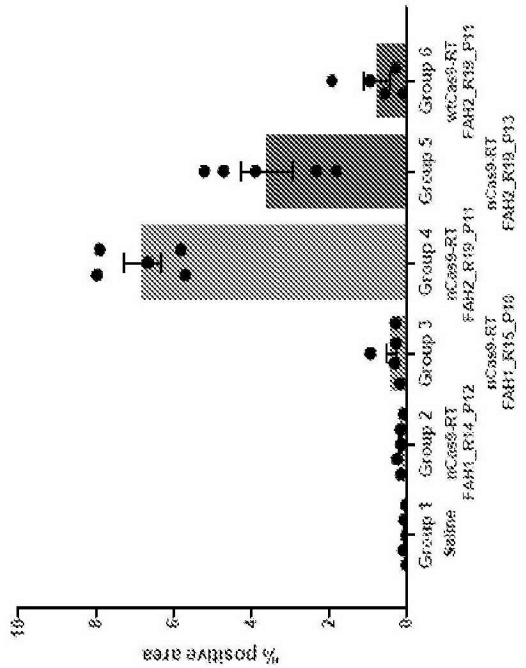
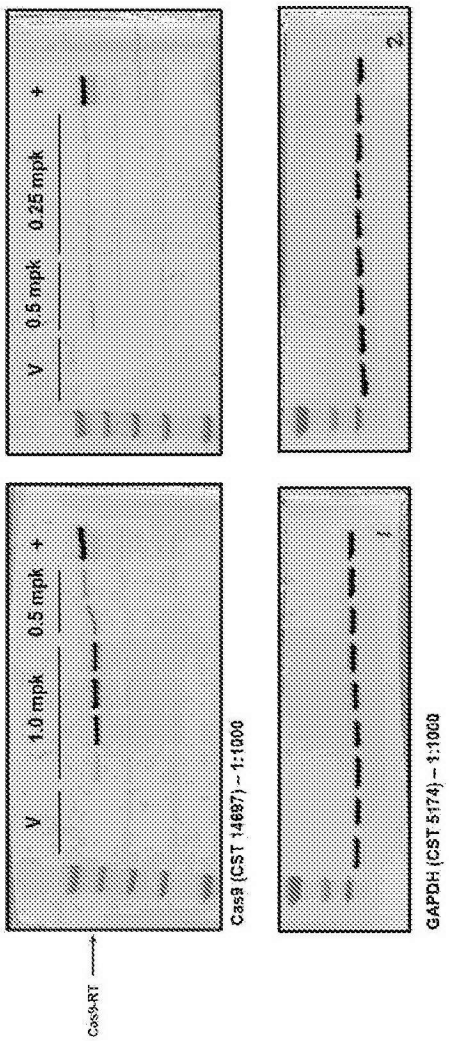

FAH IHC
(6 days post dosing)
% positive area
10
8
6
4
2
0
Group 1
Saline
Group 2
wCas9-RT
FAH1_R14_P12
Group 3
wCas9-RT
FAH1_R15_P16
Group 4
wCas9-RT
FAH2_R19_P11
Group 5
wCas9-RT
FAH2_R19_P13
Group 6
wCas9-RT
FAH2_R19_P11

FIG. 11

FIG. 12


V
1.0 mpk
0.5 mpk
+
V
0.5 mpk
0.25 mpk
+
Cas9-RT
Cas9 (CST 14697) – 1:1000
GAPDH (CST 5174) – 1:1000

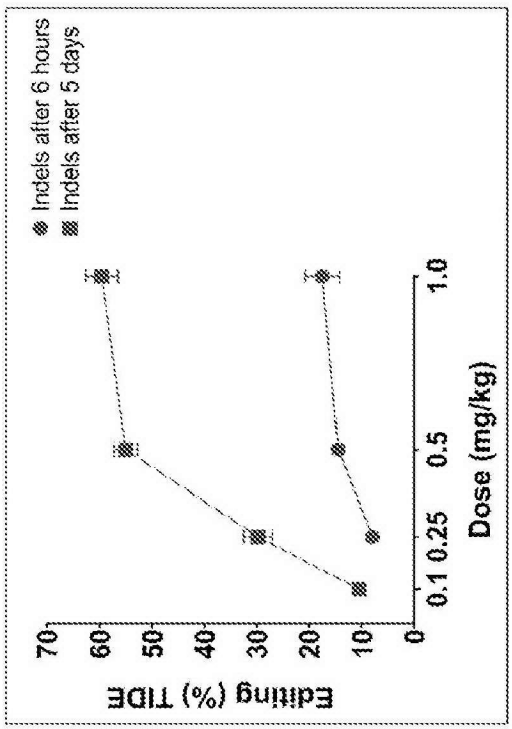

Indels after 6 hours
Indels after 5 days
Editing (%) TIDE
70
60
50
40
30
20
10
0
0.1
0.25
0.5
1.0
Dose (mg/kg)

FIG. 13

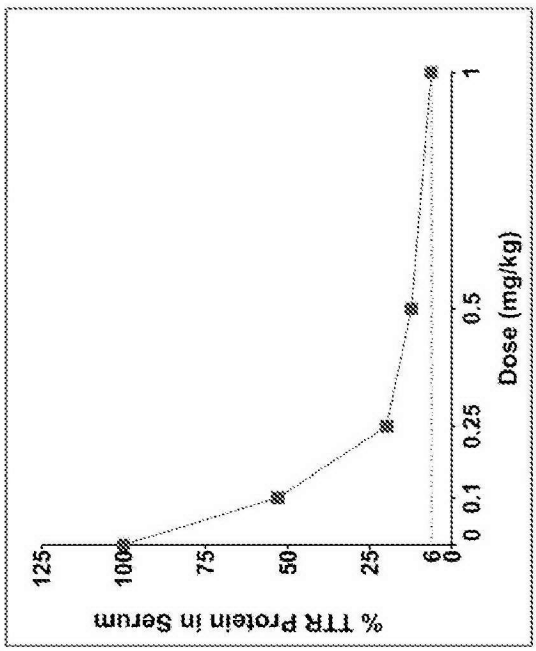


FIG. 14

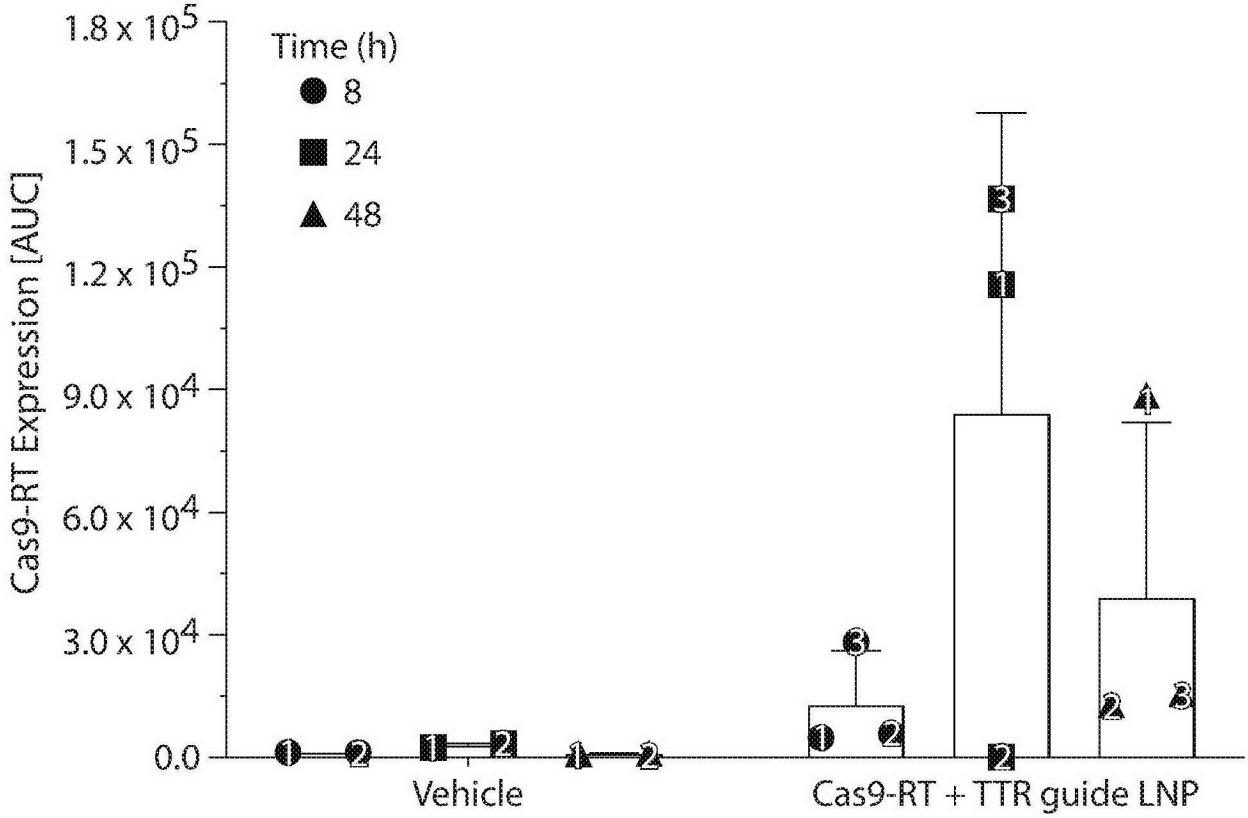

1.8 x 10^5
1.5 x 10^5
1.2 x 10^5
9.0 x 10^4
6.0 x 10^4
3.0 x 10^4
0.0
Cas9-RT Expression [AUC]
Time (h)
8
24
48
Vehicle
Cas9-RT + TTR guide LNP

FIG. 15

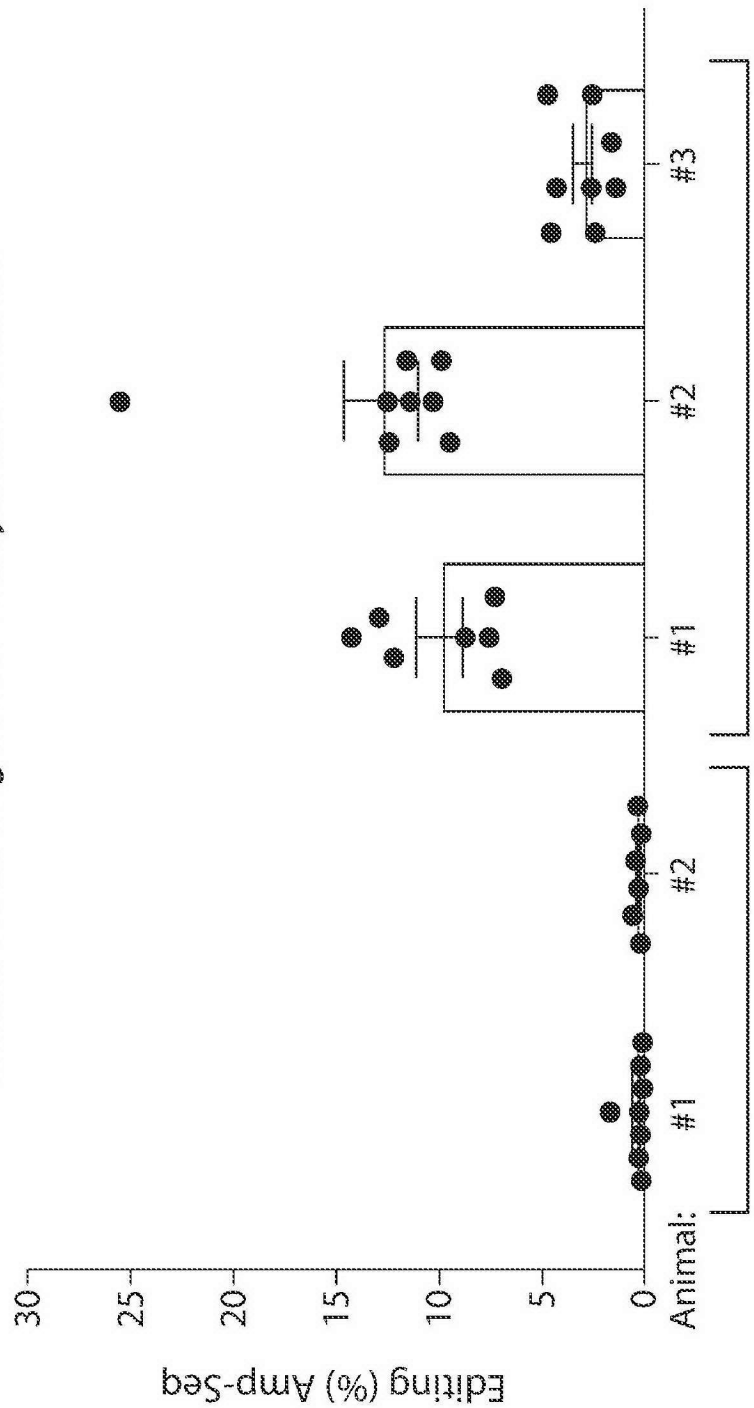

wtCas9-RT Editing of TTR 14 Days Post-Infusion
Editing (%) Amp-Seq
30
25
20
15
10
5
0
Animal:
#1
#2
Vehicle
#1
#2
#3
60-min infusion

FIG. 16

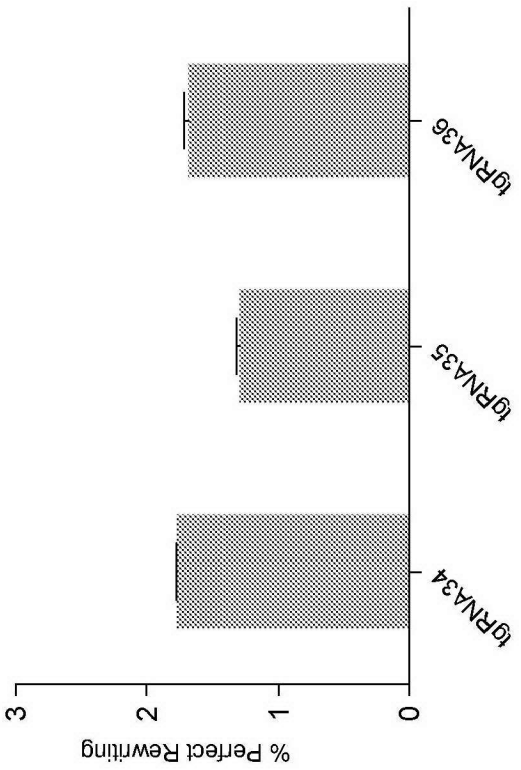


FIG. 17

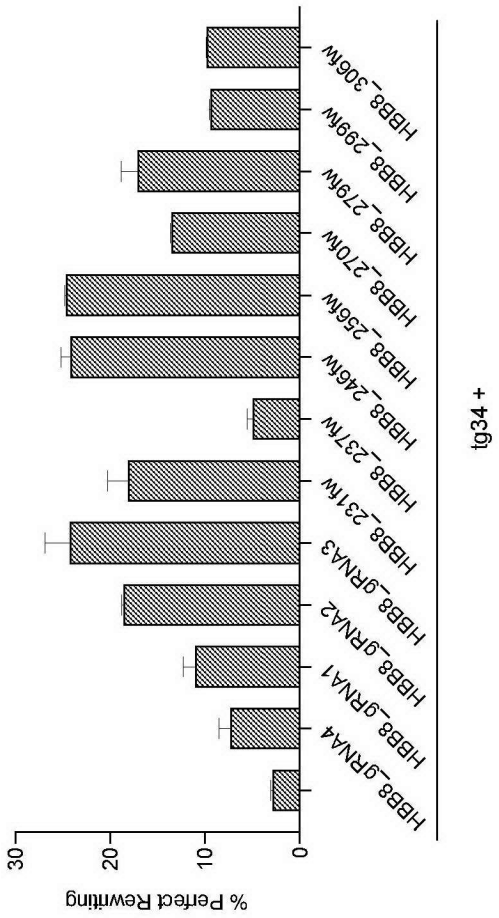


FIG. 18B

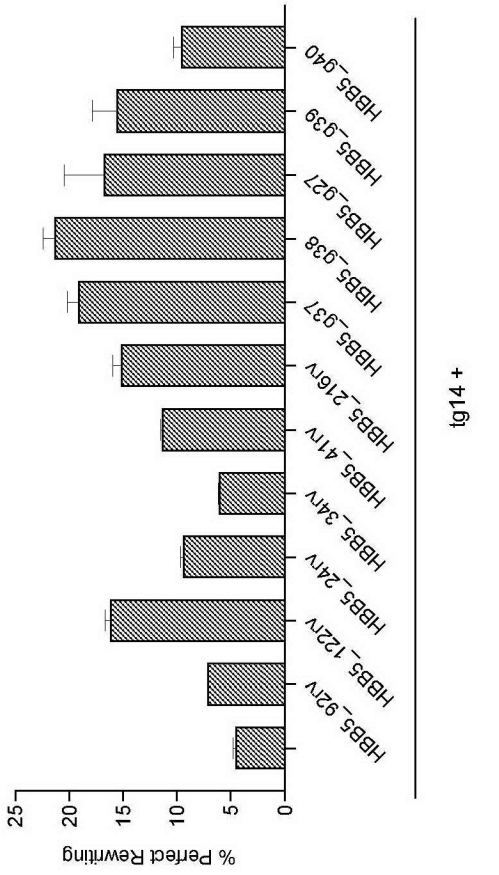


FIG. 18A

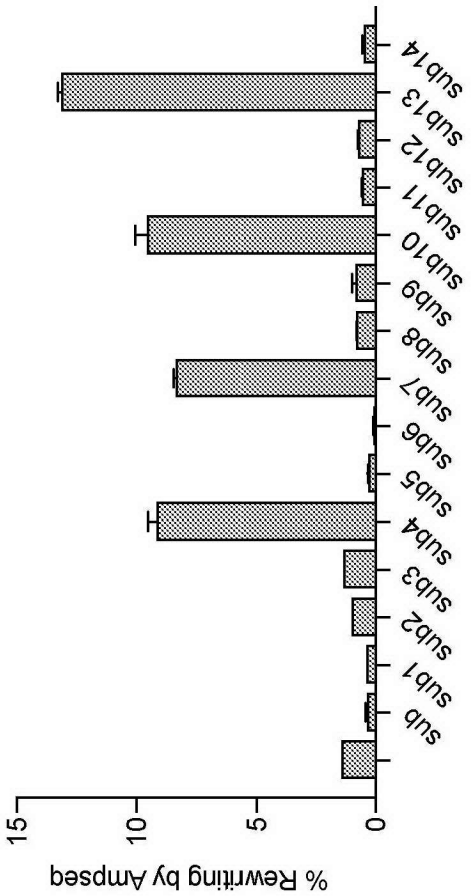


FIG. 19B

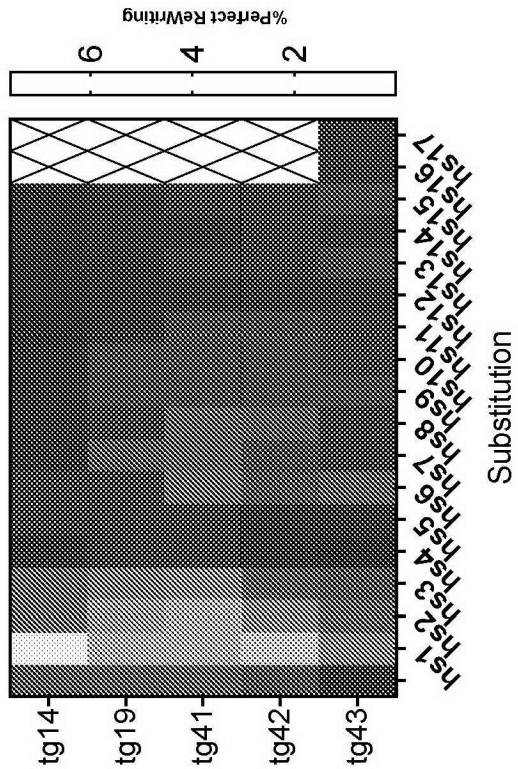


FIG. 19A

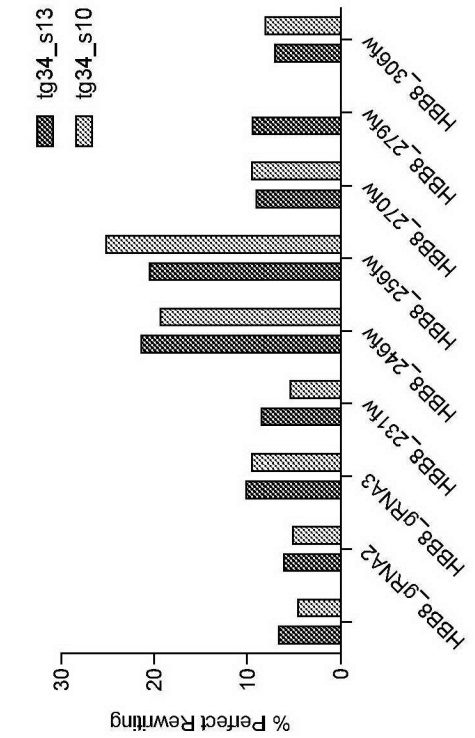


FIG. 20B

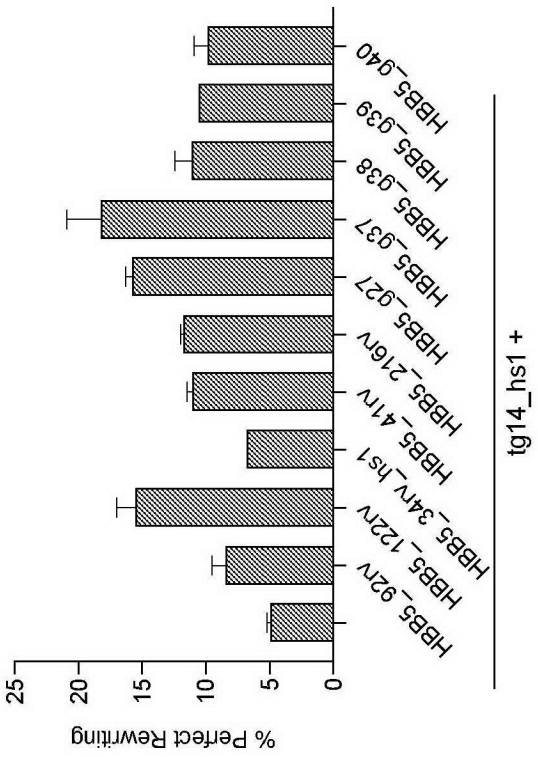


FIG. 20A

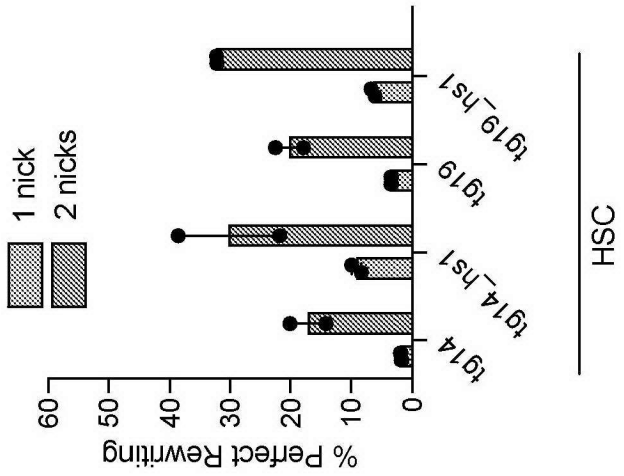

1 nick
2 nicks
% Perfect Rewriting
0
10
20
30
40
50
60
t914
t914_hs1
t919
t919_hs1
HSC

FIG. 20C

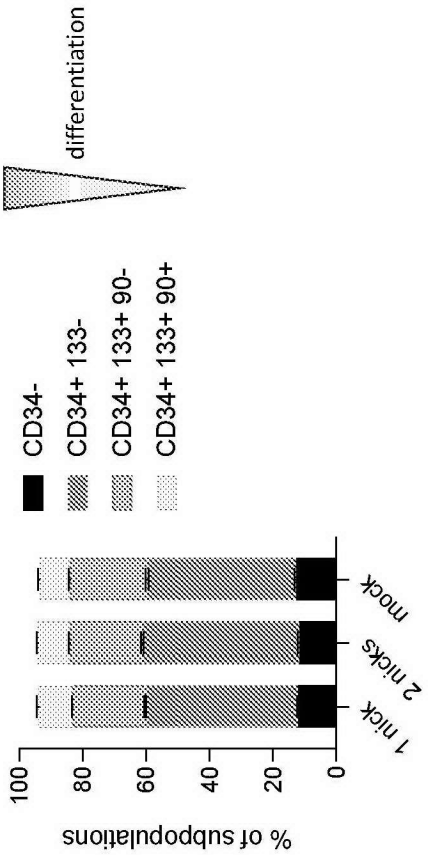


FIG. 21B

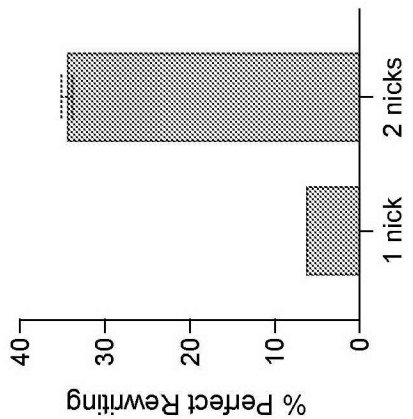


FIG. 21A

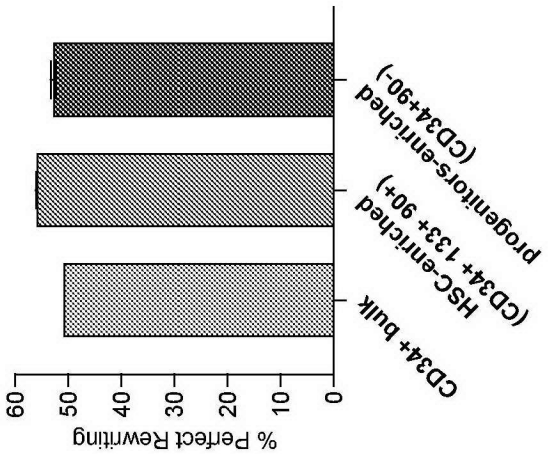


FIG. 22B

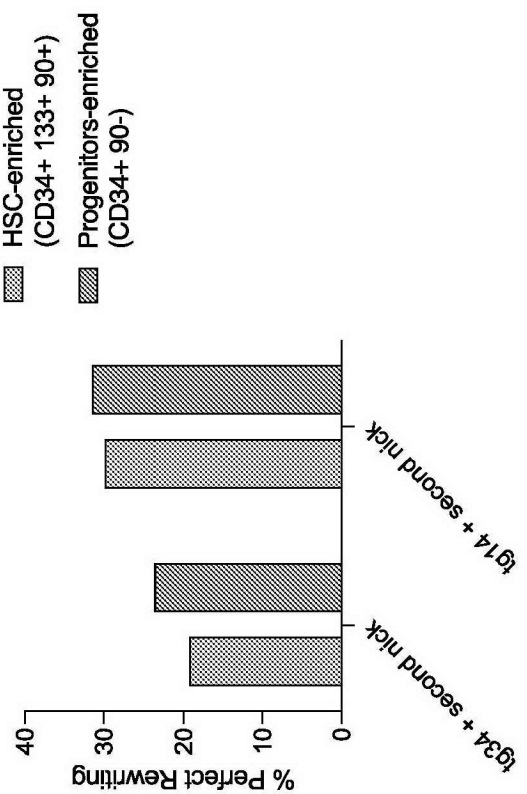


FIG. 22A

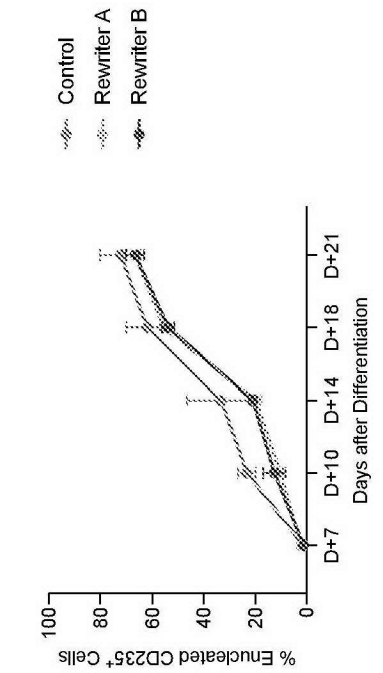


FIG. 23C

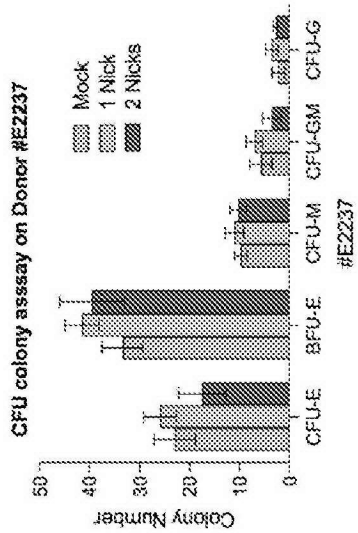


FIG. 23B

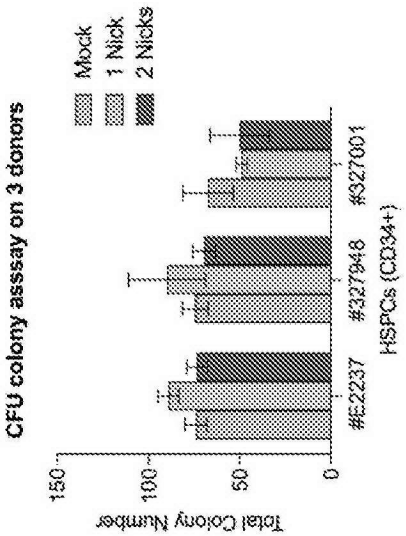


FIG. 23A