(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
06 February 2020 (06.02.2020)

WIPO | PCT

(10) International Publication Number
WO 2020/028751 A2

(51) International Patent Classification:
Not classified

(21) International Application Number:
PCT/US2019/044796

(22) International Filing Date:
02 August 2019 (02.08.2019)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
62/714,118 03 August 2018 (03.08.2018) US

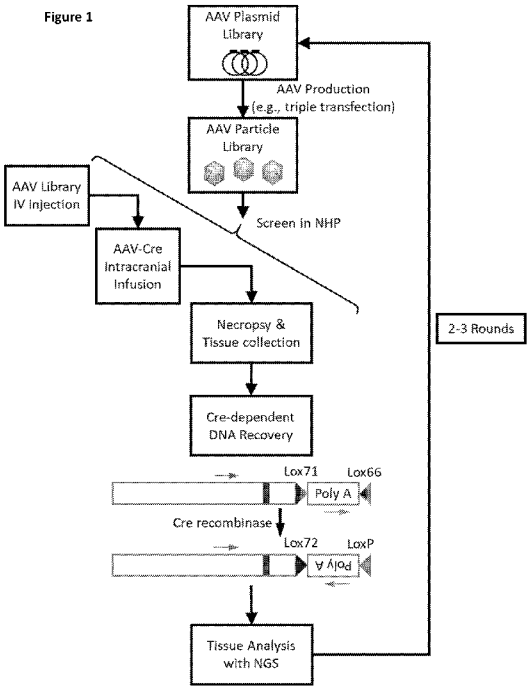
(71) Applicants: **VOYAGER THERAPEUTICS, INC.** [US/US]; 75 Sidney Street, Cambridge, Massachusetts 02139 (US). **CALIFORNIA INSTITUTE OF TECHNOLOGY** [US/US]; 1200 East California Boulevard, M/C 216-76, Pasadena, California 91125 (US).

(72) Inventors: **SAH, Dinah Wen-Yee**; c/o Voyager Therapeutics, Inc., 75 Sidney Street, Cambridge, Massachusetts 02139 (US). **HOU, Jinzhao**; c/o Voyager Therapeutics, Inc., 75 Sidney Street, Cambridge, Massachusetts 02139 (US). **ADACHI, Kei**; 3181 SW Sam Jackson Park Road, Portland, Oregon 97239 (US). **WANG, Wei**; c/o Voyager Therapeutics, Inc., 75 Sidney Street, Cambridge, Massachusetts 02139 (US). **CHEN, Qingmin**; 13 Francis Street, Belmont, Massachusetts 02478 (US). **CARROLL, Jenna**; 39 Nathaniel Road, Winchester, Massachusetts 01890 (US). **REN, Amy**; c/o Voyager Therapeutics, Inc., 75 Sidney Street, Cambridge, Massachusetts 02139 (US). **REN, Xiao-Qin**; c/o Voyager Therapeutics, Inc., 75 Sidney Street, Cambridge, Massachusetts 02139 (US). **DEVERMAN, Benjamin E.**; 211 Tremont St. Apt 1, Somerville, Massachusetts 02143 (US). **GRADINARU, Viviana**; c/o California Institute of Technology, 1200 East California Boulevard, M/C 216-76, Pasadena, California 91125 (US). **HUANG, Qin**; 7 Alfred Road, Arlington, Massachusetts 02474 (US).

(74) Agent: **WARD, Donna T.** et al.; DT Ward, PC, 142A Main Street, Groton, Massachusetts 01450 (US).

(81) Designated States *(unless otherwise indicated, for every kind of national protection available)*: AE, AG, AL, AM, AO, AT, AU, AZ, BA, BB, BG, BH, BN, BR, BW, BY, BZ, CA, CH, CL, CN, CO, CR, CU, CZ, DE, DJ, DK, DM, DO, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IR, IS, JO, JP, KE, KG, KH, KN, KP, KR, KW, KZ, LA, LC, LK, LR, LS, LU, LY, MA, MD, ME, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PA, PE, PG, PH, PL, PT, QA, RO, RS, RU, RW, SA,

(54) Title: AAV VARIANTS WITH ENHANCED TROPISM



(57) Abstract: The disclosure relates to compositions, methods, and processes for the preparation, use, and/or formulation of adeno-associated virus capsid proteins, wherein the capsid proteins comprise targeting peptide inserts for enhanced tropism to a target tissue.

WO 2020/028751 A2

[Continued on next page]

SC, SD, SE, SG, SK, SL, SM, ST, SV, SY, TH, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, ZA, ZM, ZW.

(84) **Designated States** *(unless otherwise indicated, for every kind of regional protection available)*: ARIPO (BW, GH, GM, KE, LR, LS, MW, MZ, NA, RW, SD, SL, ST, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, RU, TJ, TM), European (AL, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HR, HU, IE, IS, IT, LT, LU, LV, MC, MK, MT, NL, NO, PL, PT, RO, RS, SE, SI, SK, SM, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, KM, ML, MR, NE, SN, TD, TG).

Published:

— *without international search report and to be republished upon receipt of that report (Rule 48.2(g))*

— *with sequence listing part of description (Rule 5.2(a))*

AAV VARIANTS WITH ENHANCED TROPISM

CROSS REFERENCE TO RELATED APPLICATIONS

[0001] This application claims the benefit of U.S. Provisional Patent Application No. 62/714,118, filed August 3, 2018, entitled, "AAV VARIANTS WITH ENHANCED TROPISM", the contents of which are herein incorporated by reference in their entirety.

SEQUENCE LISTING

[0002] The instant application contains a Sequence Listing which has been filed electronically in ASCII format and is hereby incorporated by reference in its entirety. Said ASCII copy, created on August 1, 2019, is named 2057_1031PCTSL.txt and is 10,962,788 bytes in size.

FIELD OF THE DISCLOSURE

[0003] The disclosure relates to compositions, methods, and processes for the preparation, use, and/or formulation of adeno-associated virus capsid proteins, wherein the capsid proteins comprise targeting peptide inserts for enhanced tropism to a target tissue.

BACKGROUND OF THE DISCLOSURE

[0004] Recombinant adeno-associated viral vectors (AAV) have proven to be a useful biological tool and are increasingly showing promise in the field of gene therapy for the treatment of human disease.

[0005] AAV-based therapies are currently being tested for the treatment of a wide-range of human disease. In some cases, the AAV-based therapy may be brought easily into contact with the system in need, such as for treating diseases of the blood (e.g, lipoprotein lipase deficiency or hemophilias), the eye (e.g., Leber's congenital amaurosis or inherited retinal diseases), or muscle (e.g., Duchenne muscular dystrophy). In other cases, such as, for example, in treating disorders of the central nervous systems (CNS; i.e., brain and spinal cord), delivery of the AAV-based therapy becomes more complicated. Direct administration generally involves invasive surgeries, while the blood brain barrier impedes access of the AAV-based therapy to the CNS if administered systemically. Further, high doses of AAV-based therapies are necessary to yield sufficient transduction of target CNS tissue, giving rise to enhanced risk of side effects and/or production difficulties given the high volumes needed.

[0006] Though the peripheral nervous system (PNS; i.e., nervous tissue outside the brain and spinal cord) may be thought of as more accessible for therapeutic intervention, some PNS tissues, such as dorsal root ganglia remain difficult to target.

[0007] To identify AAV capsid proteins with desired tropism profiles, libraries of novel capsids have been created and screened. A variety of capsid engineering methods have been used, including DNA barcoding, directed evolution, random peptide insertions, and capsid shuffling and/or chimeras. In one such method known as CREATE, a series of targeting peptides was identified that enhanced the AAV capsid protein tropism for CNS tissues. The majority of this work has been carried out in mouse models, meaning that there still remains an issue of translatability to human subjects and conditions.

[0008] Even though such ongoing efforts to generate AAV capsids with enhanced tropism to CNS tissues and/or blood brain barrier permeability have yielded improvements, a need still exists for AAV particles with enhanced tropism for CNS or PNS tissue for the use of treating human disease. Even more so, a need exists for AAV particles with enhanced tropism for CNS or PNS tissues, which may be delivered intravenously to a subject in need, at a low dose, and yet still provide sufficient transduction of the target cell-type, tissue and/or organ.

[0009] The present disclosure addresses this need by providing novel targeting peptides and associated AAV capsid proteins and AAV particles for enhanced tropism to the human CNS or PNS following intravenous delivery. In addition, the viral genomes of these AAV particles may be manipulated to suit the needs of a wide variety of CNS or PNS-associated disorders, or neurological disease.

SUMMARY OF THE DISCLOSURE

[0010] In one aspect, the disclosure provides peptides (targeting peptides) with amino acid sequences set forth as any of SEQ ID NO: 4-14326 or SEQ ID NO: 42973-42999. Nucleic acid sequences encoding these peptides are also provided and are set forth as any of SEQ ID NO: 14327-42972 or SEQ ID NO: 4300-43053.

[0011] In one aspect, targeting sequences may be inserted into a parent sequence, for example, a targeting peptide may be inserted into a parent AAV capsid protein comprising a VP1 amino acid sequence set forth as SEQ ID NO: 2 or SEQ ID NO: 3. The parent VP1 amino acid sequence may comprise a VP2 region and/or a VP3 region. Targeting peptides may be inserted into the parent sequence in any of the VP1, VP2, or VP3 regions.

[0012] In one aspect, a targeting peptide may be inserted at any amino acid position between amino acids 586-592, inclusive, of the parent VP1 amino acid sequence.

[0013] In one aspect, a targeting peptide may be inserted between amino acids 588-589 of the parent amino acid sequence.

[0014] In one aspect, the disclosure provides AAV particles comprising an AAV capsid protein with a targeting sequence insert and a viral genome. The viral genome comprises a nucleic acid sequence encoding a payload, wherein the payload may be an RNAi agent or a polypeptide.

[0015] In one aspect, the AAV particles of the disclosure comprise a viral genome encoding an RNAi agent payload. The RNAi agent may be, but is not limited to, a dsRNA, siRNA, shRNA, pre-miRNA, pri-miRNA, miRNA, stRNA, lncRNA, piRNA, or snoRNA. When the RNAi agent is expressed, it inhibits or suppresses the expression of a gene of interest in a cell, wherein the gene of interest may be, but is not limited to, SOD1, MAPT, APOE, HTT, C9ORF72, TDP-43, APP, BACE, SNCA, ATXN1, ATXN2, ATXN3, ATXN7, SCN1A-SCN5A, or SCN8A-SCN11A.

[0016] In one aspect, the AAV particles of the disclosure comprise a viral genome encoding a polypeptide payload. The polypeptide may be, but is not limited to, an antibody, aromatic L-amino acid decarboxylase (AADC), survival motor neuron 1 (SMN1), frataxin (FXN), ApoE2, GBA1, GRN, ASPA, CLN2, GLB1, SGSH, NAGLU, IDS, NPC1, or GAN.

[0017] In one aspect, the AAV particles of the disclosure may be formulated with a pharmaceutically acceptable excipient to prepare a pharmaceutical composition. The pharmaceutical composition may be administered to a subject in need in order to treat a disease in said subject. The disease may be, but is not limited to, Huntington's Disease, Amyotrophic Lateral Sclerosis, Friedreich's Ataxia, Parkinson's Disease, Alzheimer's Disease, a tauopathy or neuropathic pain.

BRIEF DESCRIPTION OF THE FIGURES

[0018] The foregoing and other objects, features and advantages will be apparent from the following description of particular embodiments of the present disclosure, as illustrated in the accompanying figures. The figures are not necessarily to scale or comprehensive, with emphasis instead being placed upon illustrating the principles of various embodiments of the present disclosure.

[0019] Figure 1 shows a schematic for a non-limiting example of the CREATE method in non-human primate.

DETAILED DESCRIPTION

[0020] The details of one or more embodiments of the disclosure are set forth in the accompanying description below. Although any materials and methods similar or equivalent to those described herein can be used in the practice or testing of the content described herein, the preferred materials and methods are now described. Other features, objects and

advantages of the disclosure will be apparent from the description. In the description, the singular forms also include the plural unless the context clearly dictates otherwise. Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this disclosure belongs. In the case of conflict, the present description will control.

I. INTRODUCTION

[0021] According to the present disclosure, AAV particles with enhanced tropism for a target tissue (e.g., CNS) are provided, as well as associated processes for their targeting, preparation, formulation and use. Targeting peptides and nucleic acid sequences encoding the targeting peptides are provided. These targeting peptides may be inserted into an AAV capsid protein sequence to alter tropism to a particular cell-type, tissue, organ or organism, *in vivo, ex vivo* or *in vitro.*

[0022] As used herein, an "AAV particle" or "AAV vector" comprises a capsid protein and a viral genome, wherein the viral genome comprises at least one payload region and at least one inverted terminal repeat (ITR). The AAV particle and/or its component capsid and viral genome may be engineered to alter tropism to a particular cell-type, tissue, organ or organism.

[0023] As used herein, "viral genome" or "vector genome" refers to the nucleic acid sequence(s) encapsulated in an AAV particle. A viral genome comprises a nucleic acid sequence with at least one payload region encoding a payload and at least one ITR.

[0024] As used herein, a "payload region" is any nucleic acid molecule which encodes one or more "payloads" of the disclosure. As non-limiting examples, a payload region may be a nucleic acid sequence encoding a payload comprising an RNAi agent or a polypeptide.

[0025] As used herein, a "targeting peptide" refers to a peptide of 3-20 amino acids in length. These targeting peptides may be inserted into, or attached to, a parent amino acid sequence to alter the characteristics (e.g., tropism) of the parent protein. As a non-limiting example, the targeting peptide can be inserted into an AAV capsid sequence for enhanced targeting to a desired cell-type, tissue, organ or organism.

The AAV particles and payloads of the disclosure may be delivered to one or more target cells, tissues, organs, or organisms. In a preferred embodiment, the AAV particles of the disclosure demonstrate enhanced tropism for a target cell type, tissue or organ. As a non-limiting example, the AAV particle may have enhanced tropism for cells and tissues of the central or peripheral nervous systems (CNS and PNS, respectively). The AAV particles of

the disclosure may, in addition, or alternatively, have decreased tropism for an undesired target cell-type, tissue or organ.

II. COMPOSITIONS OF THE DISCLOSURE

[0026] Adeno-associated viruses (AAV) are small non-enveloped icosahedral capsid viruses of the Parvoviridae family characterized by a single stranded DNA viral genome. Parvoviridae family viruses consist of two subfamilies: Parvovirinae, which infect vertebrates, and Densovirinae, which infect invertebrates. The Parvoviridae family comprises the Dependovirus genus which includes AAV, capable of replication in vertebrate hosts including, but not limited to, human, primate, bovine, canine, equine, and ovine species.

[0027] The parvoviruses and other members of the Parvoviridae family are generally described in Kenneth I. Berns, "Parvoviridae: The Viruses and Their Replication," Chapter 69 in FIELDS VIROLOGY (3d Ed. 1996), the contents of which are incorporated by reference in their entirety.

[0028] AAV have proven to be useful as a biological tool due to their relatively simple structure, their ability to infect a wide range of cells (including quiescent and dividing cells) without integration into the host genome and without replicating, and their relatively benign immunogenic profile. The genome of the virus may be manipulated to contain a minimum of components for the assembly of a functional recombinant virus, or viral particle, which is loaded with or engineered to target a particular tissue and express or deliver a desired payload.

[0029] The wild-type AAV vector genome is a linear, single-stranded DNA (ssDNA) molecule approximately 5,000 nucleotides (nt) in length. Inverted terminal repeats (ITRs) traditionally cap the viral genome at both the 5' and the 3' end, providing origins of replication for the viral genome. While not wishing to be bound by theory, an AAV viral genome typically comprises two ITR sequences. These ITRs have a characteristic T-shaped hairpin structure defined by a self-complementary region (145nt in wild-type AAV) at the 5' and 3' ends of the ssDNA which form an energetically stable double stranded region. The double stranded hairpin structures comprise multiple functions including, but not limited to, acting as an origin for DNA replication by functioning as primers for the endogenous DNA polymerase complex of the host viral replication cell.

[0030] The wild-type AAV viral genome further comprises nucleotide sequences for two open reading frames, one for the four non-structural Rep proteins (Rep78, Rep68, Rep52, Rep40, encoded by Rep genes) and one for the three capsid, or structural, proteins (VP1, VP2, VP3, encoded by capsid genes or Cap genes). The Rep proteins are important for

replication and packaging, while the capsid proteins are assembled to create the protein shell of the AAV, or AAV capsid. Alternative splicing and alternate initiation codons and promoters result in the generation of four different Rep proteins from a single open reading frame and the generation of three capsid proteins from a single open reading frame. Though it varies by AAV serotype, as a non-limiting example, for AAV9/hu.14 (SEQ ID NO: 123 of US 7,906,111, the contents of which are herein incorporated by reference in their entirety) VP1 refers to amino acids 1-736, VP2 refers to amino acids 138-736, and VP3 refers to amino acids 203-736. In other words, VP1 is the full length capsid sequence, while VP2 and VP3 are shorter components of the whole. As a result, changes in the sequence in the VP3 region, are also changes to VP1 and VP2, however, the percent difference as compared to the parent sequence will be greatest for VP3 since it is the shortest sequence of the three. Though described here in relation to the amino acid sequence, the nucleic acid sequence encoding these proteins can be similarly described. Together, the three capsid proteins assemble to create the AAV capsid protein. While not wishing to be bound by theory, the AAV capsid protein typically comprises a molar ratio of 1:1:10 of VP1:VP2:VP3. As used herein, an "AAV serotype" is defined primarily by the AAV capsid. In some instances, the ITRs are also specifically described by the AAV serotype (e.g., AAV2/9).

[0031] For use as a biological tool, the wild-type AAV viral genome can be modified to replace the rep/cap sequences with a nucleic acid sequence comprising a payload region with at least one ITR region. Typically, in recombinant AAV viral genomes there are two ITR regions. The rep/cap sequences can be provided *in trans* during production to generate AAV particles.

[0032] In addition to the encoded heterologous payload, AAV vectors may comprise the viral genome, in whole or in part, of any naturally occurring and/or recombinant AAV serotype nucleotide sequence or variant. AAV variants may have sequences of significant homology at the nucleic acid (genome or capsid) and amino acid levels (capsids), to produce constructs which are generally physical and functional equivalents, replicate by similar mechanisms, and assemble by similar mechanisms. Chiorini et al., J. Vir. 71: 6823-33(1997); Srivastava et al., J. Vir. 45:555-64 (1983); Chiorini et al., J. Vir. 73:1309-1319 (1999); Rutledge et al., J. Vir. 72:309-319 (1998); and Wu et al., J. Vir. 74: 8635-47 (2000), the contents of each of which are incorporated herein by reference in their entirety.

[0033] In certain embodiments, AAV particles of the present disclosure are recombinant AAV viral vectors which are replication defective and lacking sequences encoding functional Rep and Cap proteins within their viral genome. These defective AAV vectors may lack

most or all parental coding sequences and essentially carry only one or two AAV ITR sequences and the nucleic acid of interest for delivery to a cell, a tissue, an organ, or an organism.

[0034] In certain embodiments, the viral genome of the AAV particles of the present disclosure comprises at least one control element which provides for the replication, transcription, and translation of a coding sequence encoded therein. Not all of the control elements need always be present as long as the coding sequence is capable of being replicated, transcribed, and/or translated in an appropriate host cell. Non-limiting examples of expression control elements include sequences for transcription initiation and/or termination, promoter and/or enhancer sequences, efficient RNA processing signals such as splicing and polyadenylation signals, sequences that stabilize cytoplasmic mRNA, sequences that enhance translation efficacy (e.g., Kozak consensus sequence), sequences that enhance protein stability, and/or sequences that enhance protein processing and/or secretion.

[0035] According to the present disclosure, AAV particles for use in therapeutics and/or diagnostics comprise a virus that has been distilled or reduced to the minimum components necessary for transduction of a nucleic acid payload or cargo of interest. In this manner, AAV particles are engineered as vehicles for specific delivery while lacking the deleterious replication and/or integration features found in wild-type viruses.

[0036] AAV vectors of the present disclosure may be produced recombinantly and may be based on adeno-associated virus (AAV) parent or reference sequences. As used herein, a "vector" is any molecule or moiety which transports, transduces, or otherwise acts as a carrier of a heterologous molecule such as the nucleic acids described herein.

[0037] In addition to single stranded AAV viral genomes (e.g., ssAAVs), the present invention also provides for self-complementary AAV (scAAVs) viral genomes. scAAV vector genomes contain DNA strands which anneal together to form double stranded DNA. By skipping second strand synthesis, scAAVs allow for rapid expression in the transduced cell.

[0038] In certain embodiments, the AAV particle of the present disclosure is an scAAV.

[0039] In certain embodiments, the AAV particle of the present disclosure is an ssAAV.

[0040] Methods for producing and/or modifying AAV particles are disclosed in the art such as pseudotyped AAV vectors (PCT Patent Publication Nos. WO200028004; WO200123001; WO2004112727; WO2005005610; and WO2005072364, the content of each of which is incorporated herein by reference in its entirety).

[0041] AAV particles may be modified to enhance the efficiency of delivery. Such modified AAV particles can be packaged efficiently and be used to successfully infect the target cells at high frequency and with minimal toxicity. In some embodiments, the capsids of the AAV particles are engineered according to the methods described in US Publication Number US20130195801, the contents of which are incorporated herein by reference in their entirety.

[0042] In certain embodiments, the AAV particles of the disclosure comprising a capsid with an inserted targeting peptide and a viral genome, may have enhanced tropism for a cell-type or tissue of the human CNS.

AAV Capsids

[0043] AAV particles of the present disclosure may comprise or be derived from any natural or recombinant AAV serotype. AAV serotypes may differ in characteristics such as, but not limited to, packaging, tropism, transduction and immunogenic profiles. While not wishing to be bound by theory, the AAV capsid protein is often considered to be the driver of AAV particle tropism to a particular tissue.

[0044] In certain embodiments, an AAV particle may have a capsid protein and ITR sequences derived from the same parent serotype (e.g., AAV2 capsid and AAV2 ITRs). In another embodiment, the AAV particle may be a pseudo-typed AAV particle, wherein the capsid protein and ITR sequences are derived from different parent serotypes (e.g., AAV9 capsid and AAV2 ITRs; AAV2/9).

[0045] The AAV particles of the present disclosure may comprise an AAV capsid protein with a targeting peptide inserted into the parent sequence. The parent capsid or serotype may comprise or be derived from any natural or recombinant AAV serotype. As used herein, a "parent" sequence is a nucleotide or amino acid sequence into which a targeting sequence is inserted (i.e., nucleotide insertion into nucleic acid sequence or amino acid sequence insertion into amino acid sequence).

[0046] In a preferred embodiment, the parent AAV capsid nucleotide sequence is as set forth in SEQ ID NO: 1.

[0047] In another embodiment, the parent AAV capsid nucleotide sequence is a K449R variant of SEQ ID NO: 1, wherein the codon encoding a lysine (e.g., AAA or AAG) at position 449 in the amino acid sequence (nucleotides 1345-1347) is exchanged for one encoding an arginine (CGT, CGC, CGA, CGG, AGA, AGG). The K449R variant has the same function as wild-type AAV9.

[0048] In a preferred embodiment, the parent AAV capsid amino acid sequence is as set forth in SEQ ID NO: 2.

[0049] In another embodiment, the parent AAV capsid amino acid sequence is as set forth in SEQ ID NO: 3.

[0050] In certain embodiments the parent AAV capsid sequence is any of those shown in Table 1.

Table 1. AAV Capsid Sequences

Serotype	SEQ ID NO	Reference Information
AAV9/hu.14 (nt)	1	US7906111 SEQ ID NO: 3; WO2015038958 SEQ ID NO: 11
AAV9/hu.14 (aa)	2	US7906111 SEQ ID NO: 123; WO2015038958 SEQ ID NO: 2
AAV9/hu.14 K449R (aa)	3	WO2017100671 SEQ ID NO: 45

[0051] Each of the patents, applications and or publications listed in Table 1 are hereby incorporated by reference in their entirety.

[0052] The parent AAV serotype and associated capsid sequence may be any of those known in the art. Non-limiting examples of such AAV serotypes include, AAV9, AAV9 K449R (or K449R AAV9), AAV1, AAVrh10, AAV-DJ, AAV-DJ8, AAV5, AAVPHP.B (PHP.B), AAVPHP.A (PHP.A), AAVG2B-26, AAVG2B-13, AAVTH1.1-32, AAVTH1.1-35, AAVPHP.B2 (PHP.B2), AAVPHP.B3 (PHP.B3), AAVPHP.N/PHP.B-DGT, AAVPHP.B-EST, AAVPHP.B-GGT, AAVPHP.B-ATP, AAVPHP.B-ATT-T, AAVPHP.B-DGT-T, AAVPHP.B-GGT-T, AAVPHP.B-SGS, AAVPHP.B-AQP, AAVPHP.B-QQP, AAVPHP.B-SNP(3), AAVPHP.B-SNP, AAVPHP.B-QGT, AAVPHP.B-NQT, AAVPHP.B-EGS, AAVPHP.B-SGN, AAVPHP.B-EGT, AAVPHP.B-DST, AAVPHP.B-DST, AAVPHP.B-STP, AAVPHP.B-PQP, AAVPHP.B-SQP, AAVPHP.B-QLP, AAVPHP.B-TMP, AAVPHP.B-TTP, AAVPHP.S/G2A12, AAVG2A15/G2A3 (G2A3), AAVG2B4 (G2B4), AAVG2B5 (G2B5), PHP.S, AAV2, AAV2G9, AAV3, AAV3a, AAV3b, AAV3-3, AAV4, AAV4-4, AAV6, AAV6.1, AAV6.2, AAV6.1.2, AAV7, AAV7.2, AAV8, AAV9.11, AAV9.13, AAV9.16, AAV9.24, AAV9.45, AAV9.47, AAV9.61, AAV9.68, AAV9.84, AAV9.9, AAV10, AAV11, AAV12, AAV16.3, AAV24.1, AAV27.3, AAV42.12, AAV42-1b, AAV42-2, AAV42-3a, AAV42-3b, AAV42-4, AAV42-5a, AAV42-5b, AAV42-6b, AAV42-8, AAV42-10, AAV42-11, AAV42-12, AAV42-13, AAV42-15, AAV42-aa, AAV43-1, AAV43-12, AAV43-20, AAV43-21, AAV43-23, AAV43-25, AAV43-5, AAV44.1, AAV44.2, AAV44.5, AAV223.1, AAV223.2, AAV223.4, AAV223.5, AAV223.6, AAV223.7, AAV1-7/rh.48, AAV1-8/rh.49, AAV2-15/rh.62, AAV2-3/rh.61, AAV2-4/rh.50,

AAV2-5/rh.51, AAV3.1/hu.6, AAV3.1/hu.9, AAV3-9/rh.52, AAV3-11/rh.53, AAV4-8/r11.64, AAV4-9/rh.54, AAV4-19/rh.55, AAV5-3/rh.57, AAV5-22/rh.58, AAV7.3/hu.7, AAV16.8/hu.10, AAV16.12/hu.11, AAV29.3/bb.1, AAV29.5/bb.2, AAV106.1/hu.37, AAV114.3/hu.40, AAV127.2/hu.41, AAV127.5/hu.42, AAV128.3/hu.44, AAV130.4/hu.48, AAV145.1/hu.53, AAV145.5/hu.54, AAV145.6/hu.55, AAV161.10/hu.60, AAV161.6/hu.61, AAV33.12/hu.17, AAV33.4/hu.15, AAV33.8/hu.16, AAV52/hu.19, AAV52.1/hu.20, AAV58.2/hu.25, AAVA3.3, AAVA3.4, AAVA3.5, AAVA3.7, AAVC1, AAVC2, AAVC5, AAVF3, AAVF5, AAVH2, AAVrh.72, AAVhu.8, AAVrh.68, AAVrh.70, AAVpi.1, AAVpi.3, AAVpi.2, AAVrh.60, AAVrh.44, AAVrh.65, AAVrh.55, AAVrh.47, AAVrh.69, AAVrh.45, AAVrh.59, AAVhu.12, AAVH6, AAVH-1/hu.1, AAVH-5/hu.3, AAVLG-10/rh.40, AAVLG-4/rh.38, AAVLG-9/hu.39, AAVN721-8/rh.43, AAVCh.5, AAVCh.5R1, AAVcy.2, AAVcy.3, AAVcy.4, AAVcy.5, AAVCy.5R1, AAVCy.5R2, AAVCy.5R3, AAVCy.5R4, AAVcy.6, AAVhu.1, AAVhu.2, AAVhu.3, AAVhu.4, AAVhu.5, AAVhu.6, AAVhu.7, AAVhu.9, AAVhu.10, AAVhu.11, AAVhu.13, AAVhu.15, AAVhu.16, AAVhu.17, AAVhu.18, AAVhu.20, AAVhu.21, AAVhu.22, AAVhu.23.2, AAVhu.24, AAVhu.25, AAVhu.27, AAVhu.28, AAVhu.29, AAVhu.29R, AAVhu.31, AAVhu.32, AAVhu.34, AAVhu.35, AAVhu.37, AAVhu.39, AAVhu.40, AAVhu.41, AAVhu.42, AAVhu.43, AAVhu.44, AAVhu.44R1, AAVhu.44R2, AAVhu.44R3, AAVhu.45, AAVhu.46, AAVhu.47, AAVhu.48, AAVhu.48R1, AAVhu.48R2, AAVhu.48R3, AAVhu.49, AAVhu.51, AAVhu.52, AAVhu.54, AAVhu.55, AAVhu.56, AAVhu.57, AAVhu.58, AAVhu.60, AAVhu.61, AAVhu.63, AAVhu.64, AAVhu.66, AAVhu.67, AAVhu.14/9, AAVhu.t 19, AAVrh.2, AAVrh.2R, AAVrh.8, AAVrh.8R, AAVrh.10, AAVrh.12, AAVrh.13, AAVrh.13R, AAVrh.14, AAVrh.17, AAVrh.18, AAVrh.19, AAVrh.20, AAVrh.21, AAVrh.22, AAVrh.23, AAVrh.24, AAVrh.25, AAVrh.31, AAVrh.32, AAVrh.33, AAVrh.34, AAVrh.35, AAVrh.36, AAVrh.37, AAVrh.37R2, AAVrh.38, AAVrh.39, AAVrh.40, AAVrh.46, AAVrh.48, AAVrh.48.1, AAVrh.48.1.2, AAVrh.48.2, AAVrh.49, AAVrh.51, AAVrh.52, AAVrh.53, AAVrh.54, AAVrh.56, AAVrh.57, AAVrh.58, AAVrh.61, AAVrh.64, AAVrh.64R1, AAVrh.64R2, AAVrh.67, AAVrh.73, AAVrh.74, AAVrh8R, AAVrh8R A586R mutant, AAVrh8R R533A mutant, AAAV, BAAV, caprine AAV, bovine AAV, AAVhE1.1, AAVhEr1.5, AAVhER1.14, AAVhEr1.8, AAVhEr1.16, AAVhEr1.18, AAVhEr1.35, AAVhEr1.7, AAVhEr1.36, AAVhEr2.29, AAVhEr2.4, AAVhEr2.16, AAVhEr2.30, AAVhEr2.31, AAVhEr2.36, AAVhER1.23, AAVhEr3.1, AAV2.5T , AAV-PAEC, AAV-LK01, AAV-LK02, AAV-LK03, AAV-LK04, AAV-LK05, AAV-LK06, AAV-LK07, AAV-LK08, AAV-LK09, AAV-

LK10, AAV-LK11, AAV-LK12, AAV-LK13, AAV-LK14, AAV-LK15, AAV-LK16, AAV-LK17, AAV-LK18, AAV-LK19, AAV-PAEC2, AAV-PAEC4, AAV-PAEC6, AAV-PAEC7, AAV-PAEC8, AAV-PAEC11, AAV-PAEC12, AAV-2-pre-miRNA-101 , AAV-8h, AAV-8b, AAV-h, AAV-b, AAV SM 10-2 , AAV Shuffle 100-1 , AAV Shuffle 100-3, AAV Shuffle 100-7, AAV Shuffle 10-2, AAV Shuffle 10-6, AAV Shuffle 10-8, AAV Shuffle 100-2, AAV SM 10-1, AAV SM 10-8 , AAV SM 100-3, AAV SM 100-10, BNP61 AAV, BNP62 AAV, BNP63 AAV, AAVrh.50, AAVrh.43, AAVrh.62, AAVrh.48, AAVhu.19, AAVhu.11, AAVhu.53, AAV4-8/rh.64, AAVLG-9/hu.39, AAV54.5/hu.23, AAV54.2/hu.22, AAV54.7/hu.24, AAV54.1/hu.21, AAV54.4R/hu.27, AAV46.2/hu.28, AAV46.6/hu.29, AAV128.1/hu.43, true type AAV (ttAAV), UPENN AAV 10, Japanese AAV 10 serotypes, AAV CBr-7.1, AAV CBr-7.10, AAV CBr-7.2, AAV CBr-7.3, AAV CBr-7.4, AAV CBr-7.5, AAV CBr-7.7, AAV CBr-7.8, AAV CBr-B7.3, AAV CBr-B7.4, AAV CBr-E1, AAV CBr-E2, AAV CBr-E3, AAV CBr-E4, AAV CBr-E5, AAV CBr-e5, AAV CBr-E6, AAV CBr-E7, AAV CBr-E8, AAV CHt-1, AAV CHt-2, AAV CHt-3, AAV CHt-6.1, AAV CHt-6.10, AAV CHt-6.5, AAV CHt-6.6, AAV CHt-6.7, AAV CHt-6.8, AAV CHt-P1, AAV CHt-P2, AAV CHt-P5, AAV CHt-P6, AAV CHt-P8, AAV CHt-P9, AAV CKd-1, AAV CKd-10, AAV CKd-2, AAV CKd-3, AAV CKd-4, AAV CKd-6, AAV CKd-7, AAV CKd-8, AAV CKd-B1, AAV CKd-B2, AAV CKd-B3, AAV CKd-B4, AAV CKd-B5, AAV CKd-B6, AAV CKd-B7, AAV CKd-B8, AAV CKd-H1, AAV CKd-H2, AAV CKd-H3, AAV CKd-H4, AAV CKd-H5, AAV CKd-H6, AAV CKd-N3, AAV CKd-N4, AAV CKd-N9, AAV CLg-F1, AAV CLg-F2, AAV CLg-F3, AAV CLg-F4, AAV CLg-F5, AAV CLg-F6, AAV CLg-F7, AAV CLg-F8, AAV CLv-1, AAV CLv1-1, AAV Clv1-10, AAV CLv1-2, AAV CLv-12, AAV CLv1-3, AAV CLv-13, AAV CLv1-4, AAV Clv1-7, AAV Clv1-8, AAV Clv1-9, AAV CLv-2, AAV CLv-3, AAV CLv-4, AAV CLv-6, AAV CLv-8, AAV CLv-D1, AAV CLv-D2, AAV CLv-D3, AAV CLv-D4, AAV CLv-D5, AAV CLv-D6, AAV CLv-D7, AAV CLv-D8, AAV CLv-E1, AAV CLv-K1, AAV CLv-K3, AAV CLv-K6, AAV CLv-L4, AAV CLv-L5, AAV CLv-L6, AAV CLv-M1, AAV CLv-M11, AAV CLv-M2, AAV CLv-M5, AAV CLv-M6, AAV CLv-M7, AAV CLv-M8, AAV CLv-M9, AAV CLv-R1, AAV CLv-R2, AAV CLv-R3, AAV CLv-R4, AAV CLv-R5, AAV CLv-R6, AAV CLv-R7, AAV CLv-R8, AAV CLv-R9, AAV CSp-1, AAV CSp-10, AAV CSp-11, AAV CSp-2, AAV CSp-3, AAV CSp-4, AAV CSp-6, AAV CSp-7, AAV CSp-8, AAV CSp-8.10, AAV CSp-8.2, AAV CSp-8.4, AAV CSp-8.5, AAV CSp-8.6, AAV CSp-8.7, AAV CSp-8.8, AAV CSp-8.9, AAV CSp-9, AAV.hu.48R3, AAV.VR-355, AAV3B, AAV4, AAV5, AAVF1/HSC1, AAVF11/HSC11, AAVF12/HSC12, AAVF13/HSC13, AAVF14/HSC14, AAVF15/HSC15, AAVF16/HSC16,

AAVF17/HSC17, AAVF2/HSC2, AAVF3/HSC3, AAVF4/HSC4, AAVF5/HSC5, AAVF6/HSC6, AAVF7/HSC7, AAVF8/HSC8, and/or AAVF9/HSC9 and variants thereof.

[0053] In some embodiments, the serotype may be AAVDJ or a variant thereof, such as AAVDJ8 (or AAV-DJ8), as described by Grimm et al. (Journal of Virology 82(12): 5887-5911 (2008), US Publication US20140359799 and US Patent No. 7,588,772, each of which is herein incorporated by reference in its entirety). The amino acid sequence of AAVDJ8 may comprise two or more mutations in order to remove the heparin binding domain (HBD). As a non-limiting example, the AAV-DJ sequence is as described by SEQ ID NO: 1 in U.S. Patent No. 7,588,772, the contents of which are herein incorporated by reference in their entirety, and the AAVDJ8 sequence may comprise two mutations: (1) R587Q where arginine (R; Arg) at amino acid 587 is changed to glutamine (Q; Gln) and (2) R590T where arginine (R; Arg) at amino acid 590 is changed to threonine (T; Thr). As another non-limiting example, the AAVDJ8 sequence may comprise three mutations: (1) K406R where lysine (K; Lys) at amino acid 406 is changed to arginine (R; Arg), (2) R587Q where arginine (R; Arg) at amino acid 587 is changed to glutamine (Q; Gln) and (3) R590T where arginine (R; Arg) at amino acid 590 is changed to threonine (T; Thr).

[0054] In certain embodiments, the parent AAV capsid sequence comprises an AAV9 sequence.

[0055] In certain embodiments, the parent AAV capsid sequence comprises an K449R AAV9 sequence.

[0056] In certain embodiments, the parent AAV capsid sequence comprises an AAVDJ sequence.

[0057] In certain embodiments, the parent AAV capsid sequence comprises an AAVDJ8 sequence.

[0058] In certain embodiments, the parent AAV capsid sequence comprises an AAVrh10 sequence.

[0059] In certain embodiments, the parent AAV capsid sequence comprises an AAV1 sequence.

[0060] In certain embodiments, the parent AAV capsid sequence comprises an AAV5 sequence.

[0061] While not wishing to be bound by theory, it is understood that a parent AAV capsid sequence comprises a VP1 region. In certain embodiments, a parent AAV capsid sequence comprises a VP1, VP2 and/or VP3 region, or any combination thereof. A parent VP1 sequence may be considered synonymous with a parent AAV capsid sequence.

[0062] In certain embodiments, the initiation codon for translation of the AAV VP1 capsid protein may be CTG, TTG, or GTG as described in US Patent No. US8163543, the contents of which are herein incorporated by reference in their entirety.

[0063] The present disclosure refers to structural capsid proteins (including VP1, VP2 and VP3) which are encoded by capsid (Cap) genes. These capsid proteins form an outer protein structural shell (i.e. capsid) of a viral vector such as AAV. VP capsid proteins synthesized from Cap polynucleotides generally include a methionine as the first amino acid in the peptide sequence (Met1), which is associated with the start codon (AUG or ATG) in the corresponding Cap nucleotide sequence. However, it is common for a first-methionine (Met1) residue or generally any first amino acid (AA1) to be cleaved off after or during polypeptide synthesis by protein processing enzymes such as Met-aminopeptidases. This "Met/AA-clipping" process often correlates with a corresponding acetylation of the second amino acid in the polypeptide sequence (e.g., alanine, valine, serine, threonine, etc.). Met-clipping commonly occurs with VP1 and VP3 capsid proteins but can also occur with VP2 capsid proteins.

[0064] Where the Met/AA-clipping is incomplete, a mixture of one or more (one, two or three) VP capsid proteins comprising the viral capsid may be produced, some of which may include a Met1/AA1 amino acid (Met+/AA+) and some of which may lack a Met1/AA1 amino acid as a result of Met/AA-clipping (Met-/AA-). For further discussion regarding Met/AA-clipping in capsid proteins, see Jin, et al. Direct Liquid Chromatography/Mass Spectrometry Analysis for Complete Characterization of Recombinant Adeno-Associated Virus Capsid Proteins. *Hum Gene Ther Methods*. 2017 Oct. 28(5):255-267; Hwang, et al. N-Terminal Acetylation of Cellular Proteins Creates Specific Degradation Signals. *Science*. 2010 February 19. 327(5968): 973–977; the contents of which are each incorporated herein by reference in its entirety.

[0065] According to the present disclosure, references to capsid proteins is not limited to either clipped (Met-/AA-) or unclipped (Met+/AA+) and may, in context, refer to independent capsid proteins, viral capsids comprised of a mixture of capsid proteins, and/or polynucleotide sequences (or fragments thereof) which encode, describe, produce or result in capsid proteins of the present disclosure. A direct reference to a "capsid protein" or "capsid polypeptide" (such as VP1, VP2 or VP2) may also comprise VP capsid proteins which include a Met1/AA1 amino acid (Met+/AA+) as well as corresponding VP capsid proteins which lack the Met1/AA1 amino acid as a result of Met/AA-clipping (Met-/AA-).

[0066] Further according to the present disclosure, a reference to a specific SEQ ID NO: (whether a protein or nucleic acid) which comprises or encodes, respectively, one or more capsid proteins which include a Met1/AA1 amino acid (Met+/AA+) should be understood to teach the VP capsid proteins which lack the Met1/AA1 amino acid as upon review of the sequence, it is readily apparent any sequence which merely lacks the first listed amino acid (whether or not Met1/AA1).

[0067] As a non-limiting example, reference to a VP1 polypeptide sequence which is 736 amino acids in length and which includes a "Met1" amino acid (Met+) encoded by the AUG/ATG start codon may also be understood to teach a VP1 polypeptide sequence which is 735 amino acids in length and which does not include the "Met1" amino acid (Met-) of the 736 amino acid Met+ sequence.

[0068] As a second non-limiting example, reference to a VP1 polypeptide sequence which is 736 amino acids in length and which includes an "AA1" amino acid (AA1+) encoded by any NNN initiator codon may also be understood to teach a VP1 polypeptide sequence which is 735 amino acids in length and which does not include the "AA1" amino acid (AA1-) of the 736 amino acid AA1+ sequence.

[0069] References to viral capsids formed from VP capsid proteins (such as reference to specific AAV capsid serotypes), can incorporate VP capsid proteins which include a Met1/AA1 amino acid (Met+/AA1+), corresponding VP capsid proteins which lack the Met1/AA1 amino acid as a result of Met/AA1-clipping (Met-/AA1-), and combinations thereof (Met+/AA1+ and Met-/AA1-).

[0070] As a non-limiting example, an AAV capsid serotype can include VP1 (Met+/AA1+), VP1 (Met-/AA1-), or a combination of VP1 (Met+/AA1+) and VP1 (Met-/AA1-). An AAV capsid serotype can also include VP3 (Met+/AA1+), VP3 (Met-/AA1-), or a combination of VP3 (Met+/AA1+) and VP3 (Met-/AA1-); and can also include similar optional combinations of VP2 (Met+/AA1) and VP2 (Met-/AA1-).

[0071] In certain embodiments, the parent AAV capsid sequence may comprise an amino acid sequence with 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%, or 100% identity to any of the those described above.

[0072] In certain embodiments, the parent AAV capsid sequence may be encoded by a nucleotide sequence with 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%, or 100% identity to any of those described above.

[0073] In certain embodiments, the parent sequence is not an AAV capsid sequence and is instead a different vector (e.g., lentivirus, plasmid, etc). In another embodiment, the parent sequence is a delivery vehicle (e.g., a nanoparticle) and the targeting peptide is attached thereto.

Capsid Engineering

[0074] Recombinant or engineered AAV vectors have shown promise for use in therapy for the treatment of human disease. However, a need still exists for AAV particles with more specific and/or enhanced tropism for target tissues. Capsid engineering methods have been used to try to identify capsids with enhanced transduction of target tissues (e.g., brain, spinal cord, DRG). A variety of methods have been used, including mutational methods, DNA barcoding, directed evolution, random peptide insertions, and capsid shuffling and/or chimeras.

[0075] Rational engineering and mutational methods have been used to direct AAV to a target tissue. In rational design, structure-function relationships are used to determine regions in which changes to the capsid sequence may be made. As non-limiting examples, surface loop structures, receptor binding sites, and/or heparin binding sites may be mutated, or otherwise altered, for rational design of recombinant AAV capsids for enhanced targeting to a target tissue. In one example of rational design, AAV capsids were modified by mutation of surface exposed tyrosines to phenylalanine, in order to evade ubiquitination, reduce proteasomal degradation and allow for increased AAV particle and viral genome expression (Lochrie MA, et al, J Virol. 2006 Jan; 80(2):821-34; Santiago-Ortiz JL and Schaffer DV, J Control Release. 2016 Oct 28;240:287-301, the contents of each of which are incorporated by reference in their entirety). Rational design also encompasses the addition of targeting peptides to a parent AAV capsid sequence, wherein the targeting peptide may have an affinity for a receptor of interest within a target tissue.

[0076] In certain embodiments, rational engineering and/or mutational methods are used to identify AAV capsids and/or targeting peptides having enhanced transduction of a target tissue (e.g., CNS or PNS).

[0077] Capsid shuffling, and/or chimeras describe a method in which fragments of at least two parent AAV capsids are combined to generate a new recombinant capsid protein. The number of parent AAV capsids used may be 2-20, or more than 20.

[0078] In certain embodiments, capsid shuffling is used to identify AAV capsids and/or targeting peptides having enhanced transduction of a target tissue (e.g., CNS or PNS).

[0079] Directed evolution involves the generation of AAV capsid libraries (~10^4-10^8) by any of a variety of mutagenesis techniques and selection of lead candidates based on response to selective pressure by properties of interest (e.g., tropism). Directed evolution of AAV capsids allows for positive selection from a pool of diverse mutants without necessitating extensive prior characterization of the mutant library. Directed evolution libraries may be generated by any molecular biology technique known in the art, and may include, DNA shuffling, random point mutagenesis, insertional mutagenesis (e.g., targeting peptides), random peptide insertions, or ancestral reconstructions. AAV capsid libraries may be subjected to more than one round of selection using directed evolution for further optimization. Directed evolution methods are most commonly used to identify AAV capsid proteins with enhanced transduction of a target tissue. Capsids with enhanced transduction of a target tissue have been identified for the targeting human airway epithelium, neural stem cells, human pluripotent stem cells, retinal cells, and other *in vitro* and *in vivo* cells.

[0080] In certain embodiments directed evolution methods are used to identify AAV capsids and/or targeting peptides having enhanced transduction of a target tissue (e.g., CNS or PNS).

[0081] One method described for high-throughput characterization of the phenotypes of a large number of AAV serotypes is known as AAV Barcode-Seq (Adachi K et al, Nature Communications 5:3075 (2014), the contents of which are herein incorporated by reference in their entirety). In this next-generation sequence (NGS) based method, AAV libraries are created comprising DNA barcode tags, which can be assessed by multi-plexed Illumina barcode sequencing. This method can be used to identify AAV variants with altered receptor binding, tropism, neutralization and or blood clearance as compared to wild-type or non-variant sequences. Amino acids of the AAV capsid that are important to these functions can also be identified in this manner.

[0082] As described in Adachi et al 2014, AAV capsid libraries were generated, wherein each mutant carried a wild-type AAV2 *rep* gene and an AAV *cap* gene derived from a series of variants or mutants, and a pair of left and right 12-nucleotide long DNA bar-codes downstream of an AAV2 polyadenylation signal (pA). In this manner, 7 different DNA barcode AAV capsid libraries were generated. Capsid libraries were then provided to mice. At a pre-set timepoint, samples were collected, DNA extracted and PCR-amplified using AAV-clone specific virus bar codes and sample-specific bar code attached PCR primers. All

the virus barcode PCR amplicons were Illumina sequenced and converted to raw sequence read number data by a computational algorithm. The core of the Barcode-Seq approach is a 96-nucleotide cassette comprising the DNA bar-codes (left and right) described above, three PCR primer binding sites and two restriction enzyme sites. As an exemplar, an AAV rep-cap genome was used, but the system can be applied to any AAV viral genome, including one devoid of rep and cap genes. The advantage of the Barcode Seq method is the collection of a large data set and correlation to desirable phenotype with few replicates and in a short period of time.

[0083] The DNA Barcode Seq method can be similarly applied to RNA.

[0084] In certain embodiments, the Barcode Seq method is used to identify AAV capsids and/or targeting peptides having enhanced transduction of a target tissue (e.g., CNS or PNS).

[0085] One method used to generate AAV particles with desirable transduction profiles, with enhanced targeting to CNS or PNS tissues after intravenous administration, is through the use of insertion of targeting peptides into a parent AAV capsid sequence.

Targeting peptides

[0086] Disclosed herein are targeting peptides and associated AAV particles comprising a capsid protein with one or more targeting peptide inserts, for enhanced or improved transduction of a target tissue (e.g., cells of the CNS or PNS).

[0087] In certain embodiments, the targeting peptide may direct an AAV particle to a cell or tissue of the CNS. The cell of the CNS may be, but is not limited to, neurons (e.g., excitatory, inhibitory, motor, sensory, autonomic, sympathetic, parasympathetic, Purkinje, Betz, etc), glial cells (e.g., microglia, astrocytes, oligodendrocytes) and/or supporting cells of the brain such as immune cells (e.g., T cells). The tissue of the CNS may be, but is not limited to, the cortex (e.g, frontal, parietal, occipital, temporal), thalamus, hypothalamus, striatum, putamen, caudate nucleus, hippocampus, entorhinal cortex, basal ganglia, or deep cerebellar nuclei.

[0088] In certain embodiments, the targeting peptide may direct an AAV particle to a cell or tissue of the PNS. The cell or tissue of the PNS may be, but is not limited to, a dorsal root ganglion (DRG).

[0089] The targeting peptide may direct an AAV particle to the CNS (e.g., the cortex) after intravenous administration.

[0090] The targeting peptide may direct and AAV particle to the PNS (e.g., DRG) after intravenous administration.

[0091] A targeting peptide may vary in length. In certain embodiments, the targeting peptide is 3-20 amino acids in length. As non-limiting examples, the targeting peptide may be 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20 or 3-5, 3-8, 3-10, 3-12, 3-15, 3-18, 3-20, 5-10, 5-15, 5-20, 10-12, 10-15, 10-20, 12-20, or 15-20 amino acids in length.

[0092] Targeting peptides of the present disclosure may be identified and/or designed by any method known in the art. As a non-limiting example, the CREATE system as described in Deverman et al., (Nature Biotechnology 34(2):204-209 (2016)) and in International Patent Application Publication Nos. WO2015038958 and WO2017100671, the contents of each of which are herein incorporated by reference in their entirety, may be used as a means of identifying targeting peptides, in either mice or other research animals, such as, but not limited to, non-human primates.

[0093] Targeting peptides and associated AAV particles may be identified from libraries of AAV capsids comprised of targeting peptide variants. In certain embodiments, the targeting peptides may be 7 amino acid sequences (7-mers). In another embodiment, the targeting peptides may be 9 amino acid sequences (9-mers). The targeting peptides may also differ in their method of creation or design, with non-limiting examples including, random peptide selection, site saturation mutagenesis, and/or optimization of a particular region of the peptide (e.g., flanking regions or central core).

[0094] In certain embodiments, a targeting peptide library comprises targeting peptides of 7 amino acids (7-mer) in length randomly generated by PCR.

[0095] In certain embodiments, a targeting peptide library comprises targeting peptides with 3 mutated amino acids. In certain embodiments, these 3 mutated amino acids are consecutive amino acids. In another embodiment, these 3 mutated amino acids are not consecutive amino acids. In certain embodiments, the parent targeting peptide is a 7-mer. In another embodiment, the parent peptide is a 9-mer.

[0096] In certain embodiments, a targeting peptide library comprises 7-mer targeting peptides, wherein the amino acids of the targeting peptide and/or the flanking sequences are evolved through site saturation mutagenesis of 3 consecutive amino acids. In certain embodiments, NNK (N = any base; K = G or T) codons are used to generate the site saturated mutation sequences.

CREATE system in mice

[0097] In some embodiments, the AAV particles of the present disclosure are prepared via the CREATE system, as described in Deverman et al., (Nature Biotechnology 34(2):204-209 (2016)) and in International Patent Application Publication Nos. WO2015038958 and

WO2017100671, the contents of each of which are herein incorporated by reference in their entirety. "CREATE" or "Cre-recombinant-based AAV targeted evolution" refers to an AAV capsid selection strategy that selects for capsids that transduce target tissues (e.g, CNS or PNS) following intravenous injection. The method has been demonstrated in a mouse model.

[0098] Libraries of AAV capsids with one or more targeting peptide inserts are developed and administered intravenously to transgenic mice. These transgenic cre-expressing mice may be developed for specific targeting, for example, GFAP-Cre mice may be used for targeting to astrocytes.

[0099] Variation of the targeting sequence as well as the transgenic animal model enables the selection of AAV variants with desired transduction profiles, for example, tropism to neurons or astrocytes, as compared to other AAV serotypes, including the parent AAV particle and capsid.

[0100] The CREATE method involves the generation of a library of targeting peptides which are then assembled into a viral genome backbone comprising a parent AAV capsid sequence. An AAV capsid library (AAV particles) is then generated, purified and administered to a transgenic animal (e.g., mouse). Target tissue is collected and AAV sequences selectively recovered from Cre expressing cells. These sequences are assessed and characterized for the identification of targeting peptides that lead to enrichment in a target tissue (i.e., enhanced transduction or tropism). Targeting peptides and associated AAV particles can then be generated for further testing and characterization. This process is considered one round of evolution or selection. In some embodiments, more than one round of evolution is conducted. As many as 15 rounds of selection may be conducted.

[0101] In more detail, the CREATE system uses a rAAV-Cap-in-cis-lox viral genome comprising AAV *cap* and regulator elements of the AAV *rep* genes and a Cre-invertible switch. Since this viral genome lacks a fully functioning *rep* gene necessary for AAV particle production, the *rep* is provided in *trans*. A modified AAV2/9 Rep-Cap plasmid may be provided, wherein stop-codons are provided in-frame to prevent the expression of VP1-VP3 proteins.

[0102] Capsid libraries are generated using the rAAV-Cap-in-cis-lox viral genome as a backbone. Targeting peptides are inserted into the parent AAV capsid protein (e.g., AAV9) at any position that results in the generation of a fully functional AAV capsid protein and AAV particle. As an exemplar, targeting peptides comprising 7 random amino acids were inserted between amino acids 588 and 589 of the VP1 sequence of K449R AAV9. Targeting

peptides may be designed by any method known in the art. In certain embodiments, targeting peptides are generated using polymerase chain reaction (PCR).

[0103] AAV particles comprising capsid proteins with targeting peptide inserts are generated and viral genomes encoding a reporter (e.g., GFP) encapsulated within. These AAV particles (or AAV capsid library) are then administered to a transgenic mouse by intravenous delivery to the tail vein. Administration of these capsid libraries to cre-expressing mice results in expression of the reporter payload in the target tissue, due to the expression of Cre.

[0104] AAV particles and/or viral genomes may be recovered from the target tissue for identification of targeting peptides and associated AAV particles that are enriched, indicating enhanced transduction of target tissue. Standard methods in the art, such as, but not limited to next generation sequencing (NGS), viral genome quantification, biochemical assays, immunohistochemistry and/or imaging of target tissue samples may be used to determine enrichment.

[0105] A target tissue may be any cell, tissue or organ of a subject. As non-limiting examples, samples may be collected from brain, spinal cord, dorsal root ganglia and associated roots, liver, heart, gastrocnemius muscle, soleus muscle, pancreas, kidney, spleen, lung, adrenal glands, stomach, sciatic nerve, saphenous nerve, thyroid gland, eyes (with or without optic nerve), pituitary gland, skeletal muscle (rectus femoris), colon, duodenum, ileum, jejunum, skin of the leg, superior cervical ganglia, urinary bladder, ovaries, uterus, prostate gland, testes, and/or any sites identified as having a lesion, or being of interest.

[0106] Targeting peptides and associated AAV capsid proteins and AAV particles identified using a CREATE system include AAVPHP.B (PHP.B), AAVPHP.A (PHP.A), AAVG2B-26, AAVG2B-13, AAVTH1.1-32, AAVTH1.1-35, AAVPHP.B2 (PHP.B2), AAVPHP.B3 (PHP.B3), AAVPHP.N/PHP.B-DGT, AAVPHP.B-EST, AAVPHP.B-GGT, AAVPHP.B-ATP, AAVPHP.B-ATT-T, AAVPHP.B-DGT-T, AAVPHP.B-GGT-T, AAVPHP.B-SGS, AAVPHP.B-AQP, AAVPHP.B-QQP, AAVPHP.B-SNP(3), AAVPHP.B-SNP, AAVPHP.B-QGT, AAVPHP.B-NQT, AAVPHP.B-EGS, AAVPHP.B-SGN, AAVPHP.B-EGT, AAVPHP.B-DST, AAVPHP.B-DST, AAVPHP.B-STP, AAVPHP.B-PQP, AAVPHP.B-SQP, AAVPHP.B-QLP, AAVPHP.B-TMP, AAVPHP.B-TTP, AAVPHP.S/G2A12, AAVG2A15/G2A3 (G2A3), AAVG2B4 (G2B4), AAVG2B5 (G2B5), and AAVPHP.S.

[0107] In certain embodiments, CREATE in mice is used to identify AAV capsids and/or targeting peptides having enhanced transduction of a target tissue (e.g., CNS or PNS).

CREATE system in NHP

[0108] The CREATE system has proven efficacious in identifying targeting peptides for enhanced transduction to the CNS of mice after intravenous administration. However, translation of findings from mouse to human is not always straightforward. Modifying the CREATE system for non-transgenic animals or model systems that more closely resemble humans may help identify targeting peptides and associated AAV capsids and particles useful for the treatment of human disease.

[0109] For adaptation of the CREATE method to non-transgenic animals, another mechanism needs to be used to alter target tissues and/or cells to express Cre. In certain embodiments, AAV Cre-vectors may be used to transduce cells and induce subsequent Cre expression. In certain embodiments, these AAV Cre-vectors may be AAV1-Cre vectors.

[0110] These AAV Cre-vectors may comprise viral genomes with a cell-type specific promoter. These cell-type specific promotors may be, but are not limited to, CAG, UBC, EF1α, synapsin, GFAP, MBP, VGLUT, VGAT, Nav1.8, parvalbumin, TH, ChaT, and/or any promoter known in the art.

[0111] In certain embodiments, these AAV-Cre vectors are delivered to a target tissue by intraparenchymal administration. In certain embodiments, the intraparenchymal administration is directly to the putamen of the subject. In certain embodiments, the intraparenchymal administration is directly to the thalamus of a subject. In certain embodiments, the intraparenchymal administration is directly to the cortex of a subject. In certain embodiments, the intraparenchymal administration is indirectly to the cortex of a subject. In certain embodiments, the intraparenchymal administration is simultaneously to one or more of the putamen, the thalamus and or the cortex of a subject, and may be bi-lateral administrations.

[0112] In certain embodiments, the subject is a non-human primate.

[0113] As for the CREATE method developed in mice, the AAV capsid libraries may be administered intravenously. In another embodiment, the AAV capsid libraries may be administered by intraparenchymal delivery. In certain embodiments, the AAV capsid library is administered prior to the delivery of the AAV-Cre vectors. In another embodiment, the AAV capsid library is administered after the delivery of the AAV-Cre vectors. The length of time between the administration of the AAV-Cre vectors and the AAV capsid libraries may be seconds, minutes, hours, days, weeks, or years.

[0114] The AAV capsid library may comprise AAV particles comprising a viral genome encoding a reporter (e.g., GFP). Only those cells of the target tissue (e.g., CNS or DRG) also

expressing Cre (co-transduced by a Cre-vector administered intraparenchymally) will express the reporter.

[0115] Target tissues may be collected and analyzed for the identification of AAV particles and targeting peptides that lead to enrichment in the target tissue, i.e., enhanced transduction. Standard methods in the art may be used to assess, analyze, or characterize sample tissues and AAV sequences, including but not limited to, next generation sequencing, viral genome quantification, biochemical assays, immunohistochemistry and/or imaging.

[0116] In certain embodiments, CREATE in NHP is used to identify AAV capsids and/or targeting peptides having enhanced transduction of a target tissue (e.g., CNS or PNS).

[0117] A non-limiting example of CREATE in NHP may be summarized as follows and is shown in Figure 1. First, an AAV plasmid library is prepared and an AAV particle library is produced using triple transfection methods (other AAV library production methods may be used). The AAV particle library is administered to one or more NHP by intravenous administration at Day 0. At Day 7, the NHP is administered AAV-Cre vectors by intracranial infusion. At Day 20, necropsy is performed and tissues collected from brain, spinal cord, dorsal root ganglia, liver, heart, muscle, kidney, pancreas, spleen, lung, etc. Capsid DNA is captured by Cre-dependent DNA recovery from transduced tissues, using an rAAV-Cap-in-cis-lox rAAV genome wherein Cre inverts the polyadenylation sequence flanked by the lox71 and lox66 sites. PCR primers selectively amplify the Cre-recombined sequences. Recovered DNA can then be processed for and analyzed by next-generation sequencing (NGS) to identify AAV variants. Two to three rounds of this process may be conducted to identify enriched variants.

Targeting peptide sequences

[0118] In certain embodiments the targeting peptide may comprise a sequence as set forth in SEQ ID NO: 4-14326 and SEQ ID NO: 42973-42999. These targeting peptides may be encoded by a sequence as set forth in SEQ ID NO: 14327-42972 and SEQ ID NO: 43027-43053. These sequences are shown in Tables 2 and 3.

[0119] In certain embodiments, the targeting peptide may comprise an amino acid sequence with 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%, or 100% identity to any of the sequences shown in Table 2 or 3.

[0120] In certain embodiments, the targeting peptide may be encoded by a nucleic acid sequence with 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%, or 100% identity to any of the sequences shown in Table 2 or 3.

[0121] In certain embodiments, a targeting peptide may comprise 4 or more contiguous amino acids of any of the targeting peptides disclosed herein. In certain embodiments the targeting peptide may comprise 4 contiguous amino acids of any of the sequences as set forth in SEQ ID NO: 4-14326 and SEQ ID NO: 42973-42999. In certain embodiments the targeting peptide may comprise 5 contiguous amino acids of any of the sequences as set forth in SEQ ID NO: 4-14326 and SEQ ID NO: 42973-42999. In certain embodiments the targeting peptide may comprise 6 contiguous amino acids of any of the sequences as set forth in SEQ ID NO: 4-14326 and SEQ ID NO: 42973-42999.

[0122] In certain embodiments, the AAV particle of the disclosure comprises an AAV capsid with a targeting peptide insert, wherein the targeting peptide has an amino acid sequence as set forth in any of SEQ ID NO: 4-14326 and SEQ ID NO: 42973-42999.

[0123] In certain embodiments, the AAV particle of the disclosure comprises an AAV capsid polynucleotide with a targeting nucleic acid insert, wherein the targeting nucleic acid insert has a nucleotide sequence as set forth in any of SEQ ID NO: 14327-42972 and SEQ ID NO: 43027-43053.

[0124] In certain embodiments, the AAV particle of the disclosure comprises an AAV capsid with a targeting peptide insert, wherein the targeting peptide has an amino acid sequence comprising at least 4 contiguous amino acids of any of the sequences as set forth in any of SEQ ID NO: 4-14326 and SEQ ID NO: 42973-42999.

[0125] In certain embodiments, the AAV particle of the disclosure comprises an AAV capsid with a targeting peptide insert, wherein the targeting peptide has an amino acid sequence substantially comprising any of the sequences as set forth in any of SEQ ID NO: 4-14326 and SEQ ID NO: 42973-42999.

[0126] In certain embodiments, the AAV particle of the disclosure comprises an AAV capsid polynucleotide with a targeting nucleic acid insert, wherein the targeting nucleic acid insert has a nucleotide sequence substantially comprising any of those set forth as SEQ ID NO: 14327-42972 and SEQ ID NO: 43027-43053.

[0127] The AAV particle of the disclosure comprising a targeting nucleic acid insert, may have a polynucleotide sequence with 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% or more, identity to the parent capsid sequence.

[0128] The AAV particle of the disclosure comprising a targeting peptide insert, may have an amino acid sequence with 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% or more, identity to the parent capsid sequence.

Table 2. Targeting peptides (7-mers)

SEQ ID NO	Peptide Sequence	SEQ ID NO	Nucleotide sequence	SEQ ID NO	Alternate Nucleotide Sequence
4	AAAASNT	14327	GCGGCTGCGGCGTCGAATACT	28650	GCAGCAGCAGCAAGCAACACA
5	AAAIDGD	14328	GCGGCGGCGATTGATGGTGAT	28651	GCAGCAGCAATCGACGGAGAC
6	AAALSTK	14329	GCTGCGGCTCTGTCGACTAAG	28652	GCAGCAGCACTCAGCACAAAA
7	AADANVN	14330	GCGGCTGATGCGAATGTTAAT	28653	GCAGCAGACGCAAACGTCAAC
8	AADFKRD	14331	GCTGCTGATTTTAAGCGTGAT	28654	GCAGCAGACTTCAAAAGAGAC
9	AADKTSR	14332	GCGGCTGATAAGACTTCTCGT	28655	GCAGCAGACAAAACAAGCAGA
10	AADPGSR	14333	GCTGCTGATCCTGGGTCGAGG	28656	GCAGCAGACCCAGGAAGCAGA
11	AADRVRP	14334	GCGGCGGATAGGGTTCGGCCG	28657	GCAGCAGACAGAGTCAGACCA
12	AAFMVER	14335	GCTGCTTTTATGGTTGAGCGT	28658	GCAGCATTCATGGTCGAAAGA
13	AAGFATD	14336	GCTGCGGGGTTTGCTACTGAT	28659	GCAGCAGGATTCGCAACAGAC
14	AAGFHLS	14337	GCGGCGGGTTTTCATCTGTCG	28660	GCAGCAGGATTCCACCTCAGC
15	AAGMIAS	14338	GCTGCGGGGATGATTGCTTCT	28661	GCAGCAGGAATGATCGCAAGC
16	AAGSTHI	14339	GCTGCTGGGTCGACGCATATT	28662	GCAGCAGGAAGCACACACATC
17	AAHANTV	14340	GCGGCTCATGCGAATACTGTT	28663	GCAGCACACGCAAACACAGTC
18	AAHPQLF	14341	GCGGCTCATCCTCAGCTGTTT	28664	GCAGCACACCCACAACTCTTC
19	AAHRTAH	14342	GCGGCTCATCGTACGGCGCAT	28665	GCAGCACACAGAACAGCACAC
20	AAIGKDE	14343	GCTGCTATTGGTAAGGATGAG	28666	GCAGCAATCGGAAAAGACGAA
21	AAIRSSY	14344	GCTGCGATTCGGTCTAGTTAT	28667	GCAGCAATCAGAAGCAGCTAC
22	AAKTSQL	14345	GCTGCGAAGACGTCTCAGCTG	28668	GCAGCAAAAACAAGCCAACTC
23	AALPTLL	14346	GCGGCGTTGCCGACGTTGCTT	28669	GCAGCACTCCCAACACTCCTC
24	AALSHLH	14347	GCGGCGTTGAGTCATTTGCAT	28670	GCAGCACTCAGCCACCTCCAC
25	AALSRVD	14348	GCTGCGTTGAGTCGGGTTGAT	28671	GCAGCACTCAGCAGAGTCGAC
26	AALTKVL	14349	GCTGCTCTTACGAAGGTTCTG	28672	GCAGCACTCACAAAAGTCCTC
27	AALTRLT	14350	GCTGCGCTTACTAGGCTGACT	28673	GCAGCACTCACAAGACTCACA
28	AAMIKRQ	14351	GCTGCTATGATTAAGCGGCAG	28674	GCAGCAATGATCAAAAGACAA
29	AAMMKTV	14352	GCTGCGATGATGAAGACTGTT	28675	GCAGCAATGATGAAAACAGTC
30	AAMVSTP	14353	GCTGCGATGGTGAGTACTCCG	28676	GCAGCAATGGTCAGCACACCA
31	AANLRTG	14354	GCTGCGAATCTTCGTACGGGT	28677	GCAGCAAACCTCAGAACAGGA
32	AANLVLQ	14355	GCTGCTAATCTTGTTCTGCAG	28678	GCAGCAAACCTCGTCCTCCAA
33	AANSTQS	14356	GCGGCGAATTCGACGCAGTCT	28679	GCAGCAAACAGCACACAAAGC
34	AAPIAAA	14357	GCGGCTCCGATTGCGGCTGCT	28680	GCAGCACCAATCGCAGCAGCA

35	AAPPFGH	14358	GCGGCTCCGCCTTTTGGTCAT	28681	GCAGCACCACCATTCGGACAC
36	AAPSSSI	14359	GCGGCTCCTAGTTCGTCTATT	28682	GCAGCACCAAGCAGCAGCATC
37	AAPSYRG	14360	GCTGCGCCGAGTTATCGGGGT	28683	GCAGCACCAAGCTACAGAGGA
38	AAPTITP	14361	GCTGCTCCTACGATTACTCCT	28684	GCAGCACCAACAATCACACCA
39	AAQLGER	14362	GCGGCGCAGTTGGGGGAGCGG	28685	GCAGCACAACTCGGAGAAAGA
40	AAQPYTH	14363	GCTGCGCAGCCTTATACTCAT	28686	GCAGCACAACCATACACACAC
41	AARPPNA	14364	GCGGCGCGTCCGCCGAATGCT	28687	GCAGCAAGACCACCAAACGCA
42	AARSTVV	14365	GCGGCGAGGAGTACGGTGGTT	28688	GCAGCAAGAAGCACAGTCGTC
43	AARTSFN	14366	GCTGCTCGTACGTCTTTTAAT	28689	GCAGCAAGAACAAGCTTCAAC
44	AARTTYT	14367	GCTGCTAGGACTACTTATACT	28690	GCAGCAAGAACAACATACACA
45	AASASRY	14368	GCTGCTTCGGCTAGTAGGTAT	28691	GCAGCAAGCGCAAGCAGATAC
46	AASSDSY	14369	GCTGCTAGTTCTGATTCTTAT	28692	GCAGCAAGCAGCGACAGCTAC
47	AASYVGI	14370	GCGGCGTCTTATGTTGGGATT	28693	GCAGCAAGCTACGTCGGAATC
48	AATCGQN	14371	GCTGCGACTTGTGGTCAGAAT	28694	GCAGCAACATGCGGACAAAAC
49	AATLATA	14372	GCGGCTACGCTGGCTACTGCT	28695	GCAGCAACACTCGCAACAGCA
50	AATPSKH	14373	GCGGCTACGCCTAGTAAGCAT	28696	GCAGCAACACCAAGCAAACAC
51	AATSLNS	14374	GCTGCTACGAGTCTTAATTCG	28697	GCAGCAACAAGCCTCAACAGC
52	AAVGASS	14375	GCGGCTGTGGGTGCGTCTTCT	28698	GCAGCAGTCGGAGCAAGCAGC
53	AAVGGLG	14376	GCTGCTGTGGGTGGGCTTGGG	28699	GCAGCAGTCGGAGGACTCGGA
54	AAWADES	14377	GCTGCGTGGGCGGATGAGAGT	28700	GCAGCATGGGCAGACGAAAGC
55	AAYSFSP	14378	GCTGCTTATTCTTTTTCGCCT	28701	GCAGCATACAGCTTCAGCCCA
56	ADAHMNR	14379	GCGGATGCTCATATGAATCGT	28702	GCAGACGCACACATGAACAGA
57	ADDHHSH	14380	GCTGATGATCATCATTCGCAT	28703	GCAGACGACCACCACAGCCAC
58	ADEEDSC	14381	GCTGATGAGGAGGATTCTTGT	28704	GCAGACGAAGAAGACAGCTGC
59	ADGDVPR	14382	GCGGATGGTGATGTGCCGCGG	28705	GCAGACGGAGACGTCCCAAGA
60	ADGKSSD	14383	GCGGATGGGAAGTCTTCTGAT	28706	GCAGACGGAAAAAGCAGCGAC
61	ADGSTTL	14384	GCGGATGGTTCGACGACTCTT	28707	GCAGACGGAAGCACAACACTC
62	ADHVPYI	14385	GCGGATCATGTTCCTTATATT	28708	GCAGACCACGTCCCATACATC
63	ADKLGHT	14386	GCTGATAAGTTGGGGCATACT	28709	GCAGACAAACTCGGACACACA
64	ADKPSDR	14387	GCTGATAAGCCGTCGGATCGG	28710	GCAGACAAACCAAGCGACAGA
65	ADKSRVG	14388	GCGGATAAGAGTCGGGTGGGG	28711	GCAGACAAAAGCAGAGTCGGA
66	ADKVRLV	14389	GCTGATAAGGTTCGGTTGGTG	28712	GCAGACAAAGTCAGACTCGTC
67	ADLAISV	14390	GCTGATCTTGCTATTAGTGTT	28713	GCAGACCTCGCAATCAGCGTC
68	ADLLPST	14391	GCTGATCTTCTGCCGAGTACT	28714	GCAGACCTCCTCCCAAGCACA
69	ADLSPTE	14392	GCTGATCTGTCGCCTACTGAG	28715	GCAGACCTCAGCCCAACAGAA
70	ADLYTRP	14393	GCGGATTTGTATACGCGGCCG	28716	GCAGACCTCTACACAAGACCA
71	ADMRSSA	14394	GCTGATATGAGGAGTAGTGCG	28717	GCAGACATGAGAAGCAGCGCA
72	ADNQVPL	14395	GCGGATAATCAGGTTCCTCTG	28718	GCAGACAACCAAGTCCCACTC
73	ADPEGAS	14396	GCTGATCCTGAGGGTGCGAGT	28719	GCAGACCCAGAAGGAGCAAGC
74	ADPERVR	14397	GCGGATCCGGAGAGGGTTCGG	28720	GCAGACCCAGAAAGAGTCAGA
75	ADPHMPK	14398	GCGGATCCGCATATGCCGAAG	28721	GCAGACCCACACATGCCAAAA
76	ADPHRNQ	14399	GCTGATCCGCATCGGAATCAG	28722	GCAGACCCACACAGAAACCAA
77	ADPMHRA	14400	GCGGATCCTATGCATCGTGCT	28723	GCAGACCCAATGCACAGAGCA
78	ADPPKFW	14401	GCGGATCCGCCTAAGTTTTGG	28724	GCAGACCCACCAAAATTCTGG
79	ADPRQKS	14402	GCTGATCCTCGGCAGAAGTCG	28725	GCAGACCCAAGACAAAAAAGC

80	ADRAHAV	14403	GCTGATCGTGCTCATGCGGTT	28726	GCAGACAGAGCACACGCAGTC
81	ADRGSHS	14404	GCGGATAGGGGGTCTCATTCT	28727	GCAGACAGAGGAAGCCACAGC
82	ADRLPFL	14405	GCGGATAGGCTTCCTTTTTTG	28728	GCAGACAGACTCCCATTCCTC
83	ADRSPIT	14406	GCGGATCGTTCGCCTATTACT	28729	GCAGACAGAAGCCCAATCACA
84	ADRYGRV	14407	GCTGATCGTTATGGGCGGGTG	28730	GCAGACAGATACGGAAGAGTC
85	ADSGRTI	14408	GCTGATTCGGGTCGTACGATT	28731	GCAGACAGCGGAAGAACAATC
86	ADSTHAA	14409	GCGGATTCGACTCATGCTGCT	28732	GCAGACAGCACACACGCAGCA
87	ADTMTSS	14410	GCTGATACTATGACGTCGTCG	28733	GCAGACACAATGACAAGCAGC
88	ADTMTTV	14411	GCTGATACGATGACTACTGTG	28734	GCAGACACAATGACAACAGTC
89	ADTRLHS	14412	GCTGATACTCGTTTGCATAGT	28735	GCAGACACAAGACTCCACAGC
90	ADTRLQT	14413	GCTGATACTAGGCTTCAGACG	28736	GCAGACACAAGACTCCAAACA
91	ADVRTLS	14414	GCTGATGTTAGGACTTTGTCT	28737	GCAGACGTCAGAACACTCAGC
92	AEAGMFD	14415	GCGGAGGCTGGGATGTTTGAT	28738	GCAGAAGCAGGAATGTTCGAC
93	AEAKNTR	14416	GCTGAGGCTAAGAATACGAGG	28739	GCAGAAGCAAAAAACACAAGA
94	AEAPTRD	14417	GCTGAGGCGCCTACGCGGGAT	28740	GCAGAAGCACCAACAAGAGAC
95	AEATSVE	14418	GCTGAGGCGACGAGTGTTGAG	28741	GCAGAAGCAACAAGCGTCGAA
96	AEGNPKI	14419	GCGGAGGGGAATCCGAAGATT	28742	GCAGAAGGAAACCCAAAAATC
97	AEGPEWR	14420	GCTGAGGGTCCGGAGTGGCGT	28743	GCAGAAGGACCAGAATGGAGA
98	AEHPNSL	14421	GCTGAGCATCCTAATTCGCTT	28744	GCAGAACACCCAAACAGCCTC
99	AEHSPSL	14422	GCTGAGCATTCTCCGTCGCTG	28745	GCAGAACACAGCCCAAGCCTC
100	AEIVRHV	14423	GCGGAGATTGTTCGGCATGTT	28746	GCAGAAATCGTCAGACACGTC
101	AELASPI	14424	GCGGAGCTTGCGTCGCCGATT	28747	GCAGAACTCGCAAGCCCAATC
102	AELKRGP	14425	GCTGAGCTGAAGAGGGGGCCG	28748	GCAGAACTCAAAAGAGGACCA
103	AELPPRQ	14426	GCGGAGCTTCCTCCTCGGCAG	28749	GCAGAACTCCCACCAAGACAA
104	AELQPHL	14427	GCTGAGCTGCAGCCTCATCTT	28750	GCAGAACTCCAACCACACCTC
105	AEPRSWS	14428	GCGGAGCCGAGGTCGTGGTCT	28751	GCAGAACCAAGAAGCTGGAGC
106	AEPTDFL	14429	GCTGAGCCGACTGATTTTCTT	28752	GCAGAACCAACAGACTTCCTC
107	AERATWS	14430	GCTGAGCGGGCGACTTGGAGT	28753	GCAGAAAGAGCAACATGGAGC
108	AERNMAP	14431	GCGGAGCGTAATATGGCTCCG	28754	GCAGAAAGAAACATGGCACCA
109	AERQQYL	14432	GCTGAGCGGCAGCAGTATTTG	28755	GCAGAAAGACAACAATACCTC
110	AESAYVP	14433	GCGGAGTCTGCGTATGTTCCG	28756	GCAGAAAGCGCATACGTCCCA
111	AETSSSS	14434	GCTGAGACGAGTTCGTCTTCG	28757	GCAGAAACAAGCAGCAGCAGC
112	AFAGVRG	14435	GCTTTTGCGGGGGTTCGTGGT	28758	GCATTCGCAGGAGTCAGAGGA
113	AFARSAP	14436	GCGTTTGCGCGGAGTGCTCCT	28759	GCATTCGCAAGAAGCGCACCA
114	AFDTRGG	14437	GCGTTTGATACGCGTGGGGGT	28760	GCATTCGACACAAGAGGAGGA
115	AFEGRSP	14438	GCGTTTGAGGGGCGGTCGCCG	28761	GCATTCGAAGGAAGAAGCCCA
116	AFESPRA	14439	GCTTTTGAGTCGCCTAGGGCT	28762	GCATTCGAAAGCCCAAGAGCA
117	AFGASMS	14440	GCTTTTGGTGCGAGTATGTCT	28763	GCATTCGGAGCAAGCATGAGC
118	AFGKGHT	14441	GCGTTTGGTAAGGGGCATACG	28764	GCATTCGGAAAAGGACACACA
119	AFGKNTV	14442	GCTTTTGGGAAGAATACTGTT	28765	GCATTCGGAAAAAACACAGTC
120	AFGTLKM	14443	GCGTTTGGTACTTTGAAGATG	28766	GCATTCGGAACACTCAAAATG
121	AFLAANA	14444	GCTTTTCTGGCTGCTAATGCG	28767	GCATTCCTCGCAGCAAACGCA
122	AFLNQLS	14445	GCTTTTCTTAATCAGCTTAGT	28768	GCATTCCTCAACCAACTCAGC
123	AFLSSAP	14446	GCGTTTCTTTCGTCGGCGCCT	28769	GCATTCCTCAGCAGCGCACCA
124	AFMSKLE	14447	GCTTTTATGTCTAAGCTGGAG	28770	GCATTCATGAGCAAACTCGAA

125	AFNGTDS	14448	GCGTTTAATGGTACGGATTCG	28771	GCATTCAACGGAACAGACAGC
126	AFNHELS	14449	GCGTTTAATCATGAGCTGTCT	28772	GCATTCAACCACGAACTCAGC
127	AFNTSHD	14450	GCTTTTAATACGAGTCATGAT	28773	GCATTCAACACAAGCCACGAC
128	AFPLPPH	14451	GCTTTTCCGTTGCCGCCTCAT	28774	GCATTCCCACTCCCACCACAC
129	AFPQSGN	14452	GCTTTTCCGCAGTCTGGTAAT	28775	GCATTCCCACAAAGCGGAAAC
130	AFQDKQT	14453	GCTTTTCAGGATAAGCAGACT	28776	GCATTCCAAGACAAACAAACA
131	AFQHQPP	14454	GCGTTTCAGCATCAGCCTCCG	28777	GCATTCCAACACCAACCACCA
132	AFQSARA	14455	GCTTTTCAGAGTGCGAGGGCT	28778	GCATTCCAAAGCGCAAGAGCA
133	AFSNAGP	14456	GCTTTTTCTAATGCGGGTCCG	28779	GCATTCAGCAACGCAGGACCA
134	AFSTTVM	14457	GCTTTTTCTACGACTGTTATG	28780	GCATTCAGCACAACAGTCATG
135	AFTGKSS	14458	GCGTTTACGGGGAAGTCTTCG	28781	GCATTCACAGGAAAAAGCAGC
136	AFVASSP	14459	GCTTTTGTGGCGAGTTCGCCT	28782	GCATTCGTCGCAAGCAGCCCA
137	AFVGKVT	14460	GCGTTTGTGGGGAAGGTGACT	28783	GCATTCGTCGGAAAAGTCACA
138	AFVPKSM	14461	GCGTTTGTGCCTAAGAGTATG	28784	GCATTCGTCCCAAAAAGCATG
139	AGAEEHM	14462	GCTGGGGCGGAGGAGCATATG	28785	GCAGGAGCAGAAGAACACATG
140	AGALMHL	14463	GCTGGGGCGCTTATGCATTTG	28786	GCAGGAGCACTCATGCACCTC
141	AGAPTGL	14464	GCGGGGGCGCCGACTGGTCTT	28787	GCAGGAGCACCAACAGGACTC
142	AGATSFY	14465	GCTGGTGCGACTTCGTTTTAT	28788	GCAGGAGCAACAAGCTTCTAC
143	AGGAGQM	14466	GCTGGGGGTGCTGGGCAGATG	28789	GCAGGAGGAGCAGGACAAATG
144	AGGQPSL	14467	GCGGGTGGTCAGCCTTCGCTG	28790	GCAGGAGGACAACCAAGCCTC
145	AGGSWPA	14468	GCTGGTGGTAGTTGGCCTGCG	28791	GCAGGAGGAAGCTGGCCAGCA
146	AGGTSMP	14469	GCTGGGGGGACGTCTATGCCG	28792	GCAGGAGGAACAAGCATGCCA
147	AGGYLVP	14470	GCTGGTGGGTATCTTGTTCCG	28793	GCAGGAGGATACCTCGTCCCA
148	AGHRADS	14471	GCGGGTCATCGGGCTGATTCT	28794	GCAGGACACAGAGCAGACAGC
149	AGHTNLP	14472	GCTGGTCATACTAATTTGCCG	28795	GCAGGACACACAAACCTCCCA
150	AGHVVSM	14473	GCTGGGCATGTTGTGTCTATG	28796	GCAGGACACGTCGTCAGCATG
151	AGITTAV	14474	GCTGGGATTACTACTGCTGTG	28797	GCAGGAATCACAACAGCAGTC
152	AGKATYI	14475	GCGGGTAAGGCTACGTATATT	28798	GCAGGAAAAGCAACATACATC
153	AGKLVSS	14476	GCGGGGAAGCTGGTGTCTTCT	28799	GCAGGAAAACTCGTCAGCAGC
154	AGLAVKP	14477	GCGGGGTTGGCGGTGAAGCCG	28800	GCAGGACTCGCAGTCAAACCA
155	AGLDFYP	14478	GCTGGGTTGGATTTTTATCCT	28801	GCAGGACTCGACTTCTACCCA
156	AGLKDVT	14479	GCTGGTTTGAAGGATGTTACG	28802	GCAGGACTCAAAGACGTCACA
157	AGLLTQI	14480	GCTGGTCTGTTGACGCAGATT	28803	GCAGGACTCCTCACACAAATC
158	AGLNGQG	14481	GCTGGTCTTAATGGGCAGGGT	28804	GCAGGACTCAACGGACAAGGA
159	AGLNHSV	14482	GCTGGTCTTAATCATTCTGTT	28805	GCAGGACTCAACCACAGCGTC
160	AGLQQLS	14483	GCGGGTCTTCAGCAGCTGTCG	28806	GCAGGACTCCAACAACTCAGC
161	AGMDSND	14484	GCTGGTATGGATAGTAATGAT	28807	GCAGGAATGGACAGCAACGAC
162	AGMHSMT	14485	GCGGGGATGCATTCTATGACT	28808	GCAGGAATGCACAGCATGACA
163	AGMPPAP	14486	GCTGGGATGCCTCCTGCTCCT	28809	GCAGGAATGCCACCAGCACCA
164	AGNHAVQ	14487	GCTGGGAATCATGCTGTGCAG	28810	GCAGGAAACCACGCAGTCCAA
165	AGNSKTS	14488	GCTGGGAATTCTAAGACTTCT	28811	GCAGGAAACAGCAAAACAAGC
166	AGNSLSS	14489	GCTGGTAATTCGCTTAGTTCT	28812	GCAGGAAACAGCCTCAGCAGC
167	AGPHVLA	14490	GCTGGTCCGCATGTTCTGGCG	28813	GCAGGACCACACGTCCTCGCA
168	AGPSNFD	14491	GCTGGGCCTTCGAATTTTGAT	28814	GCAGGACCAAGCAACTTCGAC
169	AGPTNPF	14492	GCTGGTCCGACGAATCCGTTT	28815	GCAGGACCAACAAACCCATTC

170	AGQFTKS	14493	GCTGGGCAGTTTACTAAGTCT	28816	GCAGGACAATTCACAAAAAGC
171	AGQGSQS	14494	GCGGGTCAGGGTTCTCAGAGT	28817	GCAGGACAAGGAAGCCAAAGC
172	AGQNSLV	14495	GCGGGGCAGAATTCGTTGGTT	28818	GCAGGACAAAACAGCCTCGTC
173	AGQSAPR	14496	GCGGGGCAGTCTGCTCCTCGG	28819	GCAGGACAAAGCGCACCAAGA
174	AGRDSAW	14497	GCGGGTCGGGATTCGGCGTGG	28820	GCAGGAAGAGACAGCGCATGG
175	AGRNMHP	14498	GCTGGTCGGAATATGCATCCT	28821	GCAGGAAGAAACATGCACCCA
176	AGRPPQS	14499	GCGGGTCGGCCGCCGCAGTCT	28822	GCAGGAAGACCACCACAAAGC
177	AGRVLTM	14500	GCTGGTCGGGTGCTTACGATG	28823	GCAGGAAGAGTCCTCACAATG
178	AGSGGSP	14501	GCTGGTTCGGGTGGTTCTCCG	28824	GCAGGAAGCGGAGGAAGCCCA
179	AGSGVLN	14502	GCTGGTTCGGGGGGTTCTGAAT	28825	GCAGGAAGCGGAGTCCTCAAC
180	AGSHQSE	14503	GCGGGGTCGCATCAGTCTGAG	28826	GCAGGAAGCCACCAAAGCGAA
181	AGSIISR	14504	GCGGGTTCGATTATTTCGCGT	28827	GCAGGAAGCATCATCAGCAGA
182	AGSLSVD	14505	GCTGGTTCTCTTTCGGTTGAT	28828	GCAGGAAGCCTCAGCGTCGAC
183	AGSQHPA	14506	GCTGGTAGTCAGCATCCGGCT	28829	GCAGGAAGCCAACACCCAGCA
184	AGSQTPP	14507	GCTGGGTCTCAGACGCCGCCG	28830	GCAGGAAGCCAAACACCACCA
185	AGSSRTF	14508	GCGGGTTCGAGTCGGACGTTT	28831	GCAGGAAGCAGCAGAACATTC
186	AGTGLGM	14509	GCTGGTACGGGTTTGGGGATG	28832	GCAGGAACAGGACTCGGAATG
187	AGTGPFA	14510	GCTGGTACTGGGCCTTTTGCT	28833	GCAGGAACAGGACCATTCGCA
188	AGTIRIS	14511	GCGGGGACTATTCGTATTTCG	28834	GCAGGAACAATCAGAATCAGC
189	AGTLVIM	14512	GCTGGTACGCTGGTGATTATG	28835	GCAGGAACACTCGTCATCATG
190	AGTNQRN	14513	GCTGGGACGAATCAGCGTAAT	28836	GCAGGAACAAACCAAAGAAAC
191	AGTQPMT	14514	GCGGGTACGCAGCCGATGACG	28837	GCAGGAACACAACCAATGACA
192	AGTQRAY	14515	GCTGGGACTCAGAGGGCTTAT	28838	GCAGGAACACAAAGAGCATAC
193	AGTSHSH	14516	GCGGGTACTTCTCATTCTCAT	28839	GCAGGAACAAGCCACAGCCAC
194	AGTVEHL	14517	GCGGGGACTGTGGAGCATCTT	28840	GCAGGAACAGTCGAACACCTC
195	AGVGKAQ	14518	GCTGGTGTGGGTAAGGCGCAG	28841	GCAGGAGTCGGAAAAGCACAA
196	AGVLKMS	14519	GCTGGGGTGTTGAAGATGTCG	28842	GCAGGAGTCCTCAAAATGAGC
197	AGVPRME	14520	GCTGGTGTGCCTAGGATGGAG	28843	GCAGGAGTCCCAAGAATGGAA
198	AGVPSPA	14521	GCTGGTGTTCCTTCTCCTGCT	28844	GCAGGAGTCCCAAGCCCAGCA
199	AGVQPGQ	14522	GCTGGTGTTCAGCCTGGGCAG	28845	GCAGGAGTCCAACCAGGACAA
200	AGVSEAI	14523	GCTGGGGTGTCTGAGGCTATT	28846	GCAGGAGTCAGCGAAGCAATC
201	AHAVSLQ	14524	GCGCATGCTGTGTCTTTGCAG	28847	GCACACGCAGTCAGCCTCCAA
202	AHDEVPY	14525	GCGCATGATGAGGTTCCTTAT	28848	GCACACGACGAAGTCCCATAC
203	AHDIPMS	14526	GCGCATGATATTCCGATGTCG	28849	GCACACGACATCCCAATGAGC
204	AHDNKSM	14527	GCTCATGATAATAAGAGTATG	28850	GCACACGACAACAAAAGCATG
205	AHEVLSF	14528	GCGCATGAGGTGTTGAGTTTT	28851	GCACACGAAGTCCTCAGCTTC
206	AHGESKP	14529	GCGCATGGTGAGAGTAAGCCG	28852	GCACACGGAGAAAGCAAACCA
207	AHGNAPS	14530	GCTCATGGTAATGCGCCGTCG	28853	GCACACGGAAACGCACCAAGC
208	AHGNSSL	14531	GCTCATGGGAATAGTTCTCTT	28854	GCACACGGAAACAGCAGCCTC
209	AHGSLQV	14532	GCTCATGGGAGTCTGCAGGTT	28855	GCACACGGAAGCCTCCAAGTC
210	AHGVAYI	14533	GCTCATGGGGTTGCTTATATT	28856	GCACACGGAGTCGCATACATC
211	AHGVKTS	14534	GCGCATGGGGTGAAGACGTCG	28857	GCACACGGAGTCAAAACAAGC
212	AHHSVPP	14535	GCTCATCATAGTGTGCCGCCG	28858	GCACACCACAGCGTCCCACCA
213	AHIARHG	14536	GCTCATATTGCGCGTCATGGG	28859	GCACACATCGCAAGACACGGA
214	AHKSLPL	14537	GCGCATAAGTCGCTTCCTCTG	28860	GCACACAAAAGCCTCCCACTC

215	AHLKYGS	14538	GCTCATCTTAAGTATGGGAGT	28861	GCACACCTCAAATACGGAAGC
216	AHMDRTS	14539	GCTCATATGGATCGTACTAGT	28862	GCACACATGGACAGAACAAGC
217	AHMTDGE	14540	GCTCATATGACGGATGGTGAG	28863	GCACACATGACAGACGGAGAA
218	AHNVQGA	14541	GCGCATAATGTTCAGGGGGCG	28864	GCACACAACGTCCAAGGAGCA
219	AHPPQPG	14542	GCTCATCCGCCTCAGCCGGGG	28865	GCACACCCACCACAACCAGGA
220	AHPSLPL	14543	GCTCATCCGAGTCTTCCTCTG	28866	GCACACCCAAGCCTCCCACTC
221	AHPSRGI	14544	GCTCATCCTTCGCGGGGTATT	28867	GCACACCCAAGCAGAGGAATC
222	AHPSSHG	14545	GCGCATCCGTCGTCGCATGGT	28868	GCACACCCAAGCAGCCACGGA
223	AHQVGLA	14546	GCTCATCAGGTGGGGCTGGCT	28869	GCACACCAAGTCGGACTCGCA
224	AHSHVPP	14547	GCTCATTCGCATGTTCCGCCG	28870	GCACACAGCCACGTCCCACCA
225	AHSLKQV	14548	GCTCATTCGCTTAAGCAGGTT	28871	GCACACAGCCTCAAACAAGTC
226	AHSPALV	14549	GCTCATAGTCCGGCTCTGGTT	28872	GCACACAGCCCAGCACTCGTC
227	AHSRSGP	14550	GCTCATAGTCGTAGTGGGCCT	28873	GCACACAGCAGAAGCGGACCA
228	AHTLTEP	14551	GCTCATACTCTGACGGAGCCT	28874	GCACACACACTCACAGAACCA
229	AHTNLTS	14552	GCGCATACGAATCTTACGTCG	28875	GCACACACAAACCTCACAAGC
230	AHTRIMP	14553	GCTCATACGCGTATTATGCCG	28876	GCACACACAAGAATCATGCCA
231	AHVNSFS	14554	GCTCATGTGAATAGTTTTAGT	28877	GCACACGTCAACAGCTTCAGC
232	AHVPAAD	14555	GCTCATGTTCCTGCGGCGGAT	28878	GCACACGTCCCAGCAGCAGAC
233	AHVSQSG	14556	GCTCATGTGTCTCAGTCTGGT	28879	GCACACGTCAGCCAAAGCGGA
234	AIAFRRE	14557	GCTATTGCGTTTCGGCGGGAG	28880	GCAATCGCATTCAGAAGAGAA
235	AIAPPYT	14558	GCGATTGCGCCGCCGTATACG	28881	GCAATCGCACCACCATACACA
236	AIAVSAG	14559	GCTATTGCTGTGTCTGCGGGG	28882	GCAATCGCAGTCAGCGCAGGA
237	AIDSGYH	14560	GCTATTGATTCTGGTTATCAT	28883	GCAATCGACAGCGGATACCAC
238	AIGAIGS	14561	GCTATTGGTGCGATTGGTTCG	28884	GCAATCGGAGCAATCGGAAGC
239	AIGPRGG	14562	GCTATTGGGCCTAGGGGGGGT	28885	GCAATCGGACCAAGAGGAGGA
240	AIGSTTS	14563	GCGATTGGGAGTACTACGTCT	28886	GCAATCGGAAGCACAACAAGC
241	AIHAVSP	14564	GCGATTCATGCGGTGTCGCCG	28887	GCAATCCACGCAGTCAGCCCA
242	AIHSTKS	14565	GCGATTCATTCTACGAAGTCT	28888	GCAATCCACAGCACAAAAAGC
243	AIKGQDL	14566	GCTATTAAGGGTCAGGATCTT	28889	GCAATCAAAGGACAAGACCTC
244	AINFQAG	14567	GCGATTAATTTTCAGGCGGGT	28890	GCAATCAACTTCCAAGCAGGA
245	AINHAMT	14568	GCTATTAATCATGCGATGACT	28891	GCAATCAACCACGCAATGACA
246	AIPGHIM	14569	GCTATTCCTGGTCATATTATG	28892	GCAATCCCAGGACACATCATG
247	AIPGSSR	14570	GCGATTCCTGGTTCGTCGCGT	28893	GCAATCCCAGGAAGCAGCAGA
248	AIPMTHD	14571	GCTATTCCGATGACTCATGAT	28894	GCAATCCCAATGACACACGAC
249	AIPNPLD	14572	GCTATTCCGAATCCTCTTGAT	28895	GCAATCCCAAACCCACTCGAC
250	AIRNVLA	14573	GCTATTAGGAATGTGTTGGCT	28896	GCAATCAGAAACGTCCTCGCA
251	AIRSAND	14574	GCGATTAGGTCTGCTAATGAT	28897	GCAATCAGAAGCGCAAACGAC
252	AIRSPSP	14575	GCGATTCGGTCGCCGTCGCCT	28898	GCAATCAGAAGCCCAAGCCCA
253	AIRYTDP	14576	GCGATTCGGTATACGGATCCT	28899	GCAATCAGATACACAGACCCA
254	AISVGGS	14577	GCGATTAGTGTTGGGGGGTCT	28900	GCAATCAGCGTCGGAGGAAGC
255	AITTARN	14578	GCGATTACGACGGCGCGTAAT	28901	GCAATCACAACAGCAAGAAAC
256	AIYGGLT	14579	GCGATTTATGGTGGTCTTACG	28902	GCAATCTACGGAGGACTCACA
257	AIYMQQP	14580	GCGATTTATATGCAGCAGCCT	28903	GCAATCTACATGCAACAACCA
258	AIYQGVD	14581	GCGATTTATCAGGGGGTGGAT	28904	GCAATCTACCAAGGAGTCGAC
259	AKASNQD	14582	GCTAAGGCTAGTAATCAGGAT	28905	GCAAAAGCAAGCAACCAAGAC

260	AKATALE	14583	GCTAAGGCGACTGCTCTTGAG	28906	GCAAAAGCAACAGCACTCGAA
261	AKDIGQI	14584	GCGAAGGATATTGGTCAGATT	28907	GCAAAAGACATCGGACAAATC
262	AKDIPPR	14585	GCTAAGGATATTCCTCCGCGG	28908	GCAAAAGACATCCCACCAAGA
263	AKFAPSE	14586	GCTAAGTTTGCTCCTAGTGAG	28909	GCAAAATTCGCACCAAGCGAA
264	AKGDPRM	14587	GCTAAGGGGGATCCGCGTATG	28910	GCAAAAGGAGACCCAAGAATG
265	AKGQIHV	14588	GCGAAGGGTCAGATTCATGTT	28911	GCAAAAGGACAAATCCACGTC
266	AKHTEFS	14589	GCTAAGCATACTGAGTTTTCT	28912	GCAAAACACACAGAATTCAGC
267	AKISSAS	14590	GCTAAGATTAGTAGTGCTTCT	28913	GCAAAAATCAGCAGCGCAAGC
268	AKLEAIP	14591	GCGAAGTTGGAGGCGATTCCT	28914	GCAAAACTCGAAGCAATCCCA
269	AKNRDSC	14592	GCGAAGAATCGGGATTCGTGT	28915	GCAAAAAACAGAGACAGCTGC
270	AKNSPHP	14593	GCTAAGAATTCGCCGCATCCG	28916	GCAAAAAACAGCCCACACCCA
271	AKNSTFS	14594	GCGAAGAATTCTACTTTTTCT	28917	GCAAAAAACAGCACATTCAGC
272	AKPALLV	14595	GCTAAGCCGGCGTTGCTGGTT	28918	GCAAAACCAGCACTCCTCGTC
273	AKPHLQF	14596	GCTAAGCCGCATTTGCAGTTT	28919	GCAAAACCACACCTCCAATTC
274	AKPIRPP	14597	GCGAAGCCGATTCGTCCTCCT	28920	GCAAAACCAATCAGACCACCA
275	AKPSEEK	14598	GCTAAGCCGTCTGAGGAGAAG	28921	GCAAAACCAAGCGAAGAAAAA
276	AKPTYQP	14599	GCGAAGCCGACTTATCAGCCG	28922	GCAAAACCAACATACCAACCA
277	AKRLDDA	14600	GCTAAGCGTCTGGATGATGCG	28923	GCAAAAAGACTCGACGACGCA
278	AKSIKLS	14601	GCGAAGTCTATTAAGCTTAGT	28924	GCAAAAAGCATCAAACTCAGC
279	AKSNVGL	14602	GCTAAGAGTAATGTTGGTCTT	28925	GCAAAAAGCAACGTCGGACTC
280	AKSSYPI	14603	GCTAAGTCTAGTTATCCGATT	28926	GCAAAAAGCAGCTACCCAATC
281	AKSVALS	14604	GCTAAGTCGGTGGCTCTTTCG	28927	GCAAAAAGCGTCGCACTCAGC
282	AKTIEIS	14605	GCTAAGACGATTGAGATTTCT	28928	GCAAAAACAATCGAAATCAGC
283	AKTLRDD	14606	GCGAAGACTTTGAGGGATGAT	28929	GCAAAAACACTCAGAGACGAC
284	AKTMGTM	14607	GCTAAGACGATGGGGACGATG	28930	GCAAAAACAATGGGAACAATG
285	AKTTLSA	14608	GCTAAGACGACTTTGAGTGCG	28931	GCAAAAACAACACTCAGCGCA
286	AKYSPSA	14609	GCTAAGTATAGTCCTTCTGCG	28932	GCAAAATACAGCCCAAGCGCA
287	AKYSSMP	14610	GCGAAGTATAGTAGTATGCCG	28933	GCAAAATACAGCAGCATGCCA
288	ALAIGRD	14611	GCGCTGGCTATTGGGCGGGAT	28934	GCACTCGCAATCGGAAGAGAC
289	ALALKTS	14612	GCGCTTGCGCTTAAGACTTCG	28935	GCACTCGCACTCAAAACAAGC
290	ALATKVI	14613	GCGTTGGCGACGAAGGTTATT	28936	GCACTCGCAACAAAAGTCATC
291	ALDARRV	14614	GCTTTGGATGCTCGTCGGGTG	28937	GCACTCGACGCAAGAAGAGTC
292	ALDQMTI	14615	GCTCTTGATCAGATGACTATT	28938	GCACTCGACCAAATGACAATC
293	ALECPRA	14616	GCTCTGGAGTGTCCTCGGGCT	28939	GCACTCGAATGCCCAAGAGCA
294	ALEGLRP	14617	GCTCTTGAGGGGTTGCGTCCT	28940	GCACTCGAAGGACTCAGACCA
295	ALELGSE	14618	GCGCTGGAGCTTGGTTCGGAG	28941	GCACTCGAACTCGGAAGCGAA
296	ALERTSL	14619	GCGCTGGAGAGGACGTCTTTG	28942	GCACTCGAAAGAACAAGCCTC
297	ALFPGMS	14620	GCGCTGTTTCCGGGTATGAGT	28943	GCACTCTTCCCAGGAATGAGC
298	ALGDFPS	14621	GCTCTGGGTGATTTTCCGTCT	28944	GCACTCGGAGACTTCCCAAGC
299	ALGHQAM	14622	GCGCTTGGGCATCAGGCGATG	28945	GCACTCGGACACCAAGCAATG
300	ALGNNKS	14623	GCGCTGGGGAATAATAAGTCT	28946	GCACTCGGAAACAACAAAAGC
301	ALGRNEG	14624	GCTTTGGGTCGTAATGAGGGT	28947	GCACTCGGAAGAAACGAAGGA
302	ALGVPPS	14625	GCGTTGGGGGTGCCGCCTTCT	28948	GCACTCGGAGTCCCACCAAGC
303	ALGVSAL	14626	GCGTTGGGGGTTAGTGCTTTG	28949	GCACTCGGAGTCAGCGCACTC
304	ALGYHNT	14627	GCTTTGGGGTATCATAATACT	28950	GCACTCGGATACCACAACACA

305	ALHPSAP	14628	GCTTTGCATCCGAGTGCGCCG	28951	GCACTCCACCCAAGCGCACCA
306	ALIERVN	14629	GCGCTTATTGAGCGTGTTAAT	28952	GCACTCATCGAAAGAGTCAAC
307	ALIKVHN	14630	GCGCTTATTAAGGTGCATAAT	28953	GCACTCATCAAAGTCCACAAC
308	ALIPSPP	14631	GCGTTGATTCCGAGTCCGCCT	28954	GCACTCATCCCAAGCCCACCA
309	ALLDSKL	14632	GCGCTGCTGGATTCTAAGCTG	28955	GCACTCCTCGACAGCAAACTC
310	ALLEQRP	14633	GCTCTGTTGGAGCAGCGGCCG	28956	GCACTCCTCGAACAAAGACCA
311	ALLGVNR	14634	GCTTTGCTGGGGGTGAATAGG	28957	GCACTCCTCGGAGTCAACAGA
312	ALLHSIG	14635	GCTTTGCTTCATTCTATTGGG	28958	GCACTCCTCCACAGCATCGGA
313	ALLQNAS	14636	GCGTTGTTGCAGAATGCGTCG	28959	GCACTCCTCCAAAACGCAAGC
314	ALLSSGN	14637	GCTCTTCTTTCTTCTGGGAAT	28960	GCACTCCTCAGCAGCGGAAAC
315	ALMRGTI	14638	GCTCTTATGCGGGGGACGATT	28961	GCACTCATGAGAGGAACAATC
316	ALNDAAG	14639	GCTTTGAATGATGCGGCGGGT	28962	GCACTCAACGACGCAGCAGGA
317	ALNHDKP	14640	GCGCTGAATCATGATAAGCCT	28963	GCACTCAACCACGACAAACCA
318	ALNIPEL	14641	GCGTTGAATATTCCTGAGCTT	28964	GCACTCAACATCCCAGAACTC
319	ALNTHTV	14642	GCTTTGAATACGCATACGGTT	28965	GCACTCAACACACACACAGTC
320	ALPAKSY	14643	GCTCTTCCTGCTAAGTCGTAT	28966	GCACTCCCAGCAAAAAGCTAC
321	ALPASVD	14644	GCTCTGCCGGCGAGTGTGGAT	28967	GCACTCCCAGCAAGCGTCGAC
322	ALPGTPN	14645	GCTCTTCCTGGTACTCCGAAT	28968	GCACTCCCAGGAACACCAAAC
323	ALPLSRA	14646	GCTCTGCCTTTGAGTCGGGCG	28969	GCACTCCCACTCAGCAGAGCA
324	ALPQLAV	14647	GCGTTGCCTCAGTTGGCGGTT	28970	GCACTCCCACAACTCGCAGTC
325	ALPQRRD	14648	GCTCTTCCTCAGCGTCGGGAT	28971	GCACTCCCACAAAGAAGAGAC
326	ALPSSDH	14649	GCGTTGCCGAGTAGTGATCAT	28972	GCACTCCCAAGCAGCGACCAC
327	ALPSTLV	14650	GCTTTGCCTTCGACTTTGGTG	28973	GCACTCCCAAGCACACTCGTC
328	ALPTTKA	14651	GCTTTGCCGACTACTAAGGCG	28974	GCACTCCCAACAACAAAAGCA
329	ALQAPHT	14652	GCGCTGCAGGCGCCGCATACG	28975	GCACTCCAAGCACCACACACA
330	ALQGYSV	14653	GCTCTTCAGGGGTATTCTGTG	28976	GCACTCCAAGGATACAGCGTC
331	ALQRDWS	14654	GCTCTGCAGCGGGATTGGTCG	28977	GCACTCCAAAGAGACTGGAGC
332	ALQSDTV	14655	GCTCTTCAGAGTGATACTGTT	28978	GCACTCCAAAGCGACACAGTC
333	ALQSSVR	14656	GCGTTGCAGTCTTCTGTGAGG	28979	GCACTCCAAAGCAGCGTCAGA
334	ALRMGMT	14657	GCTCTTCGGATGGGTATGACG	28980	GCACTCAGAATGGGAATGACA
335	ALRNPIN	14658	GCGCTGCGGAATCCGATTAAT	28981	GCACTCAGAAACCCAATCAAC
336	ALRTSLT	14659	GCGCTTCGTACGTCTCTGACG	28982	GCACTCAGAACAAGCCTCACA
337	ALRVAAM	14660	GCGTTGCGTGTTGCGGCGATG	28983	GCACTCAGAGTCGCAGCAATG
338	ALSAGRV	14661	GCTTTGAGTGCTGGTCGGGTG	28984	GCACTCAGCGCAGGAAGAGTC
339	ALSELQI	14662	GCGCTGTCGGAGCTTCAGATT	28985	GCACTCAGCGAACTCCAAATC
340	ALSGTFG	14663	GCTCTGTCTGGTACGTTTGGT	28986	GCACTCAGCGGAACATTCGGA
341	ALSHDGN	14664	GCGCTTTCGCATGATGGGAAT	28987	GCACTCAGCCACGACGGAAAC
342	ALSHESN	14665	GCGCTTTCGCATGAGTCTAAT	28988	GCACTCAGCCACGAAAGCAAC
343	ALSKWAM	14666	GCGCTGTCTAAGTGGGCTATG	28989	GCACTCAGCAAATGGGCAATG
344	ALSLNTI	14667	GCGTTGAGTCTGAATACTATT	28990	GCACTCAGCCTCAACACAATC
345	ALSPMPC	14668	GCGTTGTCTCCGATGCCTTGT	28991	GCACTCAGCCCAATGCCATGC
346	ALSQAER	14669	GCGTTGAGTCAGGCTGAGCGT	28992	GCACTCAGCCAAGCAGAAAGA
347	ALSRDRP	14670	GCTTTGTCTCGTGATCGGCCT	28993	GCACTCAGCAGAGACAGACCA
348	ALSSIHV	14671	GCGCTTTCGTCGATTCATGTT	28994	GCACTCAGCAGCATCCACGTC
349	ALSSSAL	14672	GCGCTTTCTAGTTCTGCTCTT	28995	GCACTCAGCAGCAGCGCACTC

350	ALSTGMP	14673	GCTCTTTCGACGGGGATGCCT	28996	GCACTCAGCACAGGAATGCCA
351	ALSTPVP	14674	GCTCTTTCGACTCCGGTGCCT	28997	GCACTCAGCACACCAGTCCCA
352	ALTHYDP	14675	GCTCTTACGCATTATGATCCG	28998	GCACTCACACACTACGACCCA
353	ALTKNVA	14676	GCTTTGACTAAGAATGTGGCT	28999	GCACTCACAAAAAACGTCGCA
354	ALTRSAV	14677	GCTTTGACGCGGTCTGCGGTT	29000	GCACTCACAAGAAGCGCAGTC
355	ALTSTHV	14678	GCTCTTACTAGTACTCATGTT	29001	GCACTCACAAGCACACACGTC
356	ALTTLAE	14679	GCTCTTACGACGCTTGCGGAG	29002	GCACTCACAACACTCGCAGAA
357	ALTTLGP	14680	GCTCTGACTACGCTTGGTCCG	29003	GCACTCACAACACTCGGACCA
358	ALTVLLE	14681	GCGTTGACGGTTCTGTTGGAG	29004	GCACTCACAGTCCTCCTCGAA
359	ALVSSNL	14682	GCGCTGGTGTCGTCTAATCTT	29005	GCACTCGTCAGCAGCAACCTC
360	ALYDNAP	14683	GCGCTGTATGATAATGCGCCT	29006	GCACTCTACGACAACGCACCA
361	ALYNTPP	14684	GCTCTTTATAATACTCCGCCG	29007	GCACTCTACAACACACCACCA
362	ALYTHLD	14685	GCGTTGTATACTCATTTGGAT	29008	GCACTCTACACACACCTCGAC
363	AMAASPA	14686	GCGATGGCGGCTTCTCCTGCT	29009	GCAATGGCAGCAAGCCCAGCA
364	AMAPKLS	14687	GCTATGGCTCCTAAGCTGTCT	29010	GCAATGGCACCAAAACTCAGC
365	AMARPSG	14688	GCTATGGCGCGGCCGTCGGGG	29011	GCAATGGCAAGACCAAGCGGA
366	AMEHSVK	14689	GCTATGGAGCATTCTGTTAAG	29012	GCAATGGAACACAGCGTCAAA
367	AMETCDL	14690	GCGATGGAGACGTGTGATCTG	29013	GCAATGGAAACATGCGACCTC
368	AMGPSAS	14691	GCGATGGGTCCGTCTGCTTCG	29014	GCAATGGGACCAAGCGCAAGC
369	AMIQMRE	14692	GCGATGATTCAGATGCGTGAG	29015	GCAATGATCCAAATGAGAGAA
370	AMKAQNT	14693	GCGATGAAGGCTCAGAATACT	29016	GCAATGAAAGCACAAAACACA
371	AMKDNRS	14694	GCTATGAAGGATAATCGGAGT	29017	GCAATGAAAGACAACAGAAGC
372	AMKLNMP	14695	GCGATGAAGCTTAATATGCCT	29018	GCAATGAAACTCAACATGCCA
373	AMMQHVA	14696	GCTATGATGCAGCATGTTGCT	29019	GCAATGATGCAACACGTCGCA
374	AMMSAES	14697	GCGATGATGAGTGCTGAGTCT	29020	GCAATGATGAGCGCAGAAAGC
375	AMPGLGV	14698	GCTATGCCTGGGCTTGGGGTT	29021	GCAATGCCAGGACTCGGAGTC
376	AMPGLQS	14699	GCTATGCCTGGGCTGCAGTCT	29022	GCAATGCCAGGACTCCAAAGC
377	AMPRLTP	14700	GCGATGCCGCGTCTGACGCCT	29023	GCAATGCCAAGACTCACACCA
378	AMPRQVS	14701	GCTATGCCTAGGCAGGTGAGT	29024	GCAATGCCAAGACAAGTCAGC
379	AMPTVVA	14702	GCTATGCCGACGGTTGTGGCG	29025	GCAATGCCAACAGTCGTCGCA
380	AMQTDRV	14703	GCTATGCAGACGGATAGGGTT	29026	GCAATGCAAACAGACAGAGTC
381	AMRPSHE	14704	GCTATGCGGCCTTCGCATGAG	29027	GCAATGAGACCAAGCCACGAA
382	AMSLIHA	14705	GCGATGTCGCTTATTCATGCG	29028	GCAATGAGCCTCATCCACGCA
383	AMSSASY	14706	GCGATGTCGTCGGCTTCTTAT	29029	GCAATGAGCAGCGCAAGCTAC
384	AMSSIAG	14707	GCGATGTCGTCTATTGCTGGG	29030	GCAATGAGCAGCATCGCAGGA
385	AMSTQLS	14708	GCGATGAGTACGCAGCTGTCT	29031	GCAATGAGCACACAACTCAGC
386	AMTDKVQ	14709	GCTATGACGGATAAGGTGCAG	29032	GCAATGACAGACAAAGTCCAA
387	AMTDVRG	14710	GCGATGACTGATGTTCGTGGT	29033	GCAATGACAGACGTCAGAGGA
388	AMTHMPS	14711	GCTATGACTCATATGCCTTCG	29034	GCAATGACACACATGCCAAGC
389	AMTLRSD	14712	GCTATGACTTTGCGTAGTGAT	29035	GCAATGACACTCAGAAGCGAC
390	AMTSPKL	14713	GCGATGACTTCTCCTAAGCTT	29036	GCAATGACAAGCCCAAAACTC
391	AMWGADA	14714	GCGATGTGGGGGGCGGATGCT	29037	GCAATGTGGGGAGCAGACGCA
392	ANAGGSP	14715	GCTAATGCTGGTGGGTCGCCG	29038	GCAAACGCAGGAGGAAGCCCA
393	ANDSRAV	14716	GCGAATGATAGTCGTGCGGTT	29039	GCAAACGACAGCAGAGCAGTC
394	ANEDFRK	14717	GCTAATGAGGATTTTCGGAAG	29040	GCAAACGAAGACTTCAGAAAA

395	ANEPDVL	14718	GCGAATGAGCCTGATGTGCTT	29041	GCAAACGAACCAGACGTCCTC
396	ANGASSP	14719	GCGAATGGGGCTAGTAGTCCG	29042	GCAAACGGAGCAAGCAGCCCA
397	ANHGATF	14720	GCTAATCATGGTGCTACTTTT	29043	GCAAACCACGGAGCAACATTC
398	ANHTTRS	14721	GCGAATCATACGACTCGGTCG	29044	GCAAACCACACAACAAGAAGC
399	ANKPQVT	14722	GCGAATAAGCCGCAGGTTACG	29045	GCAAACAAACCACAAGTCACA
400	ANLGLPP	14723	GCGAATCTTGGTTTGCCGCCT	29046	GCAAACCTCGGACTCCCACCA
401	ANLGSAR	14724	GCTAATCTTGGTAGTGCGAGG	29047	GCAAACCTCGGAAGCGCAAGA
402	ANLPGHL	14725	GCGAATCTGCCTGGTCATTTG	29048	GCAAACCTCCCAGGACACCTC
403	ANMTRVE	14726	GCGAATATGACTAGGGTTGAG	29049	GCAAACATGACAAGAGTCGAA
404	ANMTVHC	14727	GCGAATATGACTGTGCATTGT	29050	GCAAACATGACAGTCCACTGC
405	ANPAKTV	14728	GCTAATCCTGCTAAGACTGTT	29051	GCAAACCCAGCAAAAACAGTC
406	ANPGKIY	14729	GCTAATCCTGGTAAGATTTAT	29052	GCAAACCCAGGAAAAATCTAC
407	ANPGTAP	14730	GCGAATCCGGGGACTGCTCCG	29053	GCAAACCCAGGAACAGCACCA
408	ANPLLSS	14731	GCGAATCCTCTGCTGTCGTCT	29054	GCAAACCCACTCCTCAGCAGC
409	ANQGIDS	14732	GCTAATCAGGGTATTGATTCG	29055	GCAAACCAAGGAATCGACAGC
410	ANQNNKN	14733	GCGAATCAGAATAATAAGAAT	29056	GCAAACCAAAACAACAAAAAC
411	ANQSLPS	14734	GCTAATCAGTCTTTGCCGAGT	29057	GCAAACCAAAGCCTCCCAAGC
412	ANRSGHG	14735	GCGAATCGTTCTGGTCATGGT	29058	GCAAACAGAAGCGGACACGGA
413	ANSDWGP	14736	GCTAATAGTGATTGGGGTCCG	29059	GCAAACAGCGACTGGGGACCA
414	ANSEEFV	14737	GCTAATAGTGAGGAGTTTGTG	29060	GCAAACAGCGAAGAATTCGTC
415	ANSGPPP	14738	GCTAATTCTGGTCCGCCGCCG	29061	GCAAACAGCGGACCACCACCA
416	ANSHEQM	14739	GCTAATTCTCATGAGCAGATG	29062	GCAAACAGCCACGAACAAATG
417	ANSHMLK	14740	GCGAATAGTCATATGCTTAAG	29063	GCAAACAGCCACATGCTCAAA
418	ANSMMHP	14741	GCGAATTCGATGATGCATCCG	29064	GCAAACAGCATGATGCACCCA
419	ANSNSVY	14742	GCGAATTCGAATTCGGTGTAT	29065	GCAAACAGCAACAGCGTCTAC
420	ANSRLGG	14743	GCGAATTCTAGGTTGGGTGGG	29066	GCAAACAGCAGACTCGGAGGA
421	ANSRPTQ	14744	GCTAATTCGAGGCCTACTCAG	29067	GCAAACAGCAGACCAACACAA
422	ANSRSMV	14745	GCTAATTCGCGTTCGATGGTG	29068	GCAAACAGCAGAAGCATGGTC
423	ANSSSPG	14746	GCTAATTCTAGTTCTCCTGGG	29069	GCAAACAGCAGCAGCCCAGGA
424	ANSTKGL	14747	GCTAATTCGACTAAGGGTCTG	29070	GCAAACAGCACAAAAGGACTC
425	ANTDPRN	14748	GCTAATACTGATCCGAGGAAT	29071	GCAAACACAGACCCAAGAAAC
426	ANTETIW	14749	GCTAATACGGAGACGATTTGG	29072	GCAAACACAGAAACAATCTGG
427	ANTLLHV	14750	GCGAATACTCTTTTGCATGTT	29073	GCAAACACACTCCTCCACGTC
428	ANVASSG	14751	GCGAATGTGGCTTCTTCGGGT	29074	GCAAACGTCGCAAGCAGCGGA
429	ANVSSTH	14752	GCGAATGTTTCTAGTACTCAT	29075	GCAAACGTCAGCAGCACACAC
430	ANVSVQV	14753	GCTAATGTGTCTGTGCAGGTT	29076	GCAAACGTCAGCGTCCAAGTC
431	APADHRM	14754	GCTCCGGCTGATCATAGGATG	29077	GCACCAGCAGACCACAGAATG
432	APADMTS	14755	GCTCCGGCGGATATGACGAGT	29078	GCACCAGCAGACATGACAAGC
433	APADWPV	14756	GCGCCTGCGGATTGGCCGGTG	29079	GCACCAGCAGACTGGCCAGTC
434	APAGRPS	14757	GCGCCGGCGGGGAGGCCTAGT	29080	GCACCAGCAGGAAGACCAAGC
435	APALGLA	14758	GCTCCTGCTTTGGGGCTTGCT	29081	GCACCAGCACTCGGACTCGCA
436	APANDEG	14759	GCTCCTGCTAATGATGAGGGT	29082	GCACCAGCAAACGACGAAGGA
437	APAQRLY	14760	GCTCCGGCTCAGAGGTTGTAT	29083	GCACCAGCACAAAGACTCTAC
438	APARMVN	14761	GCGCCGGCTCGGATGGTGAAT	29084	GCACCAGCAAGAATGGTCAAC
439	APDGTYL	14762	GCGCCGGATGGGACTTATTTG	29085	GCACCAGACGGAACATACCTC

440	APDPSSL	14763	GCTCCGGATCCTTCGTCTCTG	29086	GCACCAGACCCAAGCAGCCTC
441	APEDAGS	14764	GCGCCTGAGGATGCTGGTTCT	29087	GCACCAGAAGACGCAGGAAGC
442	APETNDS	14765	GCTCCGGAGACGAATGATTCT	29088	GCACCAGAAACAAACGACAGC
443	APFNTQG	14766	GCTCCGTTTAATACTCAGGGG	29089	GCACCATTCAACACACAAGGA
444	APFPEKW	14767	GCGCCTTTTCCGGAGAAGTGG	29090	GCACCATTCCCAGAAAAATGG
445	APFPEQP	14768	GCGCCGTTTCCTGAGCAGCCT	29091	GCACCATTCCCAGAACAACCA
446	APGITNY	14769	GCTCCTGGTATTACGAATTAT	29092	GCACCAGGAATCACAAACTAC
447	APGLRHS	14770	GCGCCTGGGTTGCGTCATAGT	29093	GCACCAGGACTCAGACACAGC
448	APGRLSL	14771	GCGCCGGGTCGTTTGTCGCTT	29094	GCACCAGGAAGACTCAGCCTC
449	APHFPST	14772	GCTCCGCATTTTCCTTCGACT	29095	GCACCACACTTCCCAAGCACA
450	APHLPTH	14773	GCTCCTCATCTGCCTACGCAT	29096	GCACCACACCTCCCAACACAC
451	APILRTP	14774	GCTCCGATTTTGCGTACTCCG	29097	GCACCAATCCTCAGAACACCA
452	APISHQM	14775	GCGCCTATTTCTCATCAGATG	29098	GCACCAATCAGCCACCAAATG
453	APLAVRP	14776	GCTCCGTTGGCGGTTAGGCCG	29099	GCACCACTCGCAGTCAGACCA
454	APLKSVQ	14777	GCGCCTTTGAAGTCTGTGCAG	29100	GCACCACTCAAAAGCGTCCAA
455	APNLLIG	14778	GCGCCTAATTTGTTGATTGGG	29101	GCACCAAACCTCCTCATCGGA
456	APNSGVK	14779	GCTCCTAATAGTGGTGTGAAG	29102	GCACCAAACAGCGGAGTCAAA
457	APNTSVR	14780	GCTCCGAATACGTCTGTGCGT	29103	GCACCAAACACAAGCGTCAGA
458	APPNLES	14781	GCGCCTCCTAATCTGGAGTCT	29104	GCACCACCAAACCTCGAAAGC
459	APPNVRT	14782	GCGCCTCCTAATGTTCGGACT	29105	GCACCACCAAACGTCAGAACA
460	APPSLRT	14783	GCTCCGCCTTCGCTGCGTACG	29106	GCACCACCAAGCCTCAGAACA
461	APQAKTP	14784	GCGCCGCAGGCGAAGACTCCG	29107	GCACCACAAGCAAAAACACCA
462	APQGRQI	14785	GCTCCGCAGGGTCGGCAGATT	29108	GCACCACAAGGAAGACAAATC
463	APQLQPA	14786	GCTCCGCAGTTGCAGCCGGCT	29109	GCACCACAACTCCAACCAGCA
464	APQPKDP	14787	GCGCCTCAGCCTAAGGATCCG	29110	GCACCACAACCAAAAGACCCA
465	APRAVNY	14788	GCTCCTAGGGCTGTGAATTAT	29111	GCACCAAGAGCAGTCAACTAC
466	APRLTVS	14789	GCGCCGCGGCTTACTGTGTCG	29112	GCACCAAGACTCACAGTCAGC
467	APRPPLV	14790	GCTCCTCGGCCTCCTCTTGTG	29113	GCACCAAGACCACCACTCGTC
468	APRQTHN	14791	GCGCCTCGGCAGACTCATAAT	29114	GCACCAAGACAAACACACAAC
469	APRTHST	14792	GCTCCGCGTACGCATTCTACG	29115	GCACCAAGAACACACAGCACA
470	APRVLQT	14793	GCGCCGAGGGTTCTTCAGACG	29116	GCACCAAGAGTCCTCCAAACA
471	APRYELR	14794	GCGCCTCGTTATGAGCTTCGG	29117	GCACCAAGATACGAACTCAGA
472	APSGSTS	14795	GCGCCTTCTGGTAGTACGTCG	29118	GCACCAAGCGGAAGCACAAGC
473	APSGVKP	14796	GCGCCTAGTGGGGTTAAGCCT	29119	GCACCAAGCGGAGTCAAACCA
474	APSKMAI	14797	GCTCCGTCGAAGATGGCTATT	29120	GCACCAAGCAAAATGGCAATC
475	APSRCAL	14798	GCTCCGAGTAGGTGTGCGTTG	29121	GCACCAAGCAGATGCGCACTC
476	APSSAEN	14799	GCGCCGTCGTCGGCGGAGAAT	29122	GCACCAAGCAGCGCAGAAAAC
477	APSTLNN	14800	GCTCCGTCGACGCTTAATAAT	29123	GCACCAAGCACACTCAACAAC
478	APSVRPI	14801	GCGCCTTCTGTTCGGCCGATT	29124	GCACCAAGCGTCAGACCAATC
479	APSVVTT	14802	GCGCCTAGTGTTGTTACGACT	29125	GCACCAAGCGTCGTCACAACA
480	APTAGSM	14803	GCGCCTACTGCGGGTAGTATG	29126	GCACCAACAGCAGGAAGCATG
481	APTPHPS	14804	GCGCCTACTCCTCATCCTAGT	29127	GCACCAACACCACACCCAAGC
482	APTPKGI	14805	GCTCCTACGCCTAAGGGTATT	29128	GCACCAACACCAAAAGGAATC
483	APTRNPQ	14806	GCGCCTACTAGGAATCCGCAG	29129	GCACCAACAAGAAACCCACAA
484	APTTPSL	14807	GCTCCGACTACTCCTTCGCTT	29130	GCACCAACAACACCAAGCCTC

485	APTVSNI	14808	GCTCCTACTGTTTCTAATATT	29131	GCACCAACAGTCAGCAACATC
486	APVPDQT	14809	GCTCCTGTGCCGGATCAGACG	29132	GCACCAGTCCCAGACCAAACA
487	APVTDNF	14810	GCGCCGGTGACTGATAATTTT	29133	GCACCAGTCACAGACAACTTC
488	AQALRGH	14811	GCTCAGGCGCTGAGGGGTCAT	29134	GCACAAGCACTCAGAGGACAC
489	AQAPRTE	14812	GCGCAGGCTCCTCGGACTGAG	29135	GCACAAGCACCAAGAACAGAA
490	AQATSSL	14813	GCGCAGGCTACTAGTAGTCTT	29136	GCACAAGCAACAAGCAGCCTC
491	AQCSTHL	14814	GCGCAGTGTTCGACGCATCTT	29137	GCACAATGCAGCACACACCTC
492	AQDRATR	14815	GCGCAGGATCGTGCGACGCGG	29138	GCACAAGACAGAGCAACAAGA
493	AQFSTKD	14816	GCGCAGTTTTCTACTAAGGAT	29139	GCACAATTCAGCACAAAAGAC
494	AQGQTML	14817	GCTCAGGGTCAGACGATGCTT	29140	GCACAAGGACAAACAATGCTC
495	AQGQVTP	14818	GCTCAGGGTCAGGTTACGCCT	29141	GCACAAGGACAAGTCACACCA
496	AQGWTSG	14819	GCTCAGGGTTGGACTAGTGGT	29142	GCACAAGGATGGACAAGCGGA
497	AQHKLGL	14820	GCGCAGCATAAGTTGGGTTTG	29143	GCACAACACAAACTCGGACTC
498	AQHRGET	14821	GCGCAGCATCGTGGGGAGACG	29144	GCACAACACAGAGGAGAAACA
499	AQIHMEM	14822	GCGCAGATTCATATGGAGATG	29145	GCACAAATCCACATGGAAATG
500	AQKPTTM	14823	GCGCAGAAGCCGACGACGATG	29146	GCACAAAAACCAACAACAATG
501	AQKPVVI	14824	GCTCAGAAGCCTGTGGTTATT	29147	GCACAAAAACCAGTCGTCATC
502	AQKQKAP	14825	GCTCAGAAGCAGAAGGCGCCG	29148	GCACAAAAACAAAAAGCACCA
503	AQNMRNN	14826	GCGCAGAATATGCGGAATAAT	29149	GCACAAAACATGAGAAACAAC
504	AQPGTVF	14827	GCTCAGCCGGGTACTGTTTTT	29150	GCACAACCAGGAACAGTCTTC
505	AQPSLYA	14828	GCGCAGCCGTCGCTGTATGCT	29151	GCACAACCAAGCCTCTACGCA
506	AQPTRAD	14829	GCGCAGCCTACGCGGGCTGAT	29152	GCACAACCAACAAGAGCAGAC
507	AQPVSRL	14830	GCTCAGCCGGTGTCTAGGTTG	29153	GCACAACCAGTCAGCAGACTC
508	AQRLSGG	14831	GCTCAGCGTCTTAGTGGGGGT	29154	GCACAAAGACTCAGCGGAGGA
509	AQRNTSP	14832	GCTCAGCGGAATACGTCGCCG	29155	GCACAAAGAAACACAAGCCCA
510	AQRPTSV	14833	GCGCAGAGGCCTACGTCTGTG	29156	GCACAAAGACCAACAAGCGTC
511	AQSGAIS	14834	GCTCAGAGTGGGGCGATTTCG	29157	GCACAAAGCGGAGCAATCAGC
512	AQSRSPL	14835	GCGCAGTCGAGGTCTCCTTTG	29158	GCACAAAGCAGAAGCCCACTC
513	AQTSLRL	14836	GCTCAGACGAGTTTGCGTCTG	29159	GCACAAACAAGCCTCAGACTC
514	AQTSMHT	14837	GCTCAGACGTCGATGCATACT	29160	GCACAAACAAGCATGCACACA
515	AQYIPST	14838	GCTCAGTATATTCCGTCTACG	29161	GCACAATACATCCCAAGCACA
516	AQYPKPN	14839	GCTCAGTATCCTAAGCCTAAT	29162	GCACAATACCCAAAACCAAAC
517	ARAGDLV	14840	GCTCGGGCGGGTGATCTGGTT	29163	GCAAGAGCAGGAGACCTCGTC
518	ARAHDST	14841	GCTAGGGCGCATGATTCTACT	29164	GCAAGAGCACACGACAGCACA
519	ARAHLTA	14842	GCGCGGGCGCATCTGACTGCT	29165	GCAAGAGCACACCTCACAGCA
520	ARALSPN	14843	GCGCGTGCTCTTAGTCCGAAT	29166	GCAAGAGCACTCAGCCCAAAC
521	ARAPGEL	14844	GCTCGGGCTCCGGGTGAGCTT	29167	GCAAGAGCACCAGGAGAACTC
522	ARAPGPI	14845	GCTCGTGCTCCTGGTCCGATT	29168	GCAAGAGCACCAGGACCAATC
523	ARAPTLM	14846	GCGCGGGCGCCTACGTTGATG	29169	GCAAGAGCACCAACACTCATG
524	ARASPMT	14847	GCGAGGGCTTCGCCGATGACT	29170	GCAAGAGCAAGCCCAATGACA
525	ARDFNAS	14848	GCTAGGGATTTTAATGCGTCG	29171	GCAAGAGACTTCAACGCAAGC
526	ARDGVSL	14849	GCGAGGGATGGTGTGAGTCTT	29172	GCAAGAGACGGAGTCAGCCTC
527	ARDLPAY	14850	GCGAGGGATTTGCCGGCTTAT	29173	GCAAGAGACCTCCCAGCATAC
528	ARDMVPH	14851	GCTCGTGATATGGTTCCTCAT	29174	GCAAGAGACATGGTCCCACAC
529	ARDQRSP	14852	GCGCGTGATCAGCGTAGTCCG	29175	GCAAGAGACCAAAGAAGCCCA

530	AREHSQL	14853	GCGCGGGAGCATTCTCAGCTT	29176	GCAAGAGAACACAGCCAACTC
531	ARELGRS	14854	GCTCGTGAGTTGGGGCGGTCG	29177	GCAAGAGAACTCGGAAGAAGC
532	ARFDVGS	14855	GCGAGGTTTGATGTTGGGTCG	29178	GCAAGATTCGACGTCGGAAGC
533	ARFETGH	14856	GCTAGGTTTGAGACTGGTCAT	29179	GCAAGATTCGAAACAGGACAC
534	ARGLAAH	14857	GCTCGGGGTCTTGCGGCGCAT	29180	GCAAGAGGACTCGCAGCACAC
535	ARGNAQA	14858	GCGCGGGGGAATGCGCAGGCT	29181	GCAAGAGGAAACGCACAAGCA
536	ARGNVMI	14859	GCGCGTGGTAATGTTATGATT	29182	GCAAGAGGAAACGTCATGATC
537	ARGSDAS	14860	GCTCGTGGTTCGGATGCTTCG	29183	GCAAGAGGAAGCGACGCAAGC
538	ARGSMTL	14861	GCGCGTGGTTCTATGACGTTG	29184	GCAAGAGGAAGCATGACACTC
539	ARGVASP	14862	GCGAGGGGTGTTGCTAGTCCT	29185	GCAAGAGGAGTCGCAAGCCCA
540	ARHASVA	14863	GCTCGGCATGCTTCTGTGGCT	29186	GCAAGACACGCAAGCGTCGCA
541	ARHMPIE	14864	GCTAGGCATATGCCGATTGAG	29187	GCAAGACACATGCCAATCGAA
542	ARIYESP	14865	GCGCGTATTTATGAGTCGCCG	29188	GCAAGAATCTACGAAAGCCCA
543	ARLATSE	14866	GCTCGTTTGGCTACTTCTGAG	29189	GCAAGACTCGCAACAAGCGAA
544	ARLGYDG	14867	GCTCGTCTTGGTTATGATGGT	29190	GCAAGACTCGGATACGACGGA
545	ARLNFAA	14868	GCTAGGCTTAATTTTGCTGCG	29191	GCAAGACTCAACTTCGCAGCA
546	ARLQTAV	14869	GCGCGTCTGCAGACTGCTGTG	29192	GCAAGACTCCAAACAGCAGTC
547	ARMGLGL	14870	GCGCGGATGGGGCTGGGGTTG	29193	GCAAGAATGGGACTCGGACTC
548	ARMPMLE	14871	GCGCGTATGCCGATGCTGGAG	29194	GCAAGAATGCCAATGCTCGAA
549	ARMPSPP	14872	GCTAGGATGCCTAGTCCGCCG	29195	GCAAGAATGCCAAGCCCACCA
550	ARMVDPI	14873	GCTAGGATGGTTGATCCTATT	29196	GCAAGAATGGTCGACCCAATC
551	ARMVGEP	14874	GCGCGTATGGTTGGTGAGCCT	29197	GCAAGAATGGTCGGAGAACCA
552	ARNPGPD	14875	GCGAGGAATCCTGGTCCGGAT	29198	GCAAGAAACCCAGGACCAGAC
553	ARNQAAQ	14876	GCGCGTAATCAGGCGGCTCAG	29199	GCAAGAAACCAAGCAGCACAA
554	ARNSLSD	14877	GCTCGTAATAGTCTGTCGGAT	29200	GCAAGAAACAGCCTCAGCGAC
555	ARPEIKY	14878	GCTCGGCCGGAGATTAAGTAT	29201	GCAAGACCAGAAATCAAATAC
556	ARPEYRV	14879	GCGCGGCCGGAGTATCGGGTG	29202	GCAAGACCAGAATACAGAGTC
557	ARPPNSY	14880	GCGCGTCCGCCGAATTCGTAT	29203	GCAAGACCACCAAACAGCTAC
558	ARPTEHE	14881	GCTCGGCCTACTGAGCATGAG	29204	GCAAGACCAACAGAACACGAA
559	ARQHFAP	14882	GCGAGGCAGCATTTTGCGCCG	29205	GCAAGACAACACTTCGCACCA
560	ARQHVGP	14883	GCTCGTCAGCATGTTGGTCCT	29206	GCAAGACAACACGTCGGACCA
561	ARQTMNE	14884	GCTCGTCAGACGATGAATGAG	29207	GCAAGACAAACAATGAACGAA
562	ARRDPPL	14885	GCGCGTCGTGATCCTCCGCTG	29208	GCAAGAAGAGACCCACCACTC
563	ARSAALA	14886	GCTCGGTCTGCTGCTCTGGCG	29209	GCAAGAAGCGCAGCACTCGCA
564	ARSAQTN	14887	GCGCGGAGTGCTCAGACTAAT	29210	GCAAGAAGCGCACAAACAAAC
565	ARSDRVS	14888	GCGCGGTCGGATCGTGTGTCG	29211	GCAAGAAGCGACAGAGTCAGC
566	ARSEPTP	14889	GCTCGGTCTGAGCCTACTCCT	29212	GCAAGAAGCGAACCAACACCA
567	ARSGEGF	14890	GCTCGGTCTGGGGAGGGTTTT	29213	GCAAGAAGCGGAGAAGGATTC
568	ARSHIVS	14891	GCTCGTTCGCATATTGTGTCG	29214	GCAAGAAGCCACATCGTCAGC
569	ARSISVV	14892	GCTAGGAGTATTTCGGTTGTT	29215	GCAAGAAGCATCAGCGTCGTC
570	ARSIVGP	14893	GCGCGGTCTATTGTTGGTCCG	29216	GCAAGAAGCATCGTCGGACCA
571	ARSNELH	14894	GCGCGGTCGAATGAGCTTCAT	29217	GCAAGAAGCAACGAACTCCAC
572	ARSPDVL	14895	GCTCGTTCGCCTGATGTTTTG	29218	GCAAGAAGCCCAGACGTCCTC
573	ARSPHVY	14896	GCTCGGTCTCCGCATGTTTAT	29219	GCAAGAAGCCCACACGTCTAC
574	ARSRPLE	14897	GCGCGGTCGAGGCCTTTGGAG	29220	GCAAGAAGCAGACCACTCGAA

575	ARSSDLE	14898	GCTCGTAGTTCTGATCTGGAG	29221	GCAAGAAGCAGCGACCTCGAA
576	ARSSPPL	14899	GCGCGTTCTAGTCCTCCGTTG	29222	GCAAGAAGCAGCCCACCACTC
577	ARSTVLG	14900	GCGAGGTCTACGGTGTTGGGG	29223	GCAAGAAGCACAGTCCTCGGA
578	ARSVATS	14901	GCGAGGTCTGTGGCTACTTCT	29224	GCAAGAAGCGTCGCAACAAGC
579	ARSVQDS	14902	GCGAGGAGTGTGCAGGATTCT	29225	GCAAGAAGCGTCCAAGACAGC
580	ARTASLP	14903	GCTCGGACTGCGTCGCTTCCT	29226	GCAAGAACAGCAAGCCTCCCA
581	ARTGAYS	14904	GCTCGTACGGGTGCGTATAGT	29227	GCAAGAACAGGAGCATACAGC
582	ARTLPQL	14905	GCTCGGACTCTGCCGCAGCTT	29228	GCAAGAACACTCCCACAACTC
583	ARTLSTH	14906	GCTAGGACGCTGAGTACTCAT	29229	GCAAGAACACTCAGCACACAC
584	ARTPVLY	14907	GCGCGTACTCCTGTTCTGTAT	29230	GCAAGAACACCAGTCCTCTAC
585	ARTSEEP	14908	GCTAGGACTAGTGAGGAGCCT	29231	GCAAGAACAAGCGAAGAACCA
586	ARTTVGL	14909	GCTCGTACGACGGTGGGGTTG	29232	GCAAGAACAACAGTCGGACTC
587	ARTVPSM	14910	GCTCGGACTGTGCCGTCTATG	29233	GCAAGAACAGTCCCAAGCATG
588	ARVDVSM	14911	GCTCGTGTGGATGTGTCTATG	29234	GCAAGAGTCGACGTCAGCATG
589	ARVNREP	14912	GCTCGGGTTAATCGTGAGCCG	29235	GCAAGAGTCAACAGAGAACCA
590	ARVSLEA	14913	GCTCGTGTGTCTCTTGAGGCT	29236	GCAAGAGTCAGCCTCGAAGCA
591	ARVVAPE	14914	GCGAGGGTTGTTGCTCCGGAG	29237	GCAAGAGTCGTCGCACCAGAA
592	ARYGGMV	14915	GCTAGGTATGGTGGTATGGTT	29238	GCAAGATACGGAGGAATGGTC
593	ASAFKQP	14916	GCGTCTGCGTTTAAGCAGCCG	29239	GCAAGCGCATTCAAACAACCA
594	ASAGGQP	14917	GCGAGTGCTGGTGGTCAGCCT	29240	GCAAGCGCAGGAGGACAACCA
595	ASAGPPP	14918	GCTTCGGCGGGGCCTCCGCCT	29241	GCAAGCGCAGGACCACCACCA
596	ASAQQVS	14919	GCTTCGGCGCAGCAGGTTTCT	29242	GCAAGCGCACAACAAGTCAGC
597	ASASNRG	14920	GCGTCGGCGAGTAATCGTGGG	29243	GCAAGCGCAAGCAACAGAGGA
598	ASCSSTT	14921	GCGTCTTGTTCTTCTACTACG	29244	GCAAGCTGCAGCAGCACAACA
599	ASDASCS	14922	GCGTCTGATGCTTCGTGTAGT	29245	GCAAGCGACGCAAGCTGCAGC
600	ASDLSLR	14923	GCGTCTGATTTGAGTCTTCGT	29246	GCAAGCGACCTCAGCCTCAGA
601	ASDMLKS	14924	GCGTCGGATATGCTTAAGAGT	29247	GCAAGCGACATGCTCAAAAGC
602	ASDNIRA	14925	GCGAGTGATAATATTAGGGCT	29248	GCAAGCGACAACATCAGAGCA
603	ASDPMKG	14926	GCTTCTGATCCTATGAAGGGT	29249	GCAAGCGACCCAATGAAAGGA
604	ASDTTTM	14927	GCGTCTGATACTACGACGATG	29250	GCAAGCGACACAACAACAATG
605	ASDVSRP	14928	GCTAGTGATGTGTCTCGTCCT	29251	GCAAGCGACGTCAGCAGACCA
606	ASEERAN	14929	GCGTCGGAGGAGCGGGCGAAT	29252	GCAAGCGAAGAAAGAGCAAAC
607	ASENSQN	14930	GCGTCTGAGAATTCGCAGAAT	29253	GCAAGCGAAAACAGCCAAAAC
608	ASERNRL	14931	GCTTCGGAGCGGAATAGGTTG	29254	GCAAGCGAAAGAAACAGACTC
609	ASEVSNA	14932	GCGAGTGAGGTGTCTAATGCG	29255	GCAAGCGAAGTCAGCAACGCA
610	ASFCTSW	14933	GCTTCTTTTTGTACGAGTTGG	29256	GCAAGCTTCTGCACAAGCTGG
611	ASFHGGV	14934	GCGTCTTTTCATGGGGGTGTG	29257	GCAAGCTTCCACGGAGGAGTC
612	ASFMEAA	14935	GCTTCTTTTATGGAGGCGGCG	29258	GCAAGCTTCATGGAAGCAGCA
613	ASFPATS	14936	GCTTCTTTTCCTGCTACTAGT	29259	GCAAGCTTCCCAGCAACAAGC
614	ASFRLMA	14937	GCGAGTTTTCGTTTGATGGCT	29260	GCAAGCTTCAGACTCATGGCA
615	ASGRAVG	14938	GCTAGTGGGAGGGCGGTGGGG	29261	GCAAGCGGAAGAGCAGTCGGA
616	ASGRQDL	14939	GCTTCTGGGAGGCAGGATCTT	29262	GCAAGCGGAAGACAAGACCTC
617	ASGSDDS	14940	GCGAGTGGGTCTGATGATTCG	29263	GCAAGCGGAAGCGACGACAGC
618	ASGSTSG	14941	GCTTCGGGGTCGACTTCTGGT	29264	GCAAGCGGAAGCACAAGCGGA
619	ASGTRAA	14942	GCGTCTGGGACGCGGGCGGCT	29265	GCAAGCGGAACAAGAGCAGCA

620	ASGTYTS	14943	GCGAGTGGTACTTATACTAGT	29266	GCAAGCGGAACATACACAAGC
621	ASGYLPQ	14944	GCTTCTGGTTATCTTCCGCAG	29267	GCAAGCGGATACCTCCCACAA
622	ASHERDF	14945	GCGTCTCATGAGCGTGATTTT	29268	GCAAGCCACGAAAGAGACTTC
623	ASHHLTE	14946	GCGTCTCATCATCTTACTGAG	29269	GCAAGCCACCACCTCACAGAA
624	ASHRSGD	14947	GCTTCTCATCGTTCGGGTGAT	29270	GCAAGCCACAGAAGCGGAGAC
625	ASIHTTS	14948	GCTTCTATTCATACGACGAGT	29271	GCAAGCATCCACACAACAAGC
626	ASISGSA	14949	GCTAGTATTTCTGGTAGTGCT	29272	GCAAGCATCAGCGGAAGCGCA
627	ASISIGA	14950	GCGAGTATTTCTATTGGGGCG	29273	GCAAGCATCAGCATCGGAGCA
628	ASLPSPR	14951	GCGTCTTTGCCGTCTCCGAGG	29274	GCAAGCCTCCCAAGCCCAAGA
629	ASLRATG	14952	GCGTCTCTTCGGGCGACTGGT	29275	GCAAGCCTCAGAGCAACAGGA
630	ASLSAAM	14953	GCTTCTTTGTCTGCGGCTATG	29276	GCAAGCCTCAGCGCAGCAATG
631	ASLSGSM	14954	GCGTCGTTGAGTGGTAGTATG	29277	GCAAGCCTCAGCGGAAGCATG
632	ASLSNLP	14955	GCGTCGTTGTCGAATTTGCCT	29278	GCAAGCCTCAGCAACCTCCCA
633	ASLSPLL	14956	GCTTCGCTGTCTCCGCTTTTG	29279	GCAAGCCTCAGCCCACTCCTC
634	ASMKPTI	14957	GCGTCTATGAAGCCGACTATT	29280	GCAAGCATGAAACCAACAATC
635	ASMNGLP	14958	GCGAGTATGAATGGGCTGCCG	29281	GCAAGCATGAACGGACTCCCA
636	ASMNMNA	14959	GCGTCGATGAATATGAATGCT	29282	GCAAGCATGAACATGAACGCA
637	ASNKSSL	14960	GCGTCGAATAAGTCTAGTCTG	29283	GCAAGCAACAAAAGCAGCCTC
638	ASNRVSY	14961	GCTTCGAATCGGGTTTCGTAT	29284	GCAAGCAACAGAGTCAGCTAC
639	ASNSALR	14962	GCTTCGAATAGTGCTTTGCGT	29285	GCAAGCAACAGCGCACTCAGA
640	ASPAAVH	14963	GCGAGTCCTGCGGCTGTTCAT	29286	GCAAGCCCAGCAGCAGTCCAC
641	ASPLNSS	14964	GCTAGTCCTCTTAATAGTTCT	29287	GCAAGCCCACTCAACAGCAGC
642	ASPPQTT	14965	GCGAGTCCTCCGCAGACTACG	29288	GCAAGCCCACCACAAACAACA
643	ASPQFNS	14966	GCTAGTCCTCAGTTTAATTCG	29289	GCAAGCCCACAATTCAACAGC
644	ASPRGRE	14967	GCGTCGCCTAGGGGGCGGGAG	29290	GCAAGCCCAAGAGGAAGAGAA
645	ASQAACL	14968	GCGTCGCAGGCGGCGTGTTTG	29291	GCAAGCCAAGCAGCATGCCTC
646	ASQIEPT	14969	GCGAGTCAGATTGAGCCTACG	29292	GCAAGCCAAATCGAACCAACA
647	ASQIRTT	14970	GCTTCTCAGATTCGGACTACG	29293	GCAAGCCAAATCAGAACAACA
648	ASQPSRV	14971	GCTTCGCAGCCGTCTCGTGTT	29294	GCAAGCCAACCAAGCAGAGTC
649	ASQQPRS	14972	GCTTCTCAGCAGCCTCGTTCT	29295	GCAAGCCAACAACCAAGAAGC
650	ASQRLGG	14973	GCTTCTCAGCGGTTGGGTGGT	29296	GCAAGCCAAAGACTCGGAGGA
651	ASQSRDA	14974	GCGTCTCAGTCGCGTGATGCG	29297	GCAAGCCAAAGCAGAGACGCA
652	ASQYRES	14975	GCGAGTCAGTATCGGGAGTCT	29298	GCAAGCCAATACAGAGAAAGC
653	ASRAPAG	14976	GCTTCTCGGGCTCCGGCTGGT	29299	GCAAGCAGAGCACCAGCAGGA
654	ASRAPSN	14977	GCTTCTCGTGCGCCTAGTAAT	29300	GCAAGCAGAGCACCAAGCAAC
655	ASRDNVD	14978	GCTTCTCGTGATAATGTTGAT	29301	GCAAGCAGAGACAACGTCGAC
656	ASRGMST	14979	GCTAGTCGGGGTATGTCGACG	29302	GCAAGCAGAGGAATGAGCACA
657	ASRPYLV	14980	GCTTCGCGGCCGTATTTGGTT	29303	GCAAGCAGACCATACCTCGTC
658	ASRSTTS	14981	GCTTCTCGTTCTACTACTTCG	29304	GCAAGCAGAAGCACAACAAGC
659	ASRTIAP	14982	GCGTCTAGGACTATTGCTCCT	29305	GCAAGCAGAACAATCGCACCA
660	ASRTTPL	14983	GCGAGTCGGACTACTCCTTTG	29306	GCAAGCAGAACAACACCACTC
661	ASSARPI	14984	GCTAGTTCGGCGCGTCCTATT	29307	GCAAGCAGCGCAAGACCAATC
662	ASSAVLT	14985	GCTAGTAGTGCTGTGCTGACG	29308	GCAAGCAGCGCAGTCCTCACA
663	ASSERGE	14986	GCTTCGTCGGAGCGTGGTGAG	29309	GCAAGCAGCGAAAGAGGAGAA
664	ASSGDVL	14987	GCTTCGTCTGGTGATGTTCTT	29310	GCAAGCAGCGGAGACGTCCTC

665	ASSGPDK	14988	GCGTCTTCTGGTCCGGATAAG	29311	GCAAGCAGCGGACCAGACAAA
666	ASSGRSA	14989	GCTTCTAGTGGTCGTTCGGCG	29312	GCAAGCAGCGGAAGAAGCGCA
667	ASSGSGT	14990	GCTTCGTCTGGGTCTGGGACT	29313	GCAAGCAGCGGAAGCGGAACA
668	ASSKGSN	14991	GCGTCTTCGAAGGGGTCTAAT	29314	GCAAGCAGCAAAGGAAGCAAC
669	ASSKPAN	14992	GCGTCGTCTAAGCCGGCGAAT	29315	GCAAGCAGCAAACCAGCAAAC
670	ASSKPLG	14993	GCGAGTTCGAAGCCGTTGGGG	29316	GCAAGCAGCAAACCACTCGGA
671	ASSPKIY	14994	GCGTCGTCTCCTAAGATTTAT	29317	GCAAGCAGCCCAAAAATCTAC
672	ASSPVLS	14995	GCTAGTAGTCCTGTGCTGTCG	29318	GCAAGCAGCCCAGTCCTCAGC
673	ASSQHGL	14996	GCTAGTAGTCAGCATGGTCTG	29319	GCAAGCAGCCAACACGGACTC
674	ASSRTVN	14997	GCGTCTAGTCGTACGGTGAAT	29320	GCAAGCAGCAGAACAGTCAAC
675	ASSSDSR	14998	GCTTCTTCGTCTGATTCTCGT	29321	GCAAGCAGCAGCGACAGCAGA
676	ASSSLSF	14999	GCTAGTAGTTCGCTGTCTTTT	29322	GCAAGCAGCAGCCTCAGCTTC
677	ASSTSLE	15000	GCGTCTTCGACTTCTTTGGAG	29323	GCAAGCAGCACAAGCCTCGAA
678	ASSVNPS	15001	GCTAGTAGTGTTAATCCGAGT	29324	GCAAGCAGCGTCAACCCAAGC
679	ASTALLL	15002	GCTTCGACTGCGCTTCTGCTG	29325	GCAAGCACAGCACTCCTCCTC
680	ASTGIVL	15003	GCGTCGACTGGTATTGTGCTT	29326	GCAAGCACAGGAATCGTCCTC
681	ASTGSFG	15004	GCGAGTACTGGGAGTTTTGGT	29327	GCAAGCACAGGAAGCTTCGGA
682	ASTGSQE	15005	GCTTCGACTGGTAGTCAGGAG	29328	GCAAGCACAGGAAGCCAAGAA
683	ASTLQVG	15006	GCGTCTACTTTGCAGGTTGGG	29329	GCAAGCACACTCCAAGTCGGA
684	ASTPNLL	15007	GCGTCGACTCCTAATTTGCTT	29330	GCAAGCACACCAAACCTCCTC
685	ASTQKQA	15008	GCTAGTACGCAGAAGCAGGCT	29331	GCAAGCACACAAAAACAAGCA
686	ASTRMLF	15009	GCGTCGACTCGGATGTTGTTT	29332	GCAAGCACAAGAATGCTCTTC
687	ASTTFRP	15010	GCGTCGACTACGTTTCGTCCG	29333	GCAAGCACAACATTCAGACCA
688	ASTTRML	15011	GCTTCGACGACTAGGATGCTT	29334	GCAAGCACAACAAGAATGCTC
689	ASVLQEA	15012	GCGTCGGTTCTTCAGGAGGCT	29335	GCAAGCGTCCTCCAAGAAGCA
690	ASVPLIP	15013	GCGTCGGTGCCTTTGATTCCT	29336	GCAAGCGTCCCACTCATCCCA
691	ASVRMGD	15014	GCTAGTGTGCGGATGGGTGAT	29337	GCAAGCGTCAGAATGGGAGAC
692	ASVSMVA	15015	GCTAGTGTGAGTATGGTTGCG	29338	GCAAGCGTCAGCATGGTCGCA
693	ASVSTEG	15016	GCTTCTGTTAGTACGGAGGGG	29339	GCAAGCGTCAGCACAGAAGGA
694	ASWDINI	15017	GCTAGTTGGGATATTAATATT	29340	GCAAGCTGGGACATCAACATC
695	ASWDSNI	15018	GCTAGTTGGGATAGTAATATT	29341	GCAAGCTGGGACAGCAACATC
696	ASYDTSR	15019	GCTTCTTATGATACTAGTCGG	29342	GCAAGCTACGACACAAGCAGA
697	ASYDVSS	15020	GCGTCGTATGATGTTTCGTCG	29343	GCAAGCTACGACGTCAGCAGC
698	ATAATAY	15021	GCTACTGCTGCGACTGCTTAT	29344	GCAACAGCAGCAACAGCATAC
699	ATAATTS	15022	GCGACTGCTGCGACTACGAGT	29345	GCAACAGCAGCAACAACAAGC
700	ATAGLYQ	15023	GCTACTGCGGGTCTGTATCAG	29346	GCAACAGCAGGACTCTACCAA
701	ATAKILD	15024	GCGACGGCTAAGATTCTGGAT	29347	GCAACAGCAAAAATCCTCGAC
702	ATAKLLP	15025	GCTACGGCGAAGCTTTTGCCT	29348	GCAACAGCAAAACTCCTCCCA
703	ATAKPLI	15026	GCTACTGCTAAGCCTCTTATT	29349	GCAACAGCAAAACCACTCATC
704	ATARQVQ	15027	GCGACTGCGCGGCAGGTGCAG	29350	GCAACAGCAAGACAAGTCCAA
705	ATASTSS	15028	GCTACTGCTTCTACTTCTTCT	29351	GCAACAGCAAGCACAAGCAGC
706	ATASYNG	15029	GCGACGGCGTCTTATAATGGT	29352	GCAACAGCAAGCTACAACGGA
707	ATAVHDY	15030	GCGACTGCGGTGCATGATTAT	29353	GCAACAGCAGTCCACGACTAC
708	ATDHMSP	15031	GCGACTGATCATATGTCTCCT	29354	GCAACAGACCACATGAGCCCA
709	ATDYQSM	15032	GCGACTGATTATCAGAGTATG	29355	GCAACAGACTACCAAAGCATG

710	ATEAPLK	15033	GCGACGGAGGCGCCGTTGAAG	29356	GCAACAGAAGCACCACTCAAA
711	ATEGHPW	15034	GCTACGGAGGGTCATCCTTGG	29357	GCAACAGAAGGACACCCATGG
712	ATFVTSK	15035	GCTACGTTTGTTACTTCTAAG	29358	GCAACATTCGTCACAAGCAAA
713	ATGGHSP	15036	GCTACGGGGGGGCATAGTCCT	29359	GCAACAGGAGGACACAGCCCA
714	ATGTSAG	15037	GCTACTGGTACGTCTGCGGGT	29360	GCAACAGGAACAAGCGCAGGA
715	ATGVLMS	15038	GCTACTGGGGTGCTGATGAGT	29361	GCAACAGGAGTCCTCATGAGC
716	ATGVQNY	15039	GCTACGGGGGTTCAGAATTAT	29362	GCAACAGGAGTCCAAAACTAC
717	ATHILKL	15040	GCTACGCATATTTTGAAGCTT	29363	GCAACACACATCCTCAAACTC
718	ATHSLLS	15041	GCTACTCATTCTCTTCTGTCT	29364	GCAACACACAGCCTCCTCAGC
719	ATHVCVS	15042	GCGACGCATGTTTGTGTGTCT	29365	GCAACACACGTCTGCGTCAGC
720	ATIPRTP	15043	GCTACGATTCCGAGGACGCCG	29366	GCAACAATCCCAAGAACACCA
721	ATKFQGM	15044	GCGACTAAGTTTCAGGGGATG	29367	GCAACAAAATTCCAAGGAATG
722	ATKGISF	15045	GCTACGAAGGGTATTTCTTTT	29368	GCAACAAAAGGAATCAGCTTC
723	ATKHDCK	15046	GCGACTAAGCATGATTGTAAG	29369	GCAACAAAACACGACTGCAAA
724	ATLHREL	15047	GCTACGTTGCATCGTGAGCTT	29370	GCAACACTCCACAGAGAACTC
725	ATLKIPV	15048	GCTACTTTGAAGATTCCTGTT	29371	GCAACACTCAAAATCCCAGTC
726	ATLRIVE	15049	GCTACTCTTCGTATTGTGGAG	29372	GCAACACTCAGAATCGTCGAA
727	ATLRPND	15050	GCGACTCTTAGGCCTAATGAT	29373	GCAACACTCAGACCAAACGAC
728	ATLRTAT	15051	GCTACTTTGCGGACGGCTACG	29374	GCAACACTCAGAACAGCAACA
729	ATLSTNA	15052	GCGACTTTGTCGACGAATGCT	29375	GCAACACTCAGCACAAACGCA
730	ATLTLSA	15053	GCGACTCTGACGTTGAGTGCG	29376	GCAACACTCACACTCAGCGCA
731	ATLVSAE	15054	GCGACTTTGGTGAGTGCGGAG	29377	GCAACACTCGTCAGCGCAGAA
732	ATMPSTM	15055	GCTACTATGCCTTCGACTATG	29378	GCAACAATGCCAAGCACAATG
733	ATMRPRD	15056	GCTACTATGCGTCCTCGTGAT	29379	GCAACAATGAGACCAAGAGAC
734	ATMSLSS	15057	GCTACGATGTCGTTGTCTTCT	29380	GCAACAATGAGCCTCAGCAGC
735	ATMSMRG	15058	GCGACGATGTCGATGAGGGGG	29381	GCAACAATGAGCATGAGAGGA
736	ATMVTTS	15059	GCGACTATGGTGACGACGTCT	29382	GCAACAATGGTCACAACAAGC
737	ATNAHQS	15060	GCGACGAATGCTCATCAGTCG	29383	GCAACAAACGCACACCAAAGC
738	ATNRFPS	15061	GCGACGAATCGGTTTCCGTCT	29384	GCAACAAACAGATTCCCAAGC
739	ATNSSAT	15062	GCTACTAATTCTTCGGCTACT	29385	GCAACAAACAGCAGCGCAACA
740	ATNTRIA	15063	GCTACGAATACGAGGATTGCT	29386	GCAACAAACACAAGAATCGCA
741	ATPLRTS	15064	GCTACGCCTCTGCGTACTAGT	29387	GCAACACCACTCAGAACAAGC
742	ATPPMQN	15065	GCGACGCCGCCTATGCAGAAT	29388	GCAACACCACCAATGCAAAAC
743	ATPSAAI	15066	GCTACGCCTAGTGCTGCGATT	29389	GCAACACCAAGCGCAGCAATC
744	ATPTLSA	15067	GCGACTCCTACTCTTAGTGCT	29390	GCAACACCAACACTCAGCGCA
745	ATPVPHP	15068	GCGACGCCTGTTCCGCATCCG	29391	GCAACACCAGTCCCACACCCA
746	ATQNLPP	15069	GCTACTCAGAATCTGCCTCCT	29392	GCAACACAAAACCTCCCACCA
747	ATQRIVY	15070	GCGACGCAGCGGATTGTGTAT	29393	GCAACACAAAGAATCGTCTAC
748	ATQYGMN	15071	GCGACTCAGTATGGTATGAAT	29394	GCAACACAATACGGAATGAAC
749	ATRAESS	15072	GCGACGCGTGCGGAGTCGAGT	29395	GCAACAAGAGCAGAAAGCAGC
750	ATRLPDS	15073	GCTACGCGGCTTCCTGATTCT	29396	GCAACAAGACTCCCAGACAGC
751	ATRLTEK	15074	GCTACTCGGCTTACTGAGAAG	29397	GCAACAAGACTCACAGAAAAA
752	ATRPQAD	15075	GCTACTCGGCCGCAGGCTGAT	29398	GCAACAAGACCACAAGCAGAC
753	ATRTSLE	15076	GCTACTCGTACTTCGCTTGAG	29399	GCAACAAGAACAAGCCTCGAA
754	ATSITKS	15077	GCTACTAGTATTACGAAGTCG	29400	GCAACAAGCATCACAAAAAGC

755	ATSQMNF	15078	GCTACGTCTCAGATGAATTTT	29401	GCAACAAGCCAAATGAACTTC
756	ATSTLNL	15079	GCTACGTCGACTTTGAATCTT	29402	GCAACAAGCACACTCAACCTC
757	ATSTMTT	15080	GCTACTTCTACTATGACTACT	29403	GCAACAAGCACAATGACAACA
758	ATSTVFR	15081	GCTACTTCGACTGTGTTTAGG	29404	GCAACAAGCACAGTCTTCAGA
759	ATTAGSN	15082	GCTACTACGGCTGGTAGTAAT	29405	GCAACAACAGCAGGAAGCAAC
760	ATTAMGE	15083	GCGACGACTGCGATGGGTGAG	29406	GCAACAACAGCAATGGGAGAA
761	ATTGPPC	15084	GCGACGACTGGTCCTCCTTGT	29407	GCAACAACAGGACCACCATGC
762	ATTKDTT	15085	GCTACTACTAAGGATACTACT	29408	GCAACAACAAAAGACACAACA
763	ATTLIRP	15086	GCGACGACTTTGATTCGGCCG	29409	GCAACAACACTCATCAGACCA
764	ATTSRSS	15087	GCTACGACTTCGCGGTCTTCT	29410	GCAACAACAAGCAGAAGCAGC
765	ATTVASR	15088	GCTACTACTGTTGCTAGTCGT	29411	GCAACAACAGTCGCAAGCAGA
766	ATVMPTA	15089	GCTACTGTTATGCCGACGGCT	29412	GCAACAGTCATGCCAACAGCA
767	ATVMTLP	15090	GCGACGGTGATGACTTTGCCG	29413	GCAACAGTCATGACACTCCCA
768	ATVNPAV	15091	GCTACTGTTAATCCTGCGGTG	29414	GCAACAGTCAACCCAGCAGTC
769	ATVPQRT	15092	GCTACGGTGCCGCAGCGTACT	29415	GCAACAGTCCCACAAAGAACA
770	ATVRTML	15093	GCTACTGTTCGTACTATGTTG	29416	GCAACAGTCAGAACAATGCTC
771	ATVSDTL	15094	GCGACGGTGTCTGATACTCTT	29417	GCAACAGTCAGCGACACACTC
772	ATVSSLT	15095	GCTACGGTTTCGTCTCTGACG	29418	GCAACAGTCAGCAGCCTCACA
773	ATWPYKE	15096	GCGACGTGGCCGTATAAGGAG	29419	GCAACATGGCCATACAAAGAA
774	ATYARNE	15097	GCGACTTATGCGCGTAATGAG	29420	GCAACATACGCAAGAAACGAA
775	ATYTATA	15098	GCGACGTATACGGCTACTGCT	29421	GCAACATACACAGCAACAGCA
776	AVAGTLR	15099	GCGGTGGCGGGTACTTTGCGT	29422	GCAGTCGCAGGAACACTCAGA
777	AVALNTT	15100	GCTGTTGCGCTTAATACGACG	29423	GCAGTCGCACTCAACACAACA
778	AVAQMGI	15101	GCGGTTGCGCAGATGGGGATT	29424	GCAGTCGCACAAATGGGAATC
779	AVAVDFV	15102	GCTGTTGCGGTTGATTTTGTT	29425	GCAGTCGCAGTCGACTTCGTC
780	AVDHEGL	15103	GCTGTTGATCATGAGGGTTTG	29426	GCAGTCGACCACGAAGGACTC
781	AVDPGNP	15104	GCGGTGGATCCGGGTAATCCG	29427	GCAGTCGACCCAGGAAACCCA
782	AVDRSEI	15105	GCTGTGGATCGGTCGGAGATT	29428	GCAGTCGACAGAAGCGAAATC
783	AVECMPP	15106	GCTGTGGAGTGTATGCCTCCG	29429	GCAGTCGAATGCATGCCACCA
784	AVEPMWE	15107	GCGGTTGAGCCGATGTGGGAG	29430	GCAGTCGAACCAATGTGGGAA
785	AVETGYT	15108	GCTGTTGAGACGGGTTATACG	29431	GCAGTCGAAACAGGATACACA
786	AVFARLP	15109	GCTGTGTTTGCTCGGCTTCCG	29432	GCAGTCTTCGCAAGACTCCCA
787	AVGESEV	15110	GCTGTGGGTGAGTCTGAGGTG	29433	GCAGTCGGAGAAAGCGAAGTC
788	AVGNSLY	15111	GCTGTTGGGAATTCGCTGTAT	29434	GCAGTCGGAAACAGCCTCTAC
789	AVGQNMR	15112	GCTGTGGGGCAGAATATGCGG	29435	GCAGTCGGACAAAACATGAGA
790	AVHKMDM	15113	GCTGTGCATAAGATGGATATG	29436	GCAGTCCACAAAATGGACATG
791	AVHQLTL	15114	GCGGTGCATCAGCTGACGCTT	29437	GCAGTCCACCAACTCACACTC
792	AVHRENV	15115	GCTGTGCATCGTGAGAATGTT	29438	GCAGTCCACAGAGAAAACGTC
793	AVIGGMT	15116	GCTGTGATTGGGGGGATGACT	29439	GCAGTCATCGGAGGAATGACA
794	AVKGMPL	15117	GCTGTGAAGGGGATGCCTCTT	29440	GCAGTCAAAGGAATGCCACTC
795	AVKQLIV	15118	GCGGTGAAGCAGTTGATTGTT	29441	GCAGTCAAACAACTCATCGTC
796	AVLHTLG	15119	GCTGTTCTTCATACTCTGGGG	29442	GCAGTCCTCCACACACTCGGA
797	AVLKNRD	15120	GCTGTGTTGAAGAATCGGGAT	29443	GCAGTCCTCAAAAACAGAGAC
798	AVLNKED	15121	GCTGTGCTTAATAAGGAGGAT	29444	GCAGTCCTCAACAAAGAAGAC
799	AVLNSAD	15122	GCTGTTCTTAATTCTGCGGAT	29445	GCAGTCCTCAACAGCGCAGAC

800	AVLVPHA	15123	GCGGTGCTTGTTCCTCATGCG	29446	GCAGTCCTCGTCCCACACGCA
801	AVLVRED	15124	GCTGTTCTTGTGCGTGAGGAT	29447	GCAGTCCTCGTCAGAGAAGAC
802	AVMGRSE	15125	GCTGTGATGGGTCGTAGTGAG	29448	GCAGTCATGGGAAGAAGCGAA
803	AVMPRTP	15126	GCGGTTATGCCTCGGACGCCT	29449	GCAGTCATGCCAAGAACACCA
804	AVMRIAP	15127	GCTGTTATGCGTATTGCTCCT	29450	GCAGTCATGAGAATCGCACCA
805	AVNAAQA	15128	GCGGTTAATGCTGCGCAGGCT	29451	GCAGTCAACGCAGCACAAGCA
806	AVNFDVI	15129	GCTGTGAATTTTGATGTGATT	29452	GCAGTCAACTTCGACGTCATC
807	AVNPPEL	15130	GCGGTGAATCCTCCTGAGCTT	29453	GCAGTCAACCCACCAGAACTC
808	AVNRVPL	15131	GCTGTGAATCGTGTGCCTTTG	29454	GCAGTCAACAGAGTCCCACTC
809	AVPGPKS	15132	GCTGTGCCTGGGCCTAAGTCT	29455	GCAGTCCCAGGACCAAAAAGC
810	AVPLLLT	15133	GCTGTTCCGTTGCTTCTTACT	29456	GCAGTCCCACTCCTCCTCACA
811	AVPMRFP	15134	GCGGTTCCTATGCGTTTTCCT	29457	GCAGTCCCAATGAGATTCCCA
812	AVPSHAQ	15135	GCTGTGCCTAGTCATGCGCAG	29458	GCAGTCCCAAGCCACGCACAA
813	AVPVSHA	15136	GCTGTGCCGGTGTCTCATGCG	29459	GCAGTCCCAGTCAGCCACGCA
814	AVQTHGF	15137	GCGGTGCAGACGCATGGTTTT	29460	GCAGTCCAAACACACGGATTC
815	AVQTTDH	15138	GCTGTTCAGACGACTGATCAT	29461	GCAGTCCAAACAACAGACCAC
816	AVRASQQ	15139	GCGGTGCGTGCGTCTCAGCAG	29462	GCAGTCAGAGCAAGCCAACAA
817	AVRASTP	15140	GCTGTGCGTGCGAGTACTCCG	29463	GCAGTCAGAGCAAGCACACCA
818	AVRDSVL	15141	GCTGTTCGTGATTCTGTGTTG	29464	GCAGTCAGAGACAGCGTCCTC
819	AVRHQGD	15142	GCTGTTCGGCATCAGGGTGAT	29465	GCAGTCAGACACCAAGGAGAC
820	AVRLKME	15143	GCTGTTCGTTTGAAGATGGAG	29466	GCAGTCAGACTCAAAATGGAA
821	AVRPPPP	15144	GCTGTGCGTCCGCCTCCGCCT	29467	GCAGTCAGACCACCACCACCA
822	AVRRDDA	15145	GCTGTTCGTCGTGATGATGCT	29468	GCAGTCAGAAGAGACGACGCA
823	AVRSLTV	15146	GCGGTTCGGTCTCTGACTGTG	29469	GCAGTCAGAAGCCTCACAGTC
824	AVRTNPL	15147	GCTGTGCGTACTAATCCGTTG	29470	GCAGTCAGAACAAACCCACTC
825	AVSGHSL	15148	GCTGTTTCTGGTCATTCGCTG	29471	GCAGTCAGCGGACACAGCCTC
826	AVSHASD	15149	GCGGTGTCGCATGCGAGTGAT	29472	GCAGTCAGCCACGCAAGCGAC
827	AVSPYSL	15150	GCGGTTTCGCCTTATTCTTTG	29473	GCAGTCAGCCCATACAGCCTC
828	AVSRAGG	15151	GCTGTGAGTCGGGCGGGGGGT	29474	GCAGTCAGCAGAGCAGGAGGA
829	AVSRPNS	15152	GCGGTGTCTCGTCCGAATTCG	29475	GCAGTCAGCAGACCAAACAGC
830	AVTNSMI	15153	GCTGTTACGAATTCTATGATT	29476	GCAGTCACAAACAGCATGATC
831	AVTPLPL	15154	GCTGTTACGCCTTTGCCTCTT	29477	GCAGTCACACCACTCCCACTC
832	AVTSGFR	15155	GCGGTTACTAGTGGTTTTCGT	29478	GCAGTCACAAGCGGATTCAGA
833	AVTVNAY	15156	GCTGTGACTGTTAATGCGTAT	29479	GCAGTCACAGTCAACGCATAC
834	AVVGAIL	15157	GCTGTTGTGGGGGCGATTCTG	29480	GCAGTCGTCGGAGCAATCCTC
835	AVVRNQS	15158	GCGGTGGTTCGGAATCAGTCT	29481	GCAGTCGTCAGAAACCAAAGC
836	AVYNDVC	15159	GCTGTTTATAATGATGTTTGT	29482	GCAGTCTACAACGACGTCTGC
837	AVYSSEP	15160	GCTGTGTATAGTAGTGAGCCG	29483	GCAGTCTACAGCAGCGAACCA
838	AWNPNEK	15161	GCTTGGAATCCGAATGAGAAG	29484	GCATGGAACCCAAACGAAAAA
839	AWPNSLK	15162	GCTTGGCCGAATAGTCTTAAG	29485	GCATGGCCAAACAGCCTCAAA
840	AWTQQGP	15163	GCGTGGACGCAGCAGGGGCCT	29486	GCATGGACACAACAAGGACCA
841	AYAILEA	15164	GCTTATGCTATTCTGGAGGCG	29487	GCATACGCAATCCTCGAAGCA
842	AYAKAIA	15165	GCTTATGCGAAGGCTATTGCT	29488	GCATACGCAAAAGCAATCGCA
843	AYDKSLV	15166	GCTTATGATAAGTCGCTGGTT	29489	GCATACGACAAAAGCCTCGTC
844	AYDRAFS	15167	GCGTATGATAGGGCTTTTTCG	29490	GCATACGACAGAGCATTCAGC

845	AYDSAPY	15168	GCTTATGATTCTGCTCCTTAT	29491	GCATACGACAGCGCACCATAC
846	AYDSRAA	15169	GCTTATGATTCGCGGGCTGCT	29492	GCATACGACAGCAGAGCAGCA
847	AYEARTH	15170	GCGTATGAGGCGAGGACGCAT	29493	GCATACGAAGCAAGAACACAC
848	AYEGTLS	15171	GCGTATGAGGGTACTCTGAGT	29494	GCATACGAAGGAACACTCAGC
849	AYEPISK	15172	GCTTATGAGCCGATTTCTAAG	29495	GCATACGAACCAATCAGCAAA
850	AYFEVQP	15173	GCTTATTTTGAGGTTCAGCCT	29496	GCATACTTCGAAGTCCAACCA
851	AYGGPSA	15174	GCGTATGGGGGGCCGAGTGCT	29497	GCATACGGAGGACCAAGCGCA
852	AYGVIEK	15175	GCTTATGGTGTTACGGAGAAG	29498	GCATACGGAGTCACAGAAAAA
853	AYHEKGA	15176	GCTTATCATGAGAAGGGGGCT	29499	GCATACCACGAAAAAGGAGCA
854	AYHRADA	15177	GCTTATCATAGGGCGGATGCT	29500	GCATACCACAGAGCAGACGCA
855	AYHVRVD	15178	GCGTATCATGTGCGGGTTGAT	29501	GCATACCACGTCAGAGTCGAC
856	AYIQGSL	15179	GCTTATATTCAGGGTAGTCTT	29502	GCATACATCCAAGGAAGCCTC
857	AYKQQMS	15180	GCGTATAAGCAGCAGATGTCT	29503	GCATACAAACAACAAATGAGC
858	AYMPSAY	15181	GCGTATATGCCGAGTGCTTAT	29504	GCATACATGCCAAGCGCATAC
859	AYNGTRP	15182	GCGTATAATGGGACTAGGCCT	29505	GCATACAACGGAACAAGACCA
860	AYNQPGA	15183	GCTTATAATCAGCCTGGTGCG	29506	GCATACAACCAACCAGGAGCA
861	AYNTTKQ	15184	GCGTATAATACGACGAAGCAG	29507	GCATACAACACAACAAAACAA
862	AYPFKEH	15185	GCGTATCCGTTTAAGGAGCAT	29508	GCATACCCATTCAAAGAACAC
863	AYPRESG	15186	GCTTATCCGCGTGAGTCGGGT	29509	GCATACCCAAGAGAAAGCGGA
864	AYPSNAS	15187	GCGTATCCTTCTAATGCGTCG	29510	GCATACCCAAGCAACGCAAGC
865	AYPSSQF	15188	GCGTATCCTTCGAGTCAGTTT	29511	GCATACCCAAGCAGCCAATTC
866	AYPTSFA	15189	GCGTATCCGACTTCTTTTGCT	29512	GCATACCCAACAAGCTTCGCA
867	AYRASSE	15190	GCTTATCGGGCTTCGAGTGAG	29513	GCATACAGAGCAAGCAGCGAA
868	AYRDSTT	15191	GCTTATCGGGATTCTACGACT	29514	GCATACAGAGACAGCACAACA
869	AYRGSTT	15192	GCTTATCGTGGTTCGACGACT	29515	GCATACAGAGGAAGCACAACA
870	AYSDSQR	15193	GCTTATTCTGATAGTCAGCGG	29516	GCATACAGCGACAGCCAAAGA
871	AYSKSAD	15194	GCTTATTCGAAGTCTGCTGAT	29517	GCATACAGCAAAAGCGCAGAC
872	AYSNRTM	15195	GCGTATTCGAATCGTACGATG	29518	GCATACAGCAACAGAACAATG
873	AYSPTRN	15196	GCGTATTCTCCGACTCGGAAT	29519	GCATACAGCCCAACAAGAAAC
874	AYVGTTP	15197	GCGTATGTTGGTACGACTCCG	29520	GCATACGTCGGAACAACACCA
875	AYVNTPP	15198	GCTTATGTTAATACGCCTCCT	29521	GCATACGTCAACACACCACCA
876	AYVTPSS	15199	GCGTATGTTACGCCGTCGTCG	29522	GCATACGTCACACCAAGCAGC
877	CAARSTA	15200	TGTGCGGCTAGGTCTACGGCT	29523	TGCGCAGCAAGAAGCACAGCA
878	CAASQSE	15201	TGTGCGGCGTCTCAGTCGGAG	29524	TGCGCAGCAAGCCAAAGCGAA
879	CAKTTAN	15202	TGTGCTAAGACGACTGCTAAT	29525	TGCGCAAAAACAACAGCAAAC
880	CALGASY	15203	TGTGCTTTGGGGGCGTCTTAT	29526	TGCGCACTCGGAGCAAGCTAC
881	CAPLRPL	15204	TGTGCGCCGCTTAGGCCTTTG	29527	TGCGCACCACTCAGACCACTC
882	CARDTHP	15205	TGTGCTAGGGATACTCATCCG	29528	TGCGCAAGAGACACACACCCA
883	CARMKEV	15206	TGTGCTAGGATGAAGGAGGTT	29529	TGCGCAAGAATGAAAGAAGTC
884	CARSFEV	15207	TGTGCGCGGAGTTTTGAGGTT	29530	TGCGCAAGAAGCTTCGAAGTC
885	CAVFQTG	15208	TGTGCTGTGTTTCAGACGGGT	29531	TGCGCAGTCTTCCAAACAGGA
886	CAVGVRS	15209	TGTGCTGTGGGTGTTAGGTCG	29532	TGCGCAGTCGGAGTCAGAAGC
887	CCAPGLS	15210	TGTTGTGCGCCGGGTTTGAGT	29533	TGCTGCGCACCAGGACTCAGC
888	CDALNLA	15211	TGTGATGCGCTTAATCTTGCG	29534	TGCGACGCACTCAACCTCGCA
889	CDSSNSS	15212	TGTGATTCGAGTAATTCGTCG	29535	TGCGACAGCAGCAACAGCAGC

890	CEASSKV	15213	TGTGAGGCTTCTTCGAAGGTT	29536	TGCGAAGCAAGCAGCAAAGTC
891	CEKLVRV	15214	TGTGAGAAGCTGGTGCGTGTG	29537	TGCGAAAAACTCGTCAGAGTC
892	CEMEATL	15215	TGTGAGATGGAGGCGACGTTG	29538	TGCGAAATGGAAGCAACACTC
893	CEPCQEL	15216	TGTGAGCCGTGTCAGGAGCTT	29539	TGCGAACCATGCCAAGAACTC
894	CEPYERS	15217	TGTGAGCCTTATGAGAGGTCT	29540	TGCGAACCATACGAAAGAAGC
895	CETITLA	15218	TGTGAGACTATTACGTTGGCG	29541	TGCGAAACAATCACACTCGCA
896	CETWQMH	15219	TGTGAGACTTGGCAGATGCAT	29542	TGCGAAACATGGCAAATGCAC
897	CEVEKKE	15220	TGTGAGGTTGAGAAGAAGGAG	29543	TGCGAAGTCGAAAAAAAAGAA
898	CEVGAPS	15221	TGTGAGGTGGGGGCGCCTTCT	29544	TGCGAAGTCGGAGCACCAAGC
899	CFPKTVS	15222	TGTTTTCCTAAGACGGTGAGT	29545	TGCTTCCCAAAAACAGTCAGC
900	CFTSERG	15223	TGTTTTACGTCTGAGCGTGGG	29546	TGCTTCACAAGCGAAAGAGGA
901	CGLVICD	15224	TGTGGTTTGGTTATTTGTGAT	29547	TGCGGACTCGTCATCTGCGAC
902	CGMRQSS	15225	TGTGGTATGCGGCAGAGTTCT	29548	TGCGGAATGAGACAAAGCAGC
903	CGNHEAS	15226	TGTGGGAATCATGAGGCGTCG	29549	TGCGGAAACCACGAAGCAAGC
904	CGSFITH	15227	TGTGGGTCTTTTATTACGCAT	29550	TGCGGAAGCTTCATCACACAC
905	CHPKMEF	15228	TGTCATCCGAAGATGGAGTTT	29551	TGCCACCCAAAAATGGAATTC
906	CHTASCS	15229	TGTCATACGGCGTCTTGTTCG	29552	TGCCACACAGCAAGCTGCAGC
907	CIARPEC	15230	TGTATTGCTAGGCCTGAGTGT	29553	TGCATCGCAAGACCAGAATGC
908	CIQSSLH	15231	TGTATTCAGTCGAGTCTGCAT	29554	TGCATCCAAAGCAGCCTCCAC
909	CIVVETV	15232	TGTATTGTTGTTGAGACTGTG	29555	TGCATCGTCGTCGAAACAGTC
910	CKEVPRA	15233	TGTAAGGAGGTTCCGCGTGCG	29556	TGCAAAGAAGTCCCAAGAGCA
911	CKGTHNY	15234	TGTAAGGGGACTCATAATTAT	29557	TGCAAAGGAACACACAACTAC
912	CKHGTPM	15235	TGTAAGCATGGGACTCCTATG	29558	TGCAAACACGGAACACCAATG
913	CKSNSTC	15236	TGTAAGTCGAATAGTACTTGT	29559	TGCAAAAGCAACAGCACATGC
914	CKSSIGS	15237	TGTAAGTCGTCGATTGGGTCT	29560	TGCAAAAGCAGCATCGGAAGC
915	CLEDCMR	15238	TGTTTGGAGGATTGTATGCGG	29561	TGCCTCGAAGACTGCATGAGA
916	CLEIPIS	15239	TGTTTGGAGATTCCTATTTCG	29562	TGCCTCGAAATCCCAATCAGC
917	CLESDRP	15240	TGTTTGGAGTCGGATCGTCCG	29563	TGCCTCGAAAGCGACAGACCA
918	CLGTHML	15241	TGTCTTGGGACTCATATGCTT	29564	TGCCTCGGAACACACATGCTC
919	CLPADSE	15242	TGTTTGCCTGCTGATAGTGAG	29565	TGCCTCCCAGCAGACAGCGAA
920	CLQTGLT	15243	TGTTTGCAGACTGGGTTGACG	29566	TGCCTCCAAACAGGACTCACA
921	CLRTSVP	15244	TGTTTGCGTACTTCTGTTCCT	29567	TGCCTCAGAACAAGCGTCCCA
922	CLSSGSV	15245	TGTCTTTCGAGTGGTTCTGTG	29568	TGCCTCAGCAGCGGAAGCGTC
923	CMAELMD	15246	TGTATGGCTGAGCTTATGGAT	29569	TGCATGGCAGAACTCATGGAC
924	CMAELRD	15247	TGTATGGCTGAGCTTAGGGAT	29570	TGCATGGCAGAACTCAGAGAC
925	CMPRTCE	15248	TGTATGCCTAGGACGTGTGAG	29571	TGCATGCCAAGAACATGCGAA
926	CMTIPNA	15249	TGTATGACGATTCCGAATGCT	29572	TGCATGACAATCCCAAACGCA
927	CNASCGR	15250	TGTAATGCGTCTTGTGGGAGG	29573	TGCAACGCAAGCTGCGGAAGA
928	CNEITEP	15251	TGTAATGAGATTACTGAGCCT	29574	TGCAACGAAATCACAGAACCA
929	CNPKTSS	15252	TGTAATCCTAAGACTAGTAGT	29575	TGCAACCCAAAAACAAGCAGC
930	CNSSSCT	15253	TGTAATAGTTCTAGTTGTACG	29576	TGCAACAGCAGCAGCTGCACA
931	CPAENQL	15254	TGTCCGGCTGAGAATCAGTTG	29577	TGCCCAGCAGAAAACCAACTC
932	CPAKSCG	15255	TGTCCGGCTAAGTCGTGTGGT	29578	TGCCCAGCAAAAAGCTGCGGA
933	CPDRYQC	15256	TGTCCTGATCGGTATCAGTGT	29579	TGCCCAGACAGATACCAATGC
934	CPLAPYS	15257	TGTCCGCTGGCTCCGTATAGT	29580	TGCCCACTCGCACCATACAGC

935	CPLDSTI	15258	TGTCCGCTGGATTCGACGATT	29581	TGCCCACTCGACAGCACAATC
936	CPLGDRH	15259	TGTCCGTTGGGTGATCGGCAT	29582	TGCCCACTCGGAGACAGACAC
937	CPMVCSA	15260	TGTCCTATGGTGTGTTCTGCG	29583	TGCCCAATGGTCTGCAGCGCA
938	CPPQPLP	15261	TGTCCGCCGCAGCCTTTGCCG	29584	TGCCCACCACAACCACTCCCA
939	CPRTGLN	15262	TGTCCGCGTACGGGGCTTAAT	29585	TGCCCAAGAACAGGACTCAAC
940	CPSERMG	15263	TGTCCTTCTGAGCGGATGGGG	29586	TGCCCAAGCGAAAGAATGGGA
941	CPSILHC	15264	TGTCCGTCGATTCTGCATTGT	29587	TGCCCAAGCATCCTCCACTGC
942	CPSRAPC	15265	TGTCCTTCTCGTGCGCCGTGT	29588	TGCCCAAGCAGAGCACCATGC
943	CPTPSSC	15266	TGTCCGACGCCTTCTTCTTGT	29589	TGCCCAACACCAAGCAGCTGC
944	CPTTKSA	15267	TGTCCTACGACGAAGTCTGCG	29590	TGCCCAACAACAAAAAGCGCA
945	CQARSCI	15268	TGTCAGGCTCGGTCTTGTATT	29591	TGCCAAGCAAGAAGCTGCATC
946	CRASSSP	15269	TGTAGGGCGTCTTCGTCGCCG	29592	TGCAGAGCAAGCAGCAGCCCA
947	CRAVERP	15270	TGTCGTGCGGTTGAGAGGCCT	29593	TGCAGAGCAGTCGAAAGACCA
948	CRMMNRP	15271	TGTCGGATGATGAATCGGCCT	29594	TGCAGAATGATGAACAGACCA
949	CRMNDLV	15272	TGTCGTATGAATGATCTGGTG	29595	TGCAGAATGAACGACCTCGTC
950	CRRTMDM	15273	TGTAGGAGGACGATGGATATG	29596	TGCAGAAGAACAATGGACATG
951	CRSENKL	15274	TGTCGTTCGGAGAATAAGCTG	29597	TGCAGAAGCGAAAACAAACTC
952	CRSGGEA	15275	TGTCGTTCTGGGGGTGAGGCG	29598	TGCAGAAGCGGAGGAGAAGCA
953	CSALHKC	15276	TGTTCTGCTTTGCATAAGTGT	29599	TGCAGCGCACTCCACAAATGC
954	CSANFTG	15277	TGTAGTGCTAATTTTACGGGT	29600	TGCAGCGCAAACTTCACAGGA
955	CSESLMA	15278	TGTAGTGAGTCGCTGATGGCT	29601	TGCAGCGAAAGCCTCATGGCA
956	CSESSIF	15279	TGTTCTGAGTCTTCTATTTTT	29602	TGCAGCGAAAGCAGCATCTTC
957	CSGTTNC	15280	TGTAGTGGTACGACTAATTGT	29603	TGCAGCGGAACAACAAACTGC
958	CSPPHFP	15281	TGTTCGCCGCCGCATTTTCCG	29604	TGCAGCCCACCACACTTCCCA
959	CSPSGVI	15282	TGTAGTCCTTCGGGGGTTATT	29605	TGCAGCCCAAGCGGAGTCATC
960	CSSRPFA	15283	TGTTCTTCTAGGCCGTTTGCT	29606	TGCAGCAGCAGACCATTCGCA
961	CSSTTKC	15284	TGTAGTTCTACGACGAAGTGT	29607	TGCAGCAGCACAACAAAATGC
962	CTAELPF	15285	TGTACTGCGGAGTTGCCTTTT	29608	TGCACAGCAGAACTCCCATTC
963	CTDHPAC	15286	TGTACGGATCATCCTGCGTGT	29609	TGCACAGACCACCCAGCATGC
964	CTDSTCL	15287	TGTACTGATTCTACGTGTTTG	29610	TGCACAGACAGCACATGCCTC
965	CTGPLCS	15288	TGTACGGGTCCTTTGTGTTCG	29611	TGCACAGGACCACTCTGCAGC
966	CTKSICT	15289	TGTACGAAGTCGATTTGTACT	29612	TGCACAAAAAGCATCTGCACA
967	CTSTKIY	15290	TGTACTAGTACGAAGATTTAT	29613	TGCACAAGCACAAAAATCTAC
968	CTTDALS	15291	TGTACGACGGATGCTTTGAGT	29614	TGCACAACAGACGCACTCAGC
969	CTYTLID	15292	TGTACTTATACTCTTATTGAT	29615	TGCACATACACACTCATCGAC
970	CVPDSSK	15293	TGTGTTCCTGATTCGTCTAAG	29616	TGCGTCCCAGACAGCAGCAAA
971	CVRLTTP	15294	TGTGTGAGGCTGACGACGCCT	29617	TGCGTCAGACTCACAACACCA
972	CVTPEKV	15295	TGTGTTACTCCTGAGAAGGTG	29618	TGCGTCACACCAGAAAAAGTC
973	CVVNQQG	15296	TGTGTTGTGAATCAGCAGGGT	29619	TGCGTCGTCAACCAACAAGGA
974	CVVSRQD	15297	TGTGTGGTGAGTCGGCAGGAT	29620	TGCGTCGTCAGCAGACAAGAC
975	CYIGTQC	15298	TGTTATATTGGGACTCAGTGT	29621	TGCTACATCGGAACACAATGC
976	CYLSTCT	15299	TGTTATCTTAGTACGTGTACG	29622	TGCTACCTCAGCACATGCACA
977	CYNRTEC	15300	TGTTATAATCGGACGGAGTGT	29623	TGCTACAACAGAACAGAATGC
978	CYPPENA	15301	TGTTATCCGCCTGAGAATGCT	29624	TGCTACCCACCAGAAAACGCA
979	DAAGTSK	15302	GATGCGGCGGGTACGTCTAAG	29625	GACGCAGCAGGAACAAGCAAA

980	DAAKSAY	15303	GATGCTGCGAAGAGTGCTTAT	29626	GACGCAGCAAAAAGCGCATAC
981	DAATKAT	15304	GATGCTGCGACTAAGGCGACT	29627	GACGCAGCAACAAAAGCAACA
982	DAERAKP	15305	GATGCTGAGCGTGCGAAGCCG	29628	GACGCAGAAAGAGCAAAACCA
983	DAEWPMY	15306	GATGCTGAGTGGCCTATGTAT	29629	GACGCAGAATGGCCAATGTAC
984	DAGIGGP	15307	GATGCTGGTATTGGGGGTCCT	29630	GACGCAGGAATCGGAGGACCA
985	DAGNWQP	15308	GATGCGGGGAATTGGCAGCCT	29631	GACGCAGGAAACTGGCAACCA
986	DAGPRAQ	15309	GATGCGGGGCCTAGGGCTCAG	29632	GACGCAGGACCAAGAGCACAA
987	DAHNAPR	15310	GATGCTCATAATGCTCCGCGT	29633	GACGCACACAACGCACCAAGA
988	DAHRLVT	15311	GATGCTCATCGTTTGGTGACG	29634	GACGCACACAGACTCGTCACA
989	DAIKAMS	15312	GATGCTATTAAGGCTATGTCG	29635	GACGCAATCAAAGCAATGAGC
990	DAINMGG	15313	GATGCTATTAATATGGGGGGT	29636	GACGCAATCAACATGGGAGGA
991	DAIPLAS	15314	GATGCGATTCCTCTTGCTAGT	29637	GACGCAATCCCACTCGCAAGC
992	DAKVMVP	15315	GATGCTAAGGTTATGGTTCCG	29638	GACGCAAAAGTCATGGTCCCA
993	DALKGAK	15316	GATGCGTTGAAGGGGGCGAAG	29639	GACGCACTCAAAGGAGCAAAA
994	DAPNSVM	15317	GATGCTCCTAATAGTGTGATG	29640	GACGCACCAAACAGCGTCATG
995	DAPPLRT	15318	GATGCTCCTCCGCTTCGTACT	29641	GACGCACCACCACTCAGAACA
996	DAPRESL	15319	GATGCTCCGCGTGAGTCGCTT	29642	GACGCACCAAGAGAAAGCCTC
997	DAPRNAE	15320	GATGCTCCTCGGAATGCGGAG	29643	GACGCACCAAGAAACGCAGAA
998	DAQPSQM	15321	GATGCGCAGCCGTCGCAGATG	29644	GACGCACAACCAAGCCAAATG
999	DAQYSQR	15322	GATGCGCAGTATTCTCAGCGT	29645	GACGCACAATACAGCCAAAGA
1000	DARAHPL	15323	GATGCGCGTGCTCATCCTTTG	29646	GACGCAAGAGCACACCCACTC
1001	DARFSMQ	15324	GATGCGCGGTTTAGTATGCAG	29647	GACGCAAGATTCAGCATGCAA
1002	DARLAPE	15325	GATGCGAGGCTTGCGCCGGAG	29648	GACGCAAGACTCGCACCAGAA
1003	DARMLIS	15326	GATGCGAGGATGCTTATTTCT	29649	GACGCAAGAATGCTCATCAGC
1004	DARRDIV	15327	GATGCTCGTAGGGATATTGTT	29650	GACGCAAGAAGAGACATCGTC
1005	DARTATF	15328	GATGCGAGGACGGCTACTTTT	29651	GACGCAAGAACAGCAACATTC
1006	DARVTRF	15329	GATGCTCGGGTTACTCGTTTT	29652	GACGCAAGAGTCACAAGATTC
1007	DASLMKM	15330	GATGCTAGTCTGATGAAGATG	29653	GACGCAAGCCTCATGAAAATG
1008	DASPNRE	15331	GATGCGTCGCCGAATCGTGAG	29654	GACGCAAGCCCAAACAGAGAA
1009	DASTIKD	15332	GATGCGTCTACTATTAAGGAT	29655	GACGCAAGCACAATCAAAGAC
1010	DAVADDP	15333	GATGCTGTGGCGGATGATCCT	29656	GACGCAGTCGCAGACGACCCA
1011	DAVERVS	15334	GATGCTGTGGAGCGGGTTTCT	29657	GACGCAGTCGAAAGAGTCAGC
1012	DAVVERS	15335	GATGCTGTTGTTGAGCGGAGT	29658	GACGCAGTCGTCGAAAGAAGC
1013	DCDTQKT	15336	GATTGTGATACGCAGAAGACT	29659	GACTGCGACACACAAAAAACA
1014	DCLLSGP	15337	GATTGTCTTTTGAGTGGTCCT	29660	GACTGCCTCCTCAGCGGACCA
1015	DCPFQKG	15338	GATTGTCCGTTTCAGAAGGGG	29661	GACTGCCCATTCCAAAAAGGA
1016	DCSFKCS	15339	GATTGTTCGTTTAAGTGTTCT	29662	GACTGCAGCTTCAAATGCAGC
1017	DDEHRST	15340	GATGATGAGCATCGTTCGACG	29663	GACGACGAACACAGAAGCACA
1018	DDGHPHL	15341	GATGATGGGCATCCGCATCTG	29664	GACGACGGACACCCACACCTC
1019	DDIACDA	15342	GATGATATTGCTTGTGATGCT	29665	GACGACATCGCATGCGACGCA
1020	DDKERRE	15343	GATGATAAGGAGAGGCGGGAG	29666	GACGACAAAGAAAGAAGAGAA
1021	DDMARGR	15344	GATGATATGGCTAGGGGGCGG	29667	GACGACATGGCAAGAGGAAGA
1022	DDPHSSS	15345	GATGATCCTCATTCTTCGTCT	29668	GACGACCCACACAGCAGCAGC
1023	DDPRDGR	15346	GATGATCCGAGGGATGGGAGG	29669	GACGACCCAAGAGACGGAAGA
1024	DDRRHFV	15347	GATGATCGGAGGCATTTTGTG	29670	GACGACAGAAGACACTTCGTC

1025	DDRSFPM	15348	GATGATCGGAGTTTTCCGATG	29671	GACGACAGAAGCTTCCCAATG
1026	DDSLCQL	15349	GATGATTCGCTTTGTCAGCTG	29672	GACGACAGCCTCTGCCAACTC
1027	DDTRFDD	15350	GATGATACTAGGTTTGATGAT	29673	GACGACACAAGATTCGACGAC
1028	DDWPKVS	15351	GATGATTGGCCTAAGGTGAGT	29674	GACGACTGGCCAAAAGTCAGC
1029	DDYHAPA	15352	GATGATTATCATGCTCCGGCG	29675	GACGACTACCACGCACCAGCA
1030	DEAKKHH	15353	GATGAGGCTAAGAAGCATCAT	29676	GACGAAGCAAAAAAACACCAC
1031	DEAPHPA	15354	GATGAGGCTCCTCATCCTGCT	29677	GACGAAGCACCACACCCAGCA
1032	DEDIKRL	15355	GATGAGGATATTAAGAGGCTT	29678	GACGAAGACATCAAAAGACTC
1033	DEGKVKR	15356	GATGAGGGTAAGGTTAAGCGT	29679	GACGAAGGAAAAGTCAAAAGA
1034	DEGRHQR	15357	GATGAGGGGCGGCATCAGCGT	29680	GACGAAGGAAGACACCAAAGA
1035	DENETGP	15358	GATGAGAATGAGACGGGTCCT	29681	GACGAAAACGAAACAGGACCA
1036	DENVALP	15359	GATGAGAATGTTGCTTTGCCT	29682	GACGAAAACGTCGCACTCCCA
1037	DEPFKKA	15360	GATGAGCCTTTTAAGAAGGCT	29683	GACGAACCATTCAAAAAAGCA
1038	DEPGMTS	15361	GATGAGCCGGGGATGACGTCG	29684	GACGAACCAGGAATGACAAGC
1039	DEPRHQM	15362	GATGAGCCGAGGCATCAGATG	29685	GACGAACCAAGACACCAAATG
1040	DERGFRS	15363	GATGAGCGGGGTTTTAGGTCT	29686	GACGAAAGAGGATTCAGAAGC
1041	DERRLDP	15364	GATGAGCGTCGGCTTGATCCG	29687	GACGAAAGAAGACTCGACCCA
1042	DESTMSR	15365	GATGAGAGTACTATGTCTAGG	29688	GACGAAAGCACAATGAGCAGA
1043	DESYDRN	15366	GATGAGTCTTATGATCGGAAT	29689	GACGAAAGCTACGACAGAAAC
1044	DEVKKEG	15367	GATGAGGTTAAGAAGGAGGGT	29690	GACGAAGTCAAAAAAGAAGGA
1045	DEWAHAR	15368	GATGAGTGGGCGCATGCGCGG	29691	GACGAATGGGCACACGCAAGA
1046	DFAGNSD	15369	GATTTTGCGGGGAATTCGGAT	29692	GACTTCGCAGGAAACAGCGAC
1047	DFALASP	15370	GATTTTGCGCTGGCGAGTCCT	29693	GACTTCGCACTCGCAAGCCCA
1048	DFARQHD	15371	GATTTTGCGAGGCAGCATGAT	29694	GACTTCGCAAGACAACACGAC
1049	DFECIGV	15372	GATTTTGAGTGTATTGGGGTT	29695	GACTTCGAATGCATCGGAGTC
1050	DFENPME	15373	GATTTTGAGAATCCGATGGAG	29696	GACTTCGAAAACCCAATGGAA
1051	DFGGLAV	15374	GATTTTGGGGGGTTGGCTGTG	29697	GACTTCGGAGGACTCGCAGTC
1052	DFKAVCC	15375	GATTTTAAGGCTGTGTGTTGT	29698	GACTTCAAAGCAGTCTGCTGC
1053	DFKVVSG	15376	GATTTTAAGGTGGTTTCTGGG	29699	GACTTCAAAGTCGTCAGCGGA
1054	DFPLKPG	15377	GATTTTCCGTTGAAGCCTGGT	29700	GACTTCCCACTCAAACCAGGA
1055	DFRKPEQ	15378	GATTTTCGTAAGCCTGAGCAG	29701	GACTTCAGAAAACCAGAACAA
1056	DFSLGLL	15379	GATTTTAGTTTGGGGCTGTTG	29702	GACTTCAGCCTCGGACTCCTC
1057	DFSLNNS	15380	GATTTTAGTCTTAATAATTCT	29703	GACTTCAGCCTCAACAACAGC
1058	DFSLQDA	15381	GATTTTTCTTTGCAGGATGCT	29704	GACTTCAGCCTCCAAGACGCA
1059	DFSRRAD	15382	GATTTTAGTCGGCGGGCTGAT	29705	GACTTCAGCAGAAGAGCAGAC
1060	DFTRADG	15383	GATTTTACGCGTGCGGATGGG	29706	GACTTCACAAGAGCAGACGGA
1061	DFTVPAG	15384	GATTTTACTGTGCCTGCTGGG	29707	GACTTCACAGTCCCAGCAGGA
1062	DFVPLKS	15385	GATTTTGTTCCGCTTAAGTCT	29708	GACTTCGTCCCACTCAAAAGC
1063	DFVTIPN	15386	GATTTTGTGACTATTCCTAAT	29709	GACTTCGTCACAATCCCAAAC
1064	DGASGVP	15387	GATGGGGCTTCGGGGGTTCCT	29710	GACGGAGCAAGCGGAGTCCCA
1065	DGGHSVR	15388	GATGGTGGTCATTCGGTGCGT	29711	GACGGAGGACACAGCGTCAGA
1066	DGIRDPR	15389	GATGGGATTCGGGATCCGAGG	29712	GACGGAATCAGAGACCCAAGA
1067	DGKAKVS	15390	GATGGTAAGGCTAAGGTTTCT	29713	GACGGAAAAGCAAAAGTCAGC
1068	DGKHTDY	15391	GATGGTAAGCATACTGATTAT	29714	GACGGAAAACACACAGACTAC
1069	DGLRTES	15392	GATGGTCTTCGTACGGAGTCG	29715	GACGGACTCAGAACAGAAAGC

1070	DGLSRLP	15393	GATGGGCTGTCTCGGTTGCCG	29716	GACGGACTCAGCAGACTCCCA
1071	DGMLRDR	15394	GATGGGATGTTGAGGGATAGG	29717	GACGGAATGCTCAGAGACAGA
1072	DGNSYHP	15395	GATGGTAATTCTTATCATCCG	29718	GACGGAAACAGCTACCACCCA
1073	DGNTARG	15396	GATGGGAATACGGCGAGGGGG	29719	GACGGAAACACAGCAAGAGGA
1074	DGPEEER	15397	GATGGGCCGGAGGAGGAGCGT	29720	GACGGACCAGAAGAAGAAAGA
1075	DGPGSPN	15398	GATGGGCCGGGTTCGCCGAAT	29721	GACGGACCAGGAAGCCCAAAC
1076	DGRHLSP	15399	GATGGTCGTCATCTTTCGCCT	29722	GACGGAAGACACCTCAGCCCA
1077	DGRTVAA	15400	GATGGGCGTACTGTTGCGGCG	29723	GACGGAAGAACAGTCGCAGCA
1078	DGSFEPY	15401	GATGGTTCTTTTGAGCCTTAT	29724	GACGGAAGCTTCGAACCATAC
1079	DGSGTLN	15402	GATGGTTCGGGGACGCTGAAT	29725	GACGGAAGCGGAACACTCAAC
1080	DGSPSWA	15403	GATGGTAGTCCGAGTTGGGCT	29726	GACGGAAGCCCAAGCTGGGCA
1081	DGTDQSQ	15404	GATGGTACGGATCAGTCTCAG	29727	GACGGAACAGACCAAAGCCAA
1082	DGTRAQW	15405	GATGGTACGAGGGCTCAGTGG	29728	GACGGAACAAGAGCACAATGG
1083	DGTSLKH	15406	GATGGTACTTCTCTTAAGCAT	29729	GACGGAACAAGCCTCAAACAC
1084	DGTYRNM	15407	GATGGGACGTATCGGAATATG	29730	GACGGAACATACAGAAACATG
1085	DGVTTLS	15408	GATGGGGTTACGACTCTGTCG	29731	GACGGAGTCACAACACTCAGC
1086	DHAHRST	15409	GATCATGCGCATAGGAGTACT	29732	GACCACGCACACAGAAGCACA
1087	DHKSNSR	15410	GATCATAAGTCGAATTCTCGT	29733	GACCACAAAAGCAACAGCAGA
1088	DHLAQEC	15411	GATCATCTTGCTCAGGAGTGT	29734	GACCACCTCGCACAAGAATGC
1089	DHLDVNA	15412	GATCATCTTGATGTGAATGCT	29735	GACCACCTCGACGTCAACGCA
1090	DHNHMGS	15413	GATCATAATCATATGGGGTCT	29736	GACCACAACCACATGGGAAGC
1091	DHNLRQN	15414	GATCATAATTTGCGGCAGAAT	29737	GACCACAACCTCAGACAAAAC
1092	DHPYLSP	15415	GATCATCCGTATCTGTCTCCG	29738	GACCACCCATACCTCAGCCCA
1093	DHRTLES	15416	GATCATCGTACGCTTGAGAGT	29739	GACCACAGAACACTCGAAAGC
1094	DHSALSS	15417	GATCATTCGGCTCTTTCTTCG	29740	GACCACAGCGCACTCAGCAGC
1095	DHSGKKD	15418	GATCATAGTGGGAAGAAGGAT	29741	GACCACAGCGGAAAAAAAGAC
1096	DHSMALR	15419	GATCATTCTATGGCGCTGCGT	29742	GACCACAGCATGGCACTCAGA
1097	DHSVPGT	15420	GATCATTCTGTGCCGGGGACT	29743	GACCACAGCGTCCCAGGAACA
1098	DHTDRDG	15421	GATCATACTGATCGGGATGGT	29744	GACCACACAGACAGAGACGGA
1099	DHTPLLS	15422	GATCATACGCCGCTGCTTTCG	29745	GACCACACACCACTCCTCAGC
1100	DHWNGDS	15423	GATCATTGGAATGGGGATTCG	29746	GACCACTGGAACGGAGACAGC
1101	DHYARLP	15424	GATCATTATGCTCGTTTGCCG	29747	GACCACTACGCAAGACTCCCA
1102	DIAHPRN	15425	GATATTGCTCATCCTCGTAAT	29748	GACATCGCACACCCAAGAAAC
1103	DIAQHET	15426	GATATTGCGCAGCATGAGACT	29749	GACATCGCACAACACGAAACA
1104	DIEDTPV	15427	GATATTGAGGATACGCCGGTG	29750	GACATCGAAGACACACCAGTC
1105	DIHRSSY	15428	GATATTCATCGTTCGTCGTAT	29751	GACATCCACAGAAGCAGCTAC
1106	DIHSHLY	15429	GATATTCATAGTCATCTTTAT	29752	GACATCCACAGCCACCTCTAC
1107	DINFKAP	15430	GATATTAATTTTAAGGCTCCT	29753	GACATCAACTTCAAAGCACCA
1108	DINPTTL	15431	GATATTAATCCTACTACTCTG	29754	GACATCAACCCAACAACACTC
1109	DIPVASK	15432	GATATTCCGGTGGCTTCTAAG	29755	GACATCCCAGTCGCAAGCAAA
1110	DIPVTSA	15433	GATATTCCTGTGACTTCGGCT	29756	GACATCCCAGTCACAAGCGCA
1111	DIRHRLS	15434	GATATTCGGCATCGTCTTAGT	29757	GACATCAGACACAGACTCAGC
1112	DIRRPTP	15435	GATATTCGGCGGCCTACTCCG	29758	GACATCAGAAGACCAACACCA
1113	DIRTGSV	15436	GATATTAGGACTGGGTCGGTG	29759	GACATCAGAACAGGAAGCGTC
1114	DISLPEA	15437	GATATTAGTCTGCCTGAGGCT	29760	GACATCAGCCTCCCAGAAGCA

1115	DISNDQY	15438	GATATTTCTAATGATCAGTAT	29761	GACATCAGCAACGACCAATAC
1116	DISRPVR	15439	GATATTTCGCGGCCTGTGCGT	29762	GACATCAGCAGACCAGTCAGA
1117	DISRQNS	15440	GATATTTCGCGTCAGAATTCT	29763	GACATCAGCAGACAAAACAGC
1118	DITATTA	15441	GATATTACTGCTACGACGGCG	29764	GACATCACAGCAACAACAGCA
1119	DITGRVP	15442	GATATTACTGGTCGGGTGCCG	29765	GACATCACAGGAAGAGTCCCA
1120	DKAVGMI	15443	GATAAGGCGGTTGGGATGATT	29766	GACAAAGCAGTCGGAATGATC
1121	DKDELMM	15444	GATAAGGATGAGCTGATGATG	29767	GACAAAGACGAACTCATGATG
1122	DKEVPPM	15445	GATAAGGAGGTGCCTCCGATG	29768	GACAAAGAAGTCCCACCAATG
1123	DKEYAGL	15446	GATAAGGAGTATGCGGGGCTT	29769	GACAAAGAATACGCAGGACTC
1124	DKGKASP	15447	GATAAGGGGAAGGCGTCTCCG	29770	GACAAAGGAAAAGCAAGCCCA
1125	DKGSLTM	15448	GATAAGGGTTCGTTGACTATG	29771	GACAAAGGAAGCCTCACAATG
1126	DKIPNFS	15449	GATAAGATTCCGAATTTTTCT	29772	GACAAAATCCCAAACTTCAGC
1127	DKLHGQA	15450	GATAAGCTGCATGGGCAGGCT	29773	GACAAACTCCACGGACAAGCA
1128	DKLPGDR	15451	GATAAGCTTCCGGGTGATAGG	29774	GACAAACTCCCAGGAGACAGA
1129	DKLRANN	15452	GATAAGCTTAGGGCTAATAAT	29775	GACAAACTCAGAGCAAACAAC
1130	DKLTPRL	15453	GATAAGCTGACGCCTAGGCTT	29776	GACAAACTCACACCAAGACTC
1131	DKMNMPP	15454	GATAAGATGAATATGCCGCCG	29777	GACAAAATGAACATGCCACCA
1132	DKRDGRL	15455	GATAAGCGTGATGGTCGTTTG	29778	GACAAAAGAGACGGAAGACTC
1133	DKRSGTC	15456	GATAAGCGGAGTGGGACGTGT	29779	GACAAAAGAAGCGGAACATGC
1134	DKSIATN	15457	GATAAGTCGATTGCGACTAAT	29780	GACAAAAGCATCGCAACAAAC
1135	DKSPMMR	15458	GATAAGTCGCCTATGATGCGT	29781	GACAAAAGCCCAATGATGAGA
1136	DKSRLYA	15459	GATAAGTCTCGTTTGTATGCT	29782	GACAAAAGCAGACTCTACGCA
1137	DKSRNQM	15460	GATAAGTCGCGTAATCAGATG	29783	GACAAAAGCAGAAACCAAATG
1138	DKTAVIS	15461	GATAAGACTGCGGTGATTTCG	29784	GACAAAACAGCAGTCATCAGC
1139	DLALSRG	15462	GATCTTGCGCTGAGTCGTGGG	29785	GACCTCGCACTCAGCAGAGGA
1140	DLASVPR	15463	GATTTGGCTTCTGTTCCTCGG	29786	GACCTCGCAAGCGTCCCAAGA
1141	DLDPICT	15464	GATCTGGATCCTATTTGTACT	29787	GACCTCGACCCAATCTGCACA
1142	DLDSPHS	15465	GATCTTGATTCGCCTCATTCT	29788	GACCTCGACAGCCCACACAGC
1143	DLEHQCP	15466	GATCTGGAGCATCAGTGTCCG	29789	GACCTCGAACACCAATGCCCA
1144	DLFKIER	15467	GATTTGTTTAAGATTGAGCGT	29790	GACCTCTTCAAAATCGAAAGA
1145	DLGGLVH	15468	GATCTGGGGGGTTTGGTTCAT	29791	GACCTCGGAGGACTCGTCCAC
1146	DLGPDKG	15469	GATCTTGGGCCGGATAAGGGG	29792	GACCTCGGACCAGACAAAGGA
1147	DLHGAMR	15470	GATCTGCATGGGGCTATGCGG	29793	GACCTCCACGGAGCAATGAGA
1148	DLHIQDP	15471	GATTTGCATATTCAGGATCCG	29794	GACCTCCACATCCAAGACCCA
1149	DLIENRE	15472	GATCTTATTGAGAATCGGGAG	29795	GACCTCATCGAAAACAGAGAA
1150	DLIERGS	15473	GATCTTATTGAGCGTGGGTCT	29796	GACCTCATCGAAAGAGGAAGC
1151	DLIPSRP	15474	GATCTGATTCCTAGTCGTCCT	29797	GACCTCATCCCAAGCAGACCA
1152	DLIVRGL	15475	GATCTTATTGTTCGTGGGCTG	29798	GACCTCATCGTCAGAGGACTC
1153	DLKGGGF	15476	GATCTGAAGGGTGGGGGTTTT	29799	GACCTCAAAGGAGGAGGATTC
1154	DLKKPDF	15477	GATCTTAAGAAGCCTGATTTT	29800	GACCTCAAAAAACCAGACTTC
1155	DLKLHGP	15478	GATTTGAAGCTGCATGGGCCT	29801	GACCTCAAACTCCACGGACCA
1156	DLKPSLL	15479	GATTTGAAGCCTTCTTTGCTT	29802	GACCTCAAACCAAGCCTCCTC
1157	DLKSSER	15480	GATTTGAAGTCGTCGGAGAGG	29803	GACCTCAAAAGCAGCGAAAGA
1158	DLLERPS	15481	GATCTTTTGGAGAGGCCGTCG	29804	GACCTCCTCGAAAGACCAAGC
1159	DLLETRL	15482	GATCTTCTTGAGACGCGGCTT	29805	GACCTCCTCGAAACAAGACTC

1160	DLLTALA	15483	GATCTGTTGACTGCTTTGGCT	29806	GACCTCCTCACAGCACTCGCA
1161	DLMHTDA	15484	GATTTGATGCATACGGATGCT	29807	GACCTCATGCACACAGACGCA
1162	DLMHVSG	15485	GATCTGATGCATGTTAGTGGT	29808	GACCTCATGCACGTCAGCGGA
1163	DLMIHGL	15486	GATTTGATGATTCATGGGCTG	29809	GACCTCATGATCCACGGACTC
1164	DLNRGPR	15487	GATTTGAATAGGGGTCCTCGT	29810	GACCTCAACAGAGGACCAAGA
1165	DLNRIEC	15488	GATTTGAATAGGATTGAGTGT	29811	GACCTCAACAGAATCGAATGC
1166	DLNTTQH	15489	GATCTTAATACTACTCAGCAT	29812	GACCTCAACACAACACAACAC
1167	DLPAVSH	15490	GATTTGCCTGCGGTTAGTCAT	29813	GACCTCCCAGCAGTCAGCCAC
1168	DLPLGNS	15491	GATCTTCCGCTGGGTAATTCT	29814	GACCTCCCACTCGGAAACAGC
1169	DLPLRTT	15492	GATCTGCCGTTGAGGACTACT	29815	GACCTCCCACTCAGAACAACA
1170	DLPLTSL	15493	GATCTTCCGCTTACTTCTTTG	29816	GACCTCCCACTCACAAGCCTC
1171	DLPRQSV	15494	GATCTTCCTCGTCAGTCGGTG	29817	GACCTCCCAAGACAAAGCGTC
1172	DLPYSHP	15495	GATCTTCCGTATAGTCATCCT	29818	GACCTCCCATACAGCCACCCA
1173	DLQTGPQ	15496	GATTTGCAGACGGGGCCTCAG	29819	GACCTCCAAACAGGACCACAA
1174	DLRCAEG	15497	GATTTGCGTTGTGCTGAGGGG	29820	GACCTCAGATGCGCAGAAGGA
1175	DLREAPR	15498	GATCTTCGTGAGGCTCCGCGT	29821	GACCTCAGAGAAGCACCAAGA
1176	DLRHASS	15499	GATTTGCGTCATGCTTCTAGT	29822	GACCTCAGACACGCAAGCAGC
1177	DLRHPPS	15500	GATTTGAGGCATCCGCCTAGT	29823	GACCTCAGACACCCACCAAGC
1178	DLRPGGL	15501	GATCTTAGGCCGGGGGGTCTG	29824	GACCTCAGACCAGGAGGACTC
1179	DLRRSML	15502	GATTTGAGGCGTAGTATGTTG	29825	GACCTCAGAAGAAGCATGCTC
1180	DLRRTPF	15503	GATCTGCGTCGTACGCCTTTT	29826	GACCTCAGAAGAACACCATTC
1181	DLSALRG	15504	GATTTGAGTGCGTTGCGTGGG	29827	GACCTCAGCGCACTCAGAGGA
1182	DLSGLTR	15505	GATCTTTCGGGGTTGACGCGG	29828	GACCTCAGCGGACTCACAAGA
1183	DLTHVGS	15506	GATTTGACTCATGTTGGGAGT	29829	GACCTCACACACGTCGGAAGC
1184	DLTRWPS	15507	GATCTGACTCGGTGGCCTTCG	29830	GACCTCACAAGATGGCCAAGC
1185	DLTTAPT	15508	GATTTGACTACGGCTCCTACT	29831	GACCTCACAACAGCACCAACA
1186	DLTVSYA	15509	GATTTGACGGTGTCTTATGCT	29832	GACCTCACAGTCAGCTACGCA
1187	DLVETAS	15510	GATCTTGTGGAGACGGCTAGT	29833	GACCTCGTCGAAACAGCAAGC
1188	DLVIPTR	15511	GATTTGGTTATTCCGACTCGG	29834	GACCTCGTCATCCCAACAAGA
1189	DMDMQMA	15512	GATATGGATATGCAGATGGCT	29835	GACATGGACATGCAAATGGCA
1190	DMGARQY	15513	GATATGGGGGCTCGTCAGTAT	29836	GACATGGGAGCAAGACAATAC
1191	DMKPAVS	15514	GATATGAAGCCTGCGGTGTCG	29837	GACATGAAACCAGCAGTCAGC
1192	DMLKKFN	15515	GATATGTTGAAGAAGTTTAAT	29838	GACATGCTCAAAAAATTCAAC
1193	DMPFGPL	15516	GATATGCCTTTTGGGCCGTTG	29839	GACATGCCATTCGGACCACTC
1194	DMSARPS	15517	GATATGTCGGCGCGGCCTTCT	29840	GACATGAGCGCAAGACCAAGC
1195	DMSTRGM	15518	GATATGTCGACGCGTGGTATG	29841	GACATGAGCACAAGAGGAATG
1196	DMTTGAV	15519	GATATGACTACGGGTGCTGTG	29842	GACATGACAACAGGAGCAGTC
1197	DMVVPSD	15520	GATATGGTGGTGCCTAGTGAT	29843	GACATGGTCGTCCCAAGCGAC
1198	DMYPTNR	15521	GATATGTATCCGACTAATAGG	29844	GACATGTACCCAACAAACAGA
1199	DNASKLM	15522	GATAATGCGAGTAAGCTTATG	29845	GACAACGCAAGCAAACTCATG
1200	DNELLMS	15523	GATAATGAGCTTCTGATGTCG	29846	GACAACGAACTCCTCATGAGC
1201	DNESIPT	15524	GATAATGAGTCGATTCCGACG	29847	GACAACGAAAGCATCCCAACA
1202	DNGSADN	15525	GATAATGGTTCTGCTGATAAT	29848	GACAACGGAAGCGCAGACAAC
1203	DNLDGLC	15526	GATAATCTGGATGGGCTGTGT	29849	GACAACCTCGACGGACTCTGC
1204	DNLLGSR	15527	GATAATTTGCTGGGGTCGCGT	29850	GACAACCTCCTCGGAAGCAGA

1205	DNLPTLA	15528	GATAATCTGCCGACTTTGGCT	29851	GACAACCTCCCAACACTCGCA
1206	DNLRPRP	15529	GATAATCTGAGGCCGCGGCCT	29852	GACAACCTCAGACCAAGACCA
1207	DNLSHRM	15530	GATAATTTGTCTCATAGGATG	29853	GACAACCTCAGCCACAGAATG
1208	DNPAMDR	15531	GATAATCCTGCGATGGATCGG	29854	GACAACCCAGCAATGGACAGA
1209	DNPPTGV	15532	GATAATCCGCCTACTGGGGTG	29855	GACAACCCACCAACAGGAGTC
1210	DNQAAVP	15533	GATAATCAGGCTGCTGTTCCT	29856	GACAACCAAGCAGCAGTCCCA
1211	DNRLNVV	15534	GATAATCGGTTGAATGTGGTG	29857	GACAACAGACTCAACGTCGTC
1212	DNRPRLM	15535	GATAATAGGCCGCGTTTGATG	29858	GACAACAGACCAAGACTCATG
1213	DNRVSIP	15536	GATAATAGGGTTTCGATTCCG	29859	GACAACAGAGTCAGCATCCCA
1214	DNSAFAV	15537	GATAATTCGGCTTTTGCGGTG	29860	GACAACAGCGCATTCGCAGTC
1215	DNTNWAK	15538	GATAATACGAATTGGGCTAAG	29861	GACAACACAAACTGGGCAAAA
1216	DNTTRTA	15539	GATAATACGACTAGGACTGCG	29862	GACAACACAACAAGAACAGCA
1217	DNVGIKS	15540	GATAATGTGGGGATTAAGTCG	29863	GACAACGTCGGAATCAAAAGC
1218	DNYDPRP	15541	GATAATTATGATCCGCGTCCG	29864	GACAACTACGACCCAAGACCA
1219	DPAATLP	15542	GATCCGGCTGCTACGTTGCCT	29865	GACCCAGCAGCAACACTCCCA
1220	DPALQRA	15543	GATCCTGCGCTGCAGCGGGCG	29866	GACCCAGCACTCCAAAGAGCA
1221	DPAPTLP	15544	GATCCGGCGCCGACGTTGCCT	29867	GACCCAGCACCAACACTCCCA
1222	DPCHRSL	15545	GATCCTTGTCATAGGTCGCTG	29868	GACCCATGCCACAGAAGCCTC
1223	DPDPASN	15546	GATCCTGATCCTGCGTCGAAT	29869	GACCCAGACCCAGCAAGCAAC
1224	DPDPSLS	15547	GATCCGGATCCGTCGCTTAGT	29870	GACCCAGACCCAAGCCTCAGC
1225	DPEVDPD	15548	GATCCTGAGGTTGATCCGGAT	29871	GACCCAGAAGTCGACCCAGAC
1226	DPFTHNG	15549	GATCCGTTTACTCATAATGGG	29872	GACCCATTCACACACAACGGA
1227	DPGHQRT	15550	GATCCTGGTCATCAGCGGACG	29873	GACCCAGGACACCAAAGAACA
1228	DPGLRTD	15551	GATCCGGGTCTGCGTACTGAT	29874	GACCCAGGACTCAGAACAGAC
1229	DPGMVPG	15552	GATCCTGGGATGGTGCCTGGG	29875	GACCCAGGAATGGTCCCAGGA
1230	DPHGKYP	15553	GATCCGCATGGGAAGTATCCT	29876	GACCCACACGGAAAATACCCA
1231	DPHLSSP	15554	GATCCGCATCTGTCGTCGCCG	29877	GACCCACACCTCAGCAGCCCA
1232	DPIAAPT	15555	GATCCTATTGCGGCTCCGACG	29878	GACCCAATCGCAGCACCAACA
1233	DPLAPMA	15556	GATCCTTTGGCGCCTATGGCT	29879	GACCCACTCGCACCAATGGCA
1234	DPLYSSR	15557	GATCCGCTTTATTCGAGTCGT	29880	GACCCACTCTACAGCAGCAGA
1235	DPMARVG	15558	GATCCTATGGCGCGGGTGGGG	29881	GACCCAATGGCAAGAGTCGGA
1236	DPNLNLA	15559	GATCCTAATCTTAATCTTGCT	29882	GACCCAAACCTCAACCTCGCA
1237	DPPLMAN	15560	GATCCTCCTCTTATGGCTAAT	29883	GACCCACCACTCATGGCAAAC
1238	DPPYAVS	15561	GATCCTCCTTATGCTGTGAGT	29884	GACCCACCATACGCAGTCAGC
1239	DPPYDQR	15562	GATCCGCCGTATGATCAGAGG	29885	GACCCACCATACGACCAAAGA
1240	DPQENHA	15563	GATCCTCAGGAGAATCATGCT	29886	GACCCACAAGAAAACCACGCA
1241	DPQRLVI	15564	GATCCTCAGAGGTTGGTGATT	29887	GACCCACAAAGACTCGTCATC
1242	DPRFTLP	15565	GATCCTCGTTTTACGCTGCCG	29888	GACCCAAGATTCACACTCCCA
1243	DPRKSSA	15566	GATCCTCGTAAGTCTTCGGCT	29889	GACCCAAGAAAAAGCAGCGCA
1244	DPRLPSY	15567	GATCCGAGGCTTCCGTCTTAT	29890	GACCCAAGACTCCCAAGCTAC
1245	DPRPLAS	15568	GATCCGCGGCCGCTGGCGTCT	29891	GACCCAAGACCACTCGCAAGC
1246	DPRSAVQ	15569	GATCCTAGGTCGGCTGTGCAG	29892	GACCCAAGAAGCGCAGTCCAA
1247	DPRSSLT	15570	GATCCTAGGTCTAGTTTGACT	29893	GACCCAAGAAGCAGCCTCACA
1248	DPRTEMV	15571	GATCCGCGTACGGAGATGGTG	29894	GACCCAAGAACAGAAATGGTC
1249	DPSDDYV	15572	GATCCTTCTGATGATTATGTG	29895	GACCCAAGCGACGACTACGTC

1250	DPSRRPS	15573	GATCCGTCGAGGAGGCCTAGT	29896	GACCCAAGCAGAAGACCAAGC
1251	DPSSLRL	15574	GATCCTTCGAGTCTTCGGTTG	29897	GACCCAAGCAGCCTCAGACTC
1252	DPSYDQH	15575	GATCCTTCTTATGATCAGCAT	29898	GACCCAAGCTACGACCAACAC
1253	DPTFSSE	15576	GATCCTACGTTTTCGTCGGAG	29899	GACCCAACATTCAGCAGCGAA
1254	DPTHRIV	15577	GATCCGACGCATAGGATTGTT	29900	GACCCAACACACAGAATCGTC
1255	DPTLHRP	15578	GATCCGACTTTGCATCGTCCT	29901	GACCCAACACTCCACAGACCA
1256	DPTYRGG	15579	GATCCTACTTATCGTGGTGGG	29902	GACCCAACATACAGAGGAGGA
1257	DPVGRSL	15580	GATCCTGTGGGTCGGAGTTTG	29903	GACCCAGTCGGAAGAAGCCTC
1258	DPVIRAA	15581	GATCCTGTGATTCGTGCTGCT	29904	GACCCAGTCATCAGAGCAGCA
1259	DPVMPRR	15582	GATCCGGTTATGCCGCGTCGT	29905	GACCCAGTCATGCCAAGAAGA
1260	DPVSSRA	15583	GATCCGGTTTCGTCGAGGGCG	29906	GACCCAGTCAGCAGCAGAGCA
1261	DQAMSRN	15584	GATCAGGCGATGAGTCGGAAT	29907	GACCAAGCAATGAGCAGAAAC
1262	DQDKSAS	15585	GATCAGGATAAGTCTGCGAGT	29908	GACCAAGACAAAAGCGCAAGC
1263	DQDQGRA	15586	GATCAGGATCAGGGGCGTGCG	29909	GACCAAGACCAAGGAAGAGCA
1264	DQFHPRP	15587	GATCAGTTTCATCCTAGGCCT	29910	GACCAATTCCACCCAAGACCA
1265	DQLNPRG	15588	GATCAGCTGAATCCGCGTGGT	29911	GACCAACTCAACCCAAGAGGA
1266	DQLRSAT	15589	GATCAGTTGCGTTCGGCTACG	29912	GACCAACTCAGAAGCGCAACA
1267	DQPAYNA	15590	GATCAGCCTGCTTATAATGCG	29913	GACCAACCAGCATACAACGCA
1268	DQQFEMG	15591	GATCAGCAGTTTGAGATGGGT	29914	GACCAACAATTCGAAATGGGA
1269	DQQSFTR	15592	GATCAGCAGAGTTTTACGCGT	29915	GACCAACAAAGCTTCACAAGA
1270	DQRASSP	15593	GATCAGCGTGCGTCGTCGCCT	29916	GACCAAAGAGCAAGCAGCCCA
1271	DQRLQMI	15594	GATCAGAGGTTGCAGATGATT	29917	GACCAAAGACTCCAAATGATC
1272	DQSGTVS	15595	GATCAGTCTGGGACTGTGTCT	29918	GACCAAAGCGGAACAGTCAGC
1273	DQSPGMK	15596	GATCAGTCTCCGGGTATGAAG	29919	GACCAAAGCCCAGGAATGAAA
1274	DRALSMG	15597	GATCGGGCTTTGTCTATGGGG	29920	GACAGAGCACTCAGCATGGGA
1275	DRDTSSF	15598	GATCGTGATACTTCGTCTTTT	29921	GACAGAGACACAAGCAGCTTC
1276	DRERPYS	15599	GATCGGGAGCGTCCTTATAGT	29922	GACAGAGAAAGACCATACAGC
1277	DRFNSYA	15600	GATCGTTTTAATTCTTATGCG	29923	GACAGATTCAACAGCTACGCA
1278	DRGCKDT	15601	GATCGGGGGTGTAAGGATACG	29924	GACAGAGGATGCAAAGACACA
1279	DRGGFND	15602	GATAGGGGTGGGTTTAATGAT	29925	GACAGAGGAGGATTCAACGAC
1280	DRGLRTA	15603	GATAGGGGTCTGAGGACGGCT	29926	GACAGAGGACTCAGAACAGCA
1281	DRGNGPR	15604	GATAGGGGTAATGGTCCTCGG	29927	GACAGAGGAAACGGACCAAGA
1282	DRGSDLS	15605	GATCGGGGTAGTGATTTGTCG	29928	GACAGAGGAAGCGACCTCAGC
1283	DRGSLAR	15606	GATCGGGGTTCGCTGGCTCGG	29929	GACAGAGGAAGCCTCGCAAGA
1284	DRIETQP	15607	GATCGGATTGAGACTCAGCCG	29930	GACAGAATCGAAACACAACCA
1285	DRIMQEH	15608	GATAGGATTATGCAGGAGCAT	29931	GACAGAATCATGCAAGAACAC
1286	DRIQTAP	15609	GATCGTATTCAGACTGCGCCT	29932	GACAGAATCCAAACAGCACCA
1287	DRKKLNE	15610	GATCGGAAGAAGCTGAATGAG	29933	GACAGAAAAAAACTCAACGAA
1288	DRKLVTP	15611	GATCGTAAGCTGGTGACGCCT	29934	GACAGAAAACTCGTCACACCA
1289	DRLATMS	15612	GATAGGCTTGCGACGATGTCT	29935	GACAGACTCGCAACAATGAGC
1290	DRLNQRG	15613	GATCGGTTGAATCAGCGGGGT	29936	GACAGACTCAACCAAAGAGGA
1291	DRMTNAV	15614	GATCGGATGACTAATGCTGTT	29937	GACAGAATGACAAACGCAGTC
1292	DRNLVTR	15615	GATCGTAATTTGGTTACGCGG	29938	GACAGAAACCTCGTCACAAGA
1293	DRNVKHV	15616	GATCGGAATGTGAAGCATGTT	29939	GACAGAAACGTCAAACACGTC
1294	DRPFEAP	15617	GATCGTCCGTTTGAGGCGCCG	29940	GACAGACCATTCGAAGCACCA

1295	DRPGGKP	15618	GATCGGCCGGGGGGGAAGCCT	29941	GACAGACCAGGAGGAAAACCA
1296	DRPLHVV	15619	GATCGTCCGTTGCATGTTGTG	29942	GACAGACCACTCCACGTCGTC
1297	DRPPCSR	15620	GATAGGCCTCCTTGTAGTCGT	29943	GACAGACCACCATGCAGCAGA
1298	DRPSSPL	15621	GATCGGCCGTCTTCGCCTCTG	29944	GACAGACCAAGCAGCCCACTC
1299	DRQRPLS	15622	GATCGGCAGCGGCCGTTGTCG	29945	GACAGACAAAGACCACTCAGC
1300	DRQTLTR	15623	GATAGGCAGACTCTGACTCGT	29946	GACAGACAAACACTCACAAGA
1301	DRRMGVA	15624	GATAGGAGGATGGGTGTGGCT	29947	GACAGAAGAATGGGAGTCGCA
1302	DRRPAHD	15625	GATAGGCGTCCTGCTCATGAT	29948	GACAGAAGACCAGCACACGAC
1303	DRRSEER	15626	GATAGGCGTTCTGAGGAGCGG	29949	GACAGAAGAAGCGAAGAAAGA
1304	DRSAAII	15627	GATCGGTCTGCTGCTATTATT	29950	GACAGAAGCGCAGCAATCATC
1305	DRSGPNE	15628	GATCGTTCGGGTCCTAATGAG	29951	GACAGAAGCGGACCAAACGAA
1306	DRSIALR	15629	GATCGTTCTATTGCTCTGCGG	29952	GACAGAAGCATCGCACTCAGA
1307	DRSLAFA	15630	GATCGGTCTCTGGCGTTTGCG	29953	GACAGAAGCCTCGCATTCGCA
1308	DRSLRSL	15631	GATCGTAGTCTTCGTAGTCTT	29954	GACAGAAGCCTCAGAAGCCTC
1309	DRSNAGH	15632	GATCGTTCTAATGCGGGTCAT	29955	GACAGAAGCAACGCAGGACAC
1310	DRSQLTA	15633	GATCGGTCTCAGCTGACTGCT	29956	GACAGAAGCCAACTCACAGCA
1311	DRSQVLH	15634	GATAGGTCGCAGGTTCTTCAT	29957	GACAGAAGCCAAGTCCTCCAC
1312	DRSVVLN	15635	GATAGGTCGGTTGTTCTTAAT	29958	GACAGAAGCGTCGTCCTCAAC
1313	DRTARAP	15636	GATAGGACTGCGCGGGCGCCT	29959	GACAGAACAGCAAGAGCACCA
1314	DRTKSST	15637	GATAGGACTAAGTCGTCGACG	29960	GACAGAACAAAAAGCAGCACA
1315	DRTTVPP	15638	GATCGTACTACGGTTCCTCCT	29961	GACAGAACAACAGTCCCACCA
1316	DRTVSLL	15639	GATCGTACGGTTTCGCTGCTG	29962	GACAGAACAGTCAGCCTCCTC
1317	DRVHSSS	15640	GATAGGGTGCATTCGTCGAGT	29963	GACAGAGTCCACAGCAGCAGC
1318	DRVSTSK	15641	GATAGGGTGAGTACGAGTAAG	29964	GACAGAGTCAGCACAAGCAAA
1319	DRVTPEP	15642	GATCGGGTGACTCCGGAGCCT	29965	GACAGAGTCACACCAGAACCA
1320	DRWTSSS	15643	GATCGGTGGACGTCTAGTTCG	29966	GACAGATGGACAAGCAGCAGC
1321	DSAPVAH	15644	GATTCTGCGCCGGTGGCGCAT	29967	GACAGCGCACCAGTCGCACAC
1322	DSARSAI	15645	GATAGTGCTAGGTCGGCGATT	29968	GACAGCGCAAGAAGCGCAATC
1323	DSDMMGE	15646	GATAGTGATATGATGGGTGAG	29969	GACAGCGACATGATGGGAGAA
1324	DSDRDSK	15647	GATTCGGATAGGGATAGTAAG	29970	GACAGCGACAGAGACAGCAAA
1325	DSDRLSA	15648	GATTCTGATCGGCTTTCTGCG	29971	GACAGCGACAGACTCAGCGCA
1326	DSEKTIP	15649	GATTCGGAGAAGACGATTCCT	29972	GACAGCGAAAAAACAATCCCA
1327	DSEVPMY	15650	GATTCGGAGGTGCCTATGTAT	29973	GACAGCGAAGTCCCAATGTAC
1328	DSEVSHP	15651	GATTCTGAGGTGAGTCATCCG	29974	GACAGCGAAGTCAGCCACCCA
1329	DSFGRPQ	15652	GATTCGTTTGGTAGGCCGCAG	29975	GACAGCTTCGGAAGACCACAA
1330	DSGASLG	15653	GATTCTGGTGCTAGTCTGGGT	29976	GACAGCGGAGCAAGCCTCGGA
1331	DSGDPAR	15654	GATAGTGGTGATCCTGCGCGT	29977	GACAGCGGAGACCCAGCAAGA
1332	DSGIGYP	15655	GATTCTGGGATTGGTTATCCT	29978	GACAGCGGAATCGGATACCCA
1333	DSGSNGL	15656	GATTCTGGTTCGAATGGTCTT	29979	GACAGCGGAAGCAACGGACTC
1334	DSHYRVP	15657	GATTCTCATTATAGGGTTCCG	29980	GACAGCCACTACAGAGTCCCA
1335	DSIDPKF	15658	GATTCGATTGATCCGAAGTTT	29981	GACAGCATCGACCCAAAATTC
1336	DSIGPGT	15659	GATTCGATTGGGCCGGGGACT	29982	GACAGCATCGGACCAGGAACA
1337	DSIHIMA	15660	GATTCGATTCATATTATGGCT	29983	GACAGCATCCACATCATGGCA
1338	DSISSRA	15661	GATAGTATTTCGAGTCGGGCG	29984	GACAGCATCAGCAGCAGAGCA
1339	DSITRAS	15662	GATTCGATTACGAGGGCTTCT	29985	GACAGCATCACAAGAGCAAGC

1340	DSITTRI	15663	GATTCTATTACGACTCGTATT	29986	GACAGCATCACAACAAGAATC
1341	DSKRTIT	15664	GATTCGAAGCGGACGATTACG	29987	GACAGCAAAAGAACAATCACA
1342	DSLASRP	15665	GATTCGTTGGCGTCGAGGCCG	29988	GACAGCCTCGCAAGCAGACCA
1343	DSLGKRS	15666	GATTCGTTGGGGAAGAGGTCG	29989	GACAGCCTCGGAAAAAGAAGC
1344	DSLKLSS	15667	GATTCGCTGAAGCTGTCTTCG	29990	GACAGCCTCAAACTCAGCAGC
1345	DSMELYS	15668	GATAGTATGGAGCTTTATTCT	29991	GACAGCATGGAACTCTACAGC
1346	DSMGASG	15669	GATTCTATGGGTGCTTCGGGT	29992	GACAGCATGGGAGCAAGCGGA
1347	DSNIPPR	15670	GATTCGAATATTCCGCCGCGT	29993	GACAGCAACATCCCACCAAGA
1348	DSNNEKS	15671	GATTCTAATAATGAGAAGTCT	29994	GACAGCAACAACGAAAAAAGC
1349	DSNPSLS	15672	GATTCTAATCCGTCTTTGTCG	29995	GACAGCAACCCAAGCCTCAGC
1350	DSNRLVD	15673	GATAGTAATCGGTTGGTGGAT	29996	GACAGCAACAGACTCGTCGAC
1351	DSPKYSH	15674	GATTCGCCGAAGTATTCTCAT	29997	GACAGCCCAAAATACAGCCAC
1352	DSPSFVL	15675	GATTCTCCTAGTTTTGTGTTG	29998	GACAGCCCAAGCTTCGTCCTC
1353	DSQIYVS	15676	GATTCTCAGATTTATGTGTCG	29999	GACAGCCAAATCTACGTCAGC
1354	DSQLNAP	15677	GATTCGCAGCTGAATGCGCCT	30000	GACAGCCAACTCAACGCACCA
1355	DSQMRTM	15678	GATTCTCAGATGCGTACTATG	30001	GACAGCCAAATGAGAACAATG
1356	DSRIAAL	15679	GATTCTAGGATTGCGGCGTTG	30002	GACAGCAGAATCGCAGCACTC
1357	DSRLLSG	15680	GATAGTCGTTTGCTGTCTGGT	30003	GACAGCAGACTCCTCAGCGGA
1358	DSRMAAS	15681	GATAGTCGTATGGCTGCTAGT	30004	GACAGCAGAATGGCAGCAAGC
1359	DSRNAVT	15682	GATTCTCGGAATGCTGTGACG	30005	GACAGCAGAAACGCAGTCACA
1360	DSRPLSV	15683	GATTCGCGTCCTTTGAGTGTT	30006	GACAGCAGACCACTCAGCGTC
1361	DSRQGRV	15684	GATTCTCGTCAGGGGCGGGTG	30007	GACAGCAGACAAGGAAGAGTC
1362	DSRSLRA	15685	GATTCGAGGTCGTTGAGGGCG	30008	GACAGCAGAAGCCTCAGAGCA
1363	DSSAKES	15686	GATTCGTCGGCTAAGGAGAGT	30009	GACAGCAGCGCAAAAGAAAGC
1364	DSSEYSP	15687	GATAGTTCTGAGTATAGTCCT	30010	GACAGCAGCGAATACAGCCCA
1365	DSSHTLQ	15688	GATAGTAGTCATACTTTGCAG	30011	GACAGCAGCCACACACTCCAA
1366	DSSHTMM	15689	GATTCTAGTCATACTATGATG	30012	GACAGCAGCCACACAATGATG
1367	DSSHYPG	15690	GATTCGTCGCATTATCCTGGT	30013	GACAGCAGCCACTACCCAGGA
1368	DSSPLVR	15691	GATTCGTCGCCTCTGGTTCGG	30014	GACAGCAGCCCACTCGTCAGA
1369	DSTPEEG	15692	GATAGTACGCCGGAGGAGGGT	30015	GACAGCACACCAGAAGAAGGA
1370	DSTQFPR	15693	GATTCGACTCAGTTTCCTAGG	30016	GACAGCACACAATTCCCAAGA
1371	DSVHLGR	15694	GATAGTGTTCATTTGGGGCGT	30017	GACAGCGTCCACCTCGGAAGA
1372	DSVKASQ	15695	GATTCGGTGAAGGCTAGTCAG	30018	GACAGCGTCAAAGCAAGCCAA
1373	DTAAKDS	15696	GATACTGCTGCTAAGGATTCT	30019	GACACAGCAGCAAAAGACAGC
1374	DTASRLA	15697	GATACTGCGTCGCGTCTTGCT	30020	GACACAGCAAGCAGACTCGCA
1375	DTDGQRA	15698	GATACTGATGGGCAGCGTGCT	30021	GACACAGACGGACAAAGAGCA
1376	DTHAYDG	15699	GATACGCATGCTTATGATGGG	30022	GACACACACGCATACGACGGA
1377	DTHIIAS	15700	GATACTCATATTATTGCGTCG	30023	GACACACACATCATCGCAAGC
1378	DTHRSER	15701	GATACTCATAGGTCGGAGAGG	30024	GACACACACAGAAGCGAAAGA
1379	DTHVIAS	15702	GATACTCATGTTATTGCGAGT	30025	GACACACACGTCATCGCAAGC
1380	DTIAHAP	15703	GATACTATTGCGCATGCTCCG	30026	GACACAATCGCACACGCACCA
1381	DTLALSC	15704	GATACTTTGGCTTTGTCTTGT	30027	GACACACTCGCACTCAGCTGC
1382	DTLANSA	15705	GATACTCTGGCGAATTCTGCG	30028	GACACACTCGCAAACAGCGCA
1383	DTLGLEP	15706	GATACGTTGGGGTTGGAGCCG	30029	GACACACTCGGACTCGAACCA
1384	DTLMIRG	15707	GATACTTTGATGATTCGTGGG	30030	GACACACTCATGATCAGAGGA

1385	DTLSTTR	15708	GATACTTTGAGTACGACGCGG	30031	GACACACTCAGCACAACAAGA
1386	DTNMLHV	15709	GATACTAATATGTTGCATGTG	30032	GACACAAACATGCTCCACGTC
1387	DTPDALR	15710	GATACTCCGGATGCTCTTCGT	30033	GACACACCAGACGCACTCAGA
1388	DTPHLSL	15711	GATACGCCGCATCTTTCTTTG	30034	GACACACCACACCTCAGCCTC
1389	DTPLELA	15712	GATACTCCGCTTGAGCTGGCT	30035	GACACACCACTCGAACTCGCA
1390	DTPMPKI	15713	GATACTCCGATGCCTAAGATT	30036	GACACACCAATGCCAAAAATC
1391	DTPNDTA	15714	GATACGCCGAATGATACTGCG	30037	GACACACCAAACGACACAGCA
1392	DTQHLKP	15715	GATACGCAGCATCTTAAGCCG	30038	GACACACAACACCTCAAACCA
1393	DTQLPNP	15716	GATACTCAGTTGCCTAATCCT	30039	GACACACAACTCCCAAACCCA
1394	DTQLTLA	15717	GATACGCAGCTGACGTTGGCG	30040	GACACACAACTCACACTCGCA
1395	DTQSVSL	15718	GATACGCAGAGTGTGTCGTTG	30041	GACACACAAAGCGTCAGCCTC
1396	DTRAFTG	15719	GATACGAGGGCGTTTACGGGT	30042	GACACAAGAGCATTCACAGGA
1397	DTRHSDL	15720	GATACTCGTCATAGTGATTTG	30043	GACACAAGACACAGCGACCTC
1398	DTRRECD	15721	GATACTCGGAGGGAGTGTGAT	30044	GACACAAGAAGAGAATGCGAC
1399	DTSRTSL	15722	GATACTTCGAGGACGTCTTTG	30045	GACACAAGCAGAACAAGCCTC
1400	DTSSRMT	15723	GATACGAGTAGTCGTATGACG	30046	GACACAAGCAGCAGAATGACA
1401	DTSWKST	15724	GATACTTCTTGGAAGAGTACT	30047	GACACAAGCTGGAAAAGCACA
1402	DTTERPW	15725	GATACTACTGAGCGTCCGTGG	30048	GACACAACAGAAAGACCATGG
1403	DTTGRYL	15726	GATACTACGGGGAGGTATTTG	30049	GACACAACAGGAAGATACCTC
1404	DTTLLRG	15727	GATACTACTCTTCTGCGGGGT	30050	GACACAACACTCCTCAGAGGA
1405	DTTPIVR	15728	GATACTACGCCTATTGTGCGT	30051	GACACAACACCAATCGTCAGA
1406	DTYAIAI	15729	GATACTTATGCGATTGCTATT	30052	GACACATACGCAATCGCAATC
1407	DTYNTPA	15730	GATACGTATAATACGCCTGCG	30053	GACACATACAACACACCAGCA
1408	DVASRSL	15731	GATGTGGCGTCTCGTTCTCTG	30054	GACGTCGCAAGCAGAAGCCTC
1409	DVASSRL	15732	GATGTTGCTTCGTCGCGTCTG	30055	GACGTCGCAAGCAGCAGACTC
1410	DVDDTMW	15733	GATGTGGATGATACGATGTGG	30056	GACGTCGACGACACAATGTGG
1411	DVDLLPT	15734	GATGTTGATCTGCTTCCTACT	30057	GACGTCGACCTCCTCCCAACA
1412	DVDRLNT	15735	GATGTTGATAGGTTGAATACT	30058	GACGTCGACAGACTCAACACA
1413	DVDSHHT	15736	GATGTGGATTCGCATCATACT	30059	GACGTCGACAGCCACCACACA
1414	DVDVRHG	15737	GATGTTGATGTGAGGCATGGT	30060	GACGTCGACGTCAGACACGGA
1415	DVEPLQM	15738	GATGTTGAGCCTCTTCAGATG	30061	GACGTCGAACCACTCCAAATG
1416	DVFRTQP	15739	GATGTGTTTCGTACTCAGCCT	30062	GACGTCTTCAGAACACAACCA
1417	DVGTYGR	15740	GATGTTGGGACGTATGGTCGT	30063	GACGTCGGAACATACGGAAGA
1418	DVKTNVY	15741	GATGTTAAGACGAATGTTTAT	30064	GACGTCAAAACAAACGTCTAC
1419	DVLFSKN	15742	GATGTTTTGTTTTCTAAGAAT	30065	GACGTCCTCTTCAGCAAAAAC
1420	DVLGKHA	15743	GATGTTCTTGGTAAGCATGCT	30066	GACGTCCTCGGAAAACACGCA
1421	DVLKTDF	15744	GATGTTTTGAAGACGGATTTT	30067	GACGTCCTCAAAACAGACTTC
1422	DVLNSTD	15745	GATGTTCTGAATTCTACTGAT	30068	GACGTCCTCAACAGCACAGAC
1423	DVMSQLL	15746	GATGTGATGAGTCAGCTTCTG	30069	GACGTCATGAGCCAACTCCTC
1424	DVPNAPC	15747	GATGTTCCTAATGCGCCGTGT	30070	GACGTCCCAAACGCACCATGC
1425	DVPNPTG	15748	GATGTGCCGAATCCGACGGGG	30071	GACGTCCCAAACCCAACAGGA
1426	DVPNTMT	15749	GATGTGCCGAATACGATGACT	30072	GACGTCCCAAACACAATGACA
1427	DVPYSLE	15750	GATGTGCCGTATTCGCTTGAG	30073	GACGTCCCATACAGCCTCGAA
1428	DVQMHKH	15751	GATGTTCAGATGCATAAGCAT	30074	GACGTCCAAATGCACAAACAC
1429	DVRNTRL	15752	GATGTGAGGAATACGCGGCTG	30075	GACGTCAGAAACACAAGACTC

1430	DVRQAYF	15753	GATGTTAGGCAGGCGTATTTT	30076	GACGTCAGACAAGCATACTTC
1431	DVRVGHI	15754	GATGTGCGGGTTGGTCATATT	30077	GACGTCAGAGTCGGACACATC
1432	DVSGTIG	15755	GATGTGAGTGGTACTATTGGG	30078	GACGTCAGCGGAACAATCGGA
1433	DVSLRVT	15756	GATGTTTCTCTGCGTGTGACG	30079	GACGTCAGCCTCAGAGTCACA
1434	DVSSPLI	15757	GATGTTTCTTCGCCTCTTATT	30080	GACGTCAGCAGCCCACTCATC
1435	DVSVSDV	15758	GATGTTAGTGTTTCTGATGTT	30081	GACGTCAGCGTCAGCGACGTC
1436	DVTVGSS	15759	GATGTGACGGTTGGTAGTTCT	30082	GACGTCACAGTCGGAAGCAGC
1437	DVVAGPP	15760	GATGTTGTTGCGGGGCCGCCT	30083	GACGTCGTCGCAGGACCACCA
1438	DVVNSLN	15761	GATGTTGTGAATTCGCTTAAT	30084	GACGTCGTCAACAGCCTCAAC
1439	DVVPRSA	15762	GATGTGGTGCCTAGGTCGGCG	30085	GACGTCGTCCCAAGAAGCGCA
1440	DWGPKQR	15763	GATTGGGGTCCTAAGCAGCGG	30086	GACTGGGGACCAAAACAAAGA
1441	DWKPNHE	15764	GATTGGAAGCCGAATCATGAG	30087	GACTGGAAACCAAACCACGAA
1442	DWKQTTA	15765	GATTGGAAGCAGACTACTGCT	30088	GACTGGAAACAAACAACAGCA
1443	DWQRHGP	15766	GATTGGCAGCGTCATGGTCCT	30089	GACTGGCAAAGACACGGACCA
1444	DWTHIDK	15767	GATTGGACTCATATTGATAAG	30090	GACTGGACACACATCGACAAA
1445	DWTPRTT	15768	GATTGGACTCCGCGGACTACG	30091	GACTGGACACCAAGAACAACA
1446	DYAIGKT	15769	GATTATGCGATTGGGAAGACG	30092	GACTACGCAATCGGAAAAACA
1447	DYESFSR	15770	GATTATGAGTCTTTTTCGCGG	30093	GACTACGAAAGCTTCAGCAGA
1448	DYGPEII	15771	GATTATGGTCCTGAGATTATT	30094	GACTACGGACCAGAAATCATC
1449	DYGQLSN	15772	GATTATGGTCAGCTTTCGAAT	30095	GACTACGGACAACTCAGCAAC
1450	DYHQMHS	15773	GATTATCATCAGATGCATTCT	30096	GACTACCACCAAATGCACAGC
1451	DYHRAPG	15774	GATTATCATCGGGCGCCGGGG	30097	GACTACCACAGAGCACCAGGA
1452	DYPPEVL	15775	GATTATCCTCCGGAGGTTCTT	30098	GACTACCCACCAGAAGTCCTC
1453	DYREYTR	15776	GATTATAGGGAGTATACGCGT	30099	GACTACAGAGAATACACAAGA
1454	DYRFADS	15777	GATTATCGGTTTGCTGATAGT	30100	GACTACAGATTCGCAGACAGC
1455	DYRITNS	15778	GATTATCGTATTACGAATTCT	30101	GACTACAGAATCACAAACAGC
1456	DYRLLPE	15779	GATTATAGGTTGCTTCCTGAG	30102	GACTACAGACTCCTCCCAGAA
1457	DYRQIDQ	15780	GATTATCGTCAGATTGATCAG	30103	GACTACAGACAAATCGACCAA
1458	DYSEMSK	15781	GATTATTCTGAGATGTCGAAG	30104	GACTACAGCGAAATGAGCAAA
1459	DYSSARA	15782	GATTATTCGTCTGCGCGGGCT	30105	GACTACAGCAGCGCAAGAGCA
1460	DYSSSMR	15783	GATTATTCGTCGTCGATGCGG	30106	GACTACAGCAGCAGCATGAGA
1461	DYTLTPS	15784	GATTATACTCTGACTCCGTCT	30107	GACTACACACTCACACCAAGC
1462	DYVPVEL	15785	GATTATGTTCCTGTGGAGCTG	30108	GACTACGTCCCAGTCGAACTC
1463	EAAHPGM	15786	GAGGCTGCGCATCCGGGTATG	30109	GAAGCAGCACACCCAGGAATG
1464	EAAMTRE	15787	GAGGCTGCTATGACGCGGGAG	30110	GAAGCAGCAATGACAAGAGAA
1465	EAAPIPR	15788	GAGGCGGCTCCGATTCCTCGG	30111	GAAGCAGCACCAATCCCAAGA
1466	EAASRHD	15789	GAGGCGGCTTCGAGGCATGAT	30112	GAAGCAGCAAGCAGACACGAC
1467	EAASSPK	15790	GAGGCGGCTAGTAGTCCTAAG	30113	GAAGCAGCAAGCAGCCCAAAA
1468	EAATLTT	15791	GAGGCGGCGACTCTTACTACT	30114	GAAGCAGCAACACTCACAACA
1469	EAFHTSS	15792	GAGGCTTTTCATACGAGTTCG	30115	GAAGCATTCCACACAAGCAGC
1470	EAFSGRI	15793	GAGGCGTTTTCTGGTCGTATT	30116	GAAGCATTCAGCGGAAGAATC
1471	EAKTNRT	15794	GAGGCTAAGACTAATAGGACT	30117	GAAGCAAAAACAAACAGAACA
1472	EALAVRP	15795	GAGGCGCTGGCTGTGAGGCCT	30118	GAAGCACTCGCAGTCAGACCA
1473	EALRGPI	15796	GAGGCTCTTCGTGGTCCGATT	30119	GAAGCACTCAGAGGACCAATC
1474	EAMHSRA	15797	GAGGCTATGCATTCTCGTGCT	30120	GAAGCAATGCACAGCAGAGCA

1475	EANDETK	15798	GAGGCGAATGATGAGACTAAG	30121	GAAGCAAACGACGAAACAAAA
1476	EANRSPM	15799	GAGGCGAATCGTAGTCCGATG	30122	GAAGCAAACAGAAGCCCAATG
1477	EAQRAAP	15800	GAGGCTCAGAGGGCGGCGCCG	30123	GAAGCACAAAGAGCAGCACCA
1478	EARHVYA	15801	GAGGCGCGTCATGTGTATGCT	30124	GAAGCAAGACACGTCTACGCA
1479	EARYESG	15802	GAGGCTCGTTATGAGTCGGGG	30125	GAAGCAAGATACGAAAGCGGA
1480	EARYVHV	15803	GAGGCGCGTTATGTTCATGTG	30126	GAAGCAAGATACGTCCACGTC
1481	EASHFTM	15804	GAGGCGTCGCATTTTACTATG	30127	GAAGCAAGCCACTTCACAATG
1482	EASLAAK	15805	GAGGCGTCGTTGGCGGCTAAG	30128	GAAGCAAGCCTCGCAGCAAAA
1483	EASNAIA	15806	GAGGCTAGTAATGCTATTGCT	30129	GAAGCAAGCAACGCAATCGCA
1484	EASRVTV	15807	GAGGCTAGTCGTGTGACGGTT	30130	GAAGCAAGCAGAGTCACAGTC
1485	EASSMHS	15808	GAGGCGTCTTCGATGCATTCG	30131	GAAGCAAGCAGCATGCACAGC
1486	EASVLTR	15809	GAGGCTTCGGTTCTTACGAGG	30132	GAAGCAAGCGTCCTCACAAGA
1487	EASYMPP	15810	GAGGCTTCGTATATGCCTCCT	30133	GAAGCAAGCTACATGCCACCA
1488	EATMVKD	15811	GAGGCTACGATGGTTAAGGAT	30134	GAAGCAACAATGGTCAAAGAC
1489	EATNRHP	15812	GAGGCTACGAATCGGCATCCT	30135	GAAGCAACAAACAGACACCCA
1490	EATPPTI	15813	GAGGCTACTCCTCCGACTATT	30136	GAAGCAACACCACCAACAATC
1491	EATTNFL	15814	GAGGCTACGACTAATTTTCTT	30137	GAAGCAACAACAAACTTCCTC
1492	EATTPMP	15815	GAGGCGACGACGCCGATGCCG	30138	GAAGCAACAACACCAATGCCA
1493	EAVTPRH	15816	GAGGCTGTGACGCCGCGTCAT	30139	GAAGCAGTCACACCAAGACAC
1494	EAVTVKM	15817	GAGGCGGTTACTGTGAAGATG	30140	GAAGCAGTCACAGTCAAAATG
1495	EDAEREY	15818	GAGGATGCGGAGCGTGAGTAT	30141	GAAGACGCAGAAAGAGAATAC
1496	EDAPPSR	15819	GAGGATGCTCCTCCGTCGCGG	30142	GAAGACGCACCACCAAGCAGA
1497	EDIRMPS	15820	GAGGATATTCGTATGCCTTCT	30143	GAAGACATCAGAATGCCAAGC
1498	EDKQHLS	15821	GAGGATAAGCAGCATCTTTCT	30144	GAAGACAAACAACACCTCAGC
1499	EDLPGKM	15822	GAGGATCTGCCGGGGAAGATG	30145	GAAGACCTCCCAGGAAAAATG
1500	EDMPQLG	15823	GAGGATATGCCTCAGCTTGGT	30146	GAAGACATGCCACAACTCGGA
1501	EDPLGQM	15824	GAGGATCCTCTTGGTCAGATG	30147	GAAGACCCACTCGGACAAATG
1502	EDSHFAP	15825	GAGGATTCGCATTTTGCGCCT	30148	GAAGACAGCCACTTCGCACCA
1503	EEAMYPF	15826	GAGGAGGCGATGTATCCTTTT	30149	GAAGAAGCAATGTACCCATTC
1504	EEASLSL	15827	GAGGAGGCTTCGCTTAGTCTG	30150	GAAGAAGCAAGCCTCAGCCTC
1505	EELAKAD	15828	GAGGAGCTTGCTAAGGCTGAT	30151	GAAGAACTCGCAAAAGCAGAC
1506	EELRRHV	15829	GAGGAGTTGCGGAGGCATGTG	30152	GAAGAACTCAGAAGACACGTC
1507	EENLQRT	15830	GAGGAGAATCTTCAGCGGACT	30153	GAAGAAAACCTCCAAAGAACA
1508	EESGRVA	15831	GAGGAGTCTGGTCGGGTTGCG	30154	GAAGAAAGCGGAAGAGTCGCA
1509	EESKRSA	15832	GAGGAGTCGAAGCGTTCGGCT	30155	GAAGAAAGCAAAAGAAGCGCA
1510	EESPESI	15833	GAGGAGAGTCCGGAGTCGATT	30156	GAAGAAAGCCCAGAAAGCATC
1511	EETRKPL	15834	GAGGAGACGCGGAAGCCGCTT	30157	GAAGAAACAAGAAAACCACTC
1512	EETWHRL	15835	GAGGAGACTTGGCATAGGCTT	30158	GAAGAAACATGGCACAGACTC
1513	EEYVERI	15836	GAGGAGTATGTGGAGAGGATT	30159	GAAGAATACGTCGAAAGAATC
1514	EFDQRNI	15837	GAGTTTGATCAGCGTAATATT	30160	GAATTCGACCAAAGAAACATC
1515	EFERRTT	15838	GAGTTTGAGCGTCGTACGACG	30161	GAATTCGAAAGAAGAACAACA
1516	EFEVCCA	15839	GAGTTTGAGGTTTGTTGTGCT	30162	GAATTCGAAGTCTGCTGCGCA
1517	EFGMTVP	15840	GAGTTTGGGATGACGGTGCCG	30163	GAATTCGGAATGACAGTCCCA
1518	EFIEMRP	15841	GAGTTTATTGAGATGAGGCCT	30164	GAATTCATCGAAATGAGACCA
1519	EFNGKND	15842	GAGTTTAATGGTAAGAATGAT	30165	GAATTCAACGGAAAAAACGAC

1520	EFNKSGA	15843	GAGTTTAATAAGAGTGGTGCT	30166	GAATTCAACAAAAGCGGAGCA
1521	EFNPALS	15844	GAGTTTAATCCGGCTCTTAGT	30167	GAATTCAACCCAGCACTCAGC
1522	EFPSLDD	15845	GAGTTTCCTTCGTTGGATGAT	30168	GAATTCCCAAGCCTCGACGAC
1523	EFPTSLP	15846	GAGTTTCCTACGTCTCTTCCG	30169	GAATTCCCAACAAGCCTCCCA
1524	EFQKKSS	15847	GAGTTTCAGAAGAAGTCTTCT	30170	GAATTCCAAAAAAAAAAGCAGC
1525	EFQSLHV	15848	GAGTTTCAGTCGTTGCATGTG	30171	GAATTCCAAAGCCTCCACGTC
1526	EFRLSAV	15849	GAGTTTCGGCTGTCTGCTGTT	30172	GAATTCAGACTCAGCGCAGTC
1527	EFRSTGT	15850	GAGTTTAGGTCTACTGGGACG	30173	GAATTCAGAAGCACAGGAACA
1528	EFSQMTE	15851	GAGTTTTCGCAGATGACGGAG	30174	GAATTCAGCCAAATGACAGAA
1529	EFSRMNT	15852	GAGTTTTCTCGTATGAATACG	30175	GAATTCAGCAGAATGAACACA
1530	EFSTSLS	15853	GAGTTTTCGACTTCGCTTAGT	30176	GAATTCAGCACAAGCCTCAGC
1531	EFTHNKA	15854	GAGTTTACGCATAATAAGGCT	30177	GAATTCACACACAACAAAGCA
1532	EFTSEDL	15855	GAGTTTACGTCTGAGGATCTT	30178	GAATTCACAAGCGAAGACCTC
1533	EFVLSLS	15856	GAGTTTGTTTTGTCGTTGAGT	30179	GAATTCGTCCTCAGCCTCAGC
1534	EFYKDWD	15857	GAGTTTTATAAGGATTGGGAT	30180	GAATTCTACAAAGACTGGGAC
1535	EGANAAT	15858	GAGGGTGCGAATGCGGCTACT	30181	GAAGGAGCAAACGCAGCAACA
1536	EGDFVRA	15859	GAGGGTGATTTTGTTCGGGCG	30182	GAAGGAGACTTCGTCAGAGCA
1537	EGDNRLF	15860	GAGGGGGATAATCGGTTGTTT	30183	GAAGGAGACAACAGACTCTTC
1538	EGENQTT	15861	GAGGGGGAGAATCAGACTACT	30184	GAAGGAGAAAACCAAACAACA
1539	EGFVGPE	15862	GAGGGTTTTGTGGGTCCGGAG	30185	GAAGGATTCGTCGGACCAGAA
1540	EGGHRLI	15863	GAGGGGGGCATAGGCTTATT	30186	GAAGGAGGACACAGACTCATC
1541	EGHDTLM	15864	GAGGGGCATGATACTCTTATG	30187	GAAGGACACGACACACTCATG
1542	EGILKSL	15865	GAGGGGATTCTGAAGTCGCTT	30188	GAAGGAATCCTCAAAAGCCTC
1543	EGIPPFS	15866	GAGGGGATTCCGCCTTTTTCT	30189	GAAGGAATCCCACCATTCAGC
1544	EGISASV	15867	GAGGGTATTTCGGCGTCGGTG	30190	GAAGGAATCAGCGCAAGCGTC
1545	EGKVRLP	15868	GAGGGGAAGGTGCGGCTTCCG	30191	GAAGGAAAAGTCAGACTCCCA
1546	EGLGLRV	15869	GAGGGTTTGGGGCTTCGTGTG	30192	GAAGGACTCGGACTCAGAGTC
1547	EGMPLNH	15870	GAGGGTATGCCTCTTAATCAT	30193	GAAGGAATGCCACTCAACCAC
1548	EGPVLLA	15871	GAGGGTCCGGTTCTGCTGGCG	30194	GAAGGACCAGTCCTCCTCGCA
1549	EGRREPY	15872	GAGGGTCGTAGGGAGCCTTAT	30195	GAAGGAAGAAGAGAACCATAC
1550	EGRVVPA	15873	GAGGGGAGGGTTGTTCCTGCT	30196	GAAGGAAGAGTCGTCCCAGCA
1551	EGSFPLH	15874	GAGGGTAGTTTTCCTCTGCAT	30197	GAAGGAAGCTTCCCACTCCAC
1552	EGSGMLR	15875	GAGGGTTCTGGGATGTTGAGG	30198	GAAGGAAGCGGAATGCTCAGA
1553	EGSKMMV	15876	GAGGGTTCTAAGATGATGGTT	30199	GAAGGAAGCAAAATGATGGTC
1554	EGSPDLR	15877	GAGGGGTCTCCGGATTTGAGG	30200	GAAGGAAGCCCAGACCTCAGA
1555	EGSPRAM	15878	GAGGGTTCTCCTCGTGCGATG	30201	GAAGGAAGCCCAAGAGCAATG
1556	EGSQNDF	15879	GAGGGGTCGCAGAATGATTTT	30202	GAAGGAAGCCAAAACGACTTC
1557	EGTARLY	15880	GAGGGTACGGCGAGGTTGTAT	30203	GAAGGAACAGCAAGACTCTAC
1558	EGVVTLQ	15881	GAGGGGGTGGTGACTTTGCAG	30204	GAAGGAGTCGTCACACTCCAA
1559	EGYDSTT	15882	GAGGGGTATGATTCTACGACT	30205	GAAGGATACGACAGCACAACA
1560	EGYENGA	15883	GAGGGGTATGAGAATGGTGCT	30206	GAAGGATACGAAAACGGAGCA
1561	EHCTNTC	15884	GAGCATTGTACTAATACGTGT	30207	GAACACTGCACAAACACATGC
1562	EHGIAMD	15885	GAGCATGGTATTGCGATGGAT	30208	GAACACGGAATCGCAATGGAC
1563	EHGLNTL	15886	GAGCATGGGCTTAATACGCTT	30209	GAACACGGACTCAACACACTC
1564	EHGPALL	15887	GAGCATGGGCCGGCGCTGCTT	30210	GAACACGGACCAGCACTCCTC

1565	EHGSAMK	15888	GAGCATGGTTCTGCTATGAAG	30211	GAACACGGAAGCGCAATGAAA
1566	EHHVHSP	15889	GAGCATCATGTGCATTCTCCT	30212	GAACACCACGTCCACAGCCCA
1567	EHIPQAM	15890	GAGCATATTCCGCAGGCGATG	30213	GAACACATCCCACAAGCAATG
1568	EHKGAHF	15891	GAGCATAAGGGGGCTCATTTT	30214	GAACACAAAGGAGCACACTTC
1569	EHKLLVM	15892	GAGCATAAGTTGTTGGTGATG	30215	GAACACAAACTCCTCGTCATG
1570	EHMPSLR	15893	GAGCATATGCCTTCGTTGCGG	30216	GAACACATGCCAAGCCTCAGA
1571	EHNVGQS	15894	GAGCATAATGTGGGGCAGTCT	30217	GAACACAACGTCGGACAAAGC
1572	EHQGTTI	15895	GAGCATCAGGGTACTACTATT	30218	GAACACCAAGGAACAACAATC
1573	EHSDYQV	15896	GAGCATAGTGATTATCAGGTT	30219	GAACACAGCGACTACCAAGTC
1574	EHSELTP	15897	GAGCATAGTGAGTTGACGCCG	30220	GAACACAGCGAACTCACACCA
1575	EHSFKSA	15898	GAGCATAGTTTTAAGTCTGCT	30221	GAACACAGCTTCAAAAGCGCA
1576	EHSGTAI	15899	GAGCATTCTGGGACGGCGATT	30222	GAACACAGCGGAACAGCAATC
1577	EHSSGML	15900	GAGCATTCTTCGGGTATGCTT	30223	GAACACAGCAGCGGAATGCTC
1578	EIARGSF	15901	GAGATTGCGCGTGGTTCTTTT	30224	GAAATCGCAAGAGGAAGCTTC
1579	EIGYMSA	15902	GAGATTGGTTATATGAGTGCG	30225	GAAATCGGATACATGAGCGCA
1580	EIHYPLE	15903	GAGATTCATTATCCTCTGGAG	30226	GAAATCCACTACCCACTCGAA
1581	EIKAQMS	15904	GAGATTAAGGCGCAGATGTCT	30227	GAAATCAAAGCACAAATGAGC
1582	EIKDEKL	15905	GAGATTAAGGATGAGAAGCTT	30228	GAAATCAAAGACGAAAAACTC
1583	EIKHSMH	15906	GAGATTAAGCATTCGATGCAT	30229	GAAATCAAACACAGCATGCAC
1584	EINSQTN	15907	GAGATTAATTCTCAGACGAAT	30230	GAAATCAACAGCCAAACAAAC
1585	EIQHYHG	15908	GAGATTCAGCATTATCATGGT	30231	GAAATCCAACACTACCACGGA
1586	EIRKSII	15909	GAGATTAGGAAGTCTATTATT	30232	GAAATCAGAAAAAGCATCATC
1587	EISTQRY	15910	GAGATTTCGACTCAGCGTTAT	30233	GAAATCAGCACACAAAGATAC
1588	EKARAAS	15911	GAGAAGGCTCGGGCTGCGTCT	30234	GAAAAAGCAAGAGCAGCAAGC
1589	EKERPML	15912	GAGAAGGAGAGGCCGATGTTG	30235	GAAAAAGAAAGACCAATGCTC
1590	EKGFLHS	15913	GAGAAGGGTTTTTTGCATTCG	30236	GAAAAAGGATTCCTCCACAGC
1591	EKGLSTQ	15914	GAGAAGGGTCTGAGTACTCAG	30237	GAAAAAGGACTCAGCACACAA
1592	EKGSIMP	15915	GAGAAGGGTAGTATTATGCCT	30238	GAAAAAGGAAGCATCATGCCA
1593	EKGSLGH	15916	GAGAAGGGTTCTTTGGGTCAT	30239	GAAAAAGGAAGCCTCGGACAC
1594	EKIDRLG	15917	GAGAAGATTGATAGGTTGGGG	30240	GAAAAAATCGACAGACTCGGA
1595	EKIKIYS	15918	GAGAAGATTAAGATTTATTCT	30241	GAAAAAATCAAAATCTACAGC
1596	EKIPHSS	15919	GAGAAGATTCCGCATAGTTCT	30242	GAAAAAATCCCACACAGCAGC
1597	EKKLSAE	15920	GAGAAGAAGCTGTCTGCTGAG	30243	GAAAAAAAACTCAGCGCAGAA
1598	EKLARTG	15921	GAGAAGTTGGCGCGTACTGGG	30244	GAAAAACTCGCAAGAACAGGA
1599	EKMHANP	15922	GAGAAGATGCATGCTAATCCT	30245	GAAAAAATGCACGCAAACCCA
1600	EKPYITM	15923	GAGAAGCCTTATATTACTATG	30246	GAAAAACCATACATCACAATG
1601	EKQNLPL	15924	GAGAAGCAGAATTTGCCGCTT	30247	GAAAAACAAAACCTCCCACTC
1602	EKVIRPV	15925	GAGAAGGTGATTCGTCCTGTG	30248	GAAAAAGTCATCAGACCAGTC
1603	EKVPKLL	15926	GAGAAGGTTCCGAAGTTGCTG	30249	GAAAAAGTCCCAAAACTCCTC
1604	ELAAEAR	15927	GAGCTGGCTGCGGAGGCTCGT	30250	GAACTCGCAGCAGAAGCAAGA
1605	ELESAEI	15928	GAGCTGGAGAGTGCTGAGATT	30251	GAACTCGAAAGCGCAGAAATC
1606	ELETAKL	15929	GAGCTTGAGACGGCGAAGCTG	30252	GAACTCGAAACAGCAAAACTC
1607	ELFSDKF	15930	GAGCTGTTTTCTGATAAGTTT	30253	GAACTCTTCAGCGACAAATTC
1608	ELGPPRA	15931	GAGCTGGGTCCTCCGCGTGCG	30254	GAACTCGGACCACCAAGAGCA
1609	ELGPRTS	15932	GAGCTGGGGCCGCGGACTTCG	30255	GAACTCGGACCAAGAACAAGC

1610	ELILNSS	15933	GAGTTGATTCTGAATTCGTCG	30256	GAACTCATCCTCAACAGCAGC
1611	ELKAVAR	15934	GAGCTGAAGGCTGTTGCTAGG	30257	GAACTCAAAGCAGTCGCAAGA
1612	ELKFPDK	15935	GAGCTTAAGTTTCCGGATAAG	30258	GAACTCAAATTCCCAGACAAA
1613	ELKQASG	15936	GAGTTGAAGCAGGCGAGTGGT	30259	GAACTCAAACAAGCAAGCGGA
1614	ELKRYVG	15937	GAGTTGAAGAGGTATGTTGGG	30260	GAACTCAAAAGATACGTCGGA
1615	ELLEPDD	15938	GAGTTGCTTGAGCCGGATGAT	30261	GAACTCCTCGAACCAGACGAC
1616	ELMVNGG	15939	GAGCTTATGGTTAATGGGGGG	30262	GAACTCATGGTCAACGGAGGA
1617	ELNNLLR	15940	GAGCTTAATAATCTGCTTCGG	30263	GAACTCAACAACCTCCTCAGA
1618	ELNVHRG	15941	GAGTTGAATGTGCATAGGGGT	30264	GAACTCAACGTCCACAGAGGA
1619	ELPAKSM	15942	GAGTTGCCGGCTAAGAGTATG	30265	GAACTCCCAGCAAAAAGCATG
1620	ELPATYG	15943	GAGCTTCCGGCGACTTATGGG	30266	GAACTCCCAGCAACATACGGA
1621	ELPGTPC	15944	GAGCTGCCTGGGACGCCGTGT	30267	GAACTCCCAGGAACACCATGC
1622	ELPLDWD	15945	GAGCTTCCGCTTGATTGGGAT	30268	GAACTCCCACTCGACTGGGAC
1623	ELPSKQG	15946	GAGTTGCCTTCTAAGCAGGGT	30269	GAACTCCCAAGCAAACAAGGA
1624	ELQGRIN	15947	GAGCTGCAGGGGCGGATTAAT	30270	GAACTCCAAGGAAGAATCAAC
1625	ELQLPKS	15948	GAGTTGCAGTTGCCGAAGAGT	30271	GAACTCCAACTCCCAAAAAGC
1626	ELQVQMA	15949	GAGCTTCAGGTTCAGATGGCG	30272	GAACTCCAAGTCCAAATGGCA
1627	ELRGSVN	15950	GAGCTGCGGGGTTCGGTTAAT	30273	GAACTCAGAGGAAGCGTCAAC
1628	ELRVVHS	15951	GAGCTTCGGGTTGTTCATTCT	30274	GAACTCAGAGTCGTCCACAGC
1629	ELSARAT	15952	GAGTTGTCGGCGCGGGCGACT	30275	GAACTCAGCGCAAGAGCAACA
1630	ELSDGSG	15953	GAGCTGAGTGATGGGAGTGGG	30276	GAACTCAGCGACGGAAGCGGA
1631	ELSFQFD	15954	GAGCTTAGTTTTCAGTTTGAT	30277	GAACTCAGCTTCCAATTCGAC
1632	ELSMGSY	15955	GAGCTGTCTATGGGTAGTTAT	30278	GAACTCAGCATGGGAAGCTAC
1633	ELSRNNV	15956	GAGTTGTCGCGTAATAATGTT	30279	GAACTCAGCAGAAACAACGTC
1634	ELSVNGL	15957	GAGCTTTCGGTTAATGGTTTG	30280	GAACTCAGCGTCAACGGACTC
1635	ELSYRPT	15958	GAGCTGAGTTATCGTCCTACG	30281	GAACTCAGCTACAGACCAACA
1636	ELTTGKS	15959	GAGCTTACGACTGGTAAGTCT	30282	GAACTCACAACAGGAAAAAGC
1637	ELTVRLA	15960	GAGCTGACTGTGCGGCTTGCT	30283	GAACTCACAGTCAGACTCGCA
1638	ELTYPGR	15961	GAGCTGACTTATCCGGGTCGG	30284	GAACTCACATACCCAGGAAGA
1639	ELVMSVR	15962	GAGCTTGTTATGTCGGTGCGT	30285	GAACTCGTCATGAGCGTCAGA
1640	ELYSRPA	15963	GAGTTGTATTCGCGGCCTGCT	30286	GAACTCTACAGCAGACCAGCA
1641	EMAAHLE	15964	GAGATGGCTGCGCATCTTGAG	30287	GAAATGGCAGCACACCTCGAA
1642	EMAPYSK	15965	GAGATGGCGCCGTATTCGAAG	30288	GAAATGGCACCATACAGCAAA
1643	EMDGNAY	15966	GAGATGGATGGGAATGCTTAT	30289	GAAATGGACGGAAACGCATAC
1644	EMEMLSD	15967	GAGATGGAGATGCTTAGTGAT	30290	GAAATGGAAATGCTCAGCGAC
1645	EMGQLPD	15968	GAGATGGGTCAGTTGCCGGAT	30291	GAAATGGGACAACTCCCAGAC
1646	EMGQTLE	15969	GAGATGGGTCAGACGTTGGAG	30292	GAAATGGGACAAACACTCGAA
1647	EMHEDEK	15970	GAGATGCATGAGGATGAGAAG	30293	GAAATGCACGAAGACGAAAAA
1648	EMLERFD	15971	GAGATGCTGGAGCGTTTTGAT	30294	GAAATGCTCGAAAGATTCGAC
1649	EMLRAGF	15972	GAGATGCTTCGTGCTGGGTTT	30295	GAAATGCTCAGAGCAGGATTC
1650	EMMANST	15973	GAGATGATGGCTAATTCGACG	30296	GAAATGATGGCAAACAGCACA
1651	EMPKTPK	15974	GAGATGCCTAAGACGCCGAAG	30297	GAAATGCCAAAAACACCAAAA
1652	EMPTRQP	15975	GAGATGCCTACGCGGCAGCCT	30298	GAAATGCCAACAAGACAACCA
1653	EMPTYND	15976	GAGATGCCGACTTATAATGAT	30299	GAAATGCCAACATACAACGAC
1654	EMRQQSI	15977	GAGATGCGGCAGCAGTCGATT	30300	GAAATGAGACAACAAAGCATC

1655	EMRSSTS	15978	GAGATGAGGTCTAGTACTTCT	30301	GAAATGAGAAGCAGCACAAGC
1656	EMTQLPA	15979	GAGATGACGCAGCTTCCGGCT	30302	GAAATGACACAACTCCCAGCA
1657	EMYLTRV	15980	GAGATGTATTTGACGCGTGTG	30303	GAAATGTACCTCACAAGAGTC
1658	ENAVPGV	15981	GAGAATGCGGTTCCTGGTGTG	30304	GAAAACGCAGTCCCAGGAGTC
1659	ENDRSST	15982	GAGAATGATCGTAGTTCTACG	30305	GAAAACGACAGAAGCAGCACA
1660	ENEGTGT	15983	GAGAATGAGGGTACTGGTACT	30306	GAAAACGAAGGAACAGGAACA
1661	ENESHHL	15984	GAGAATGAGTCGCATCATTTG	30307	GAAAACGAAAGCCACCACCTC
1662	ENGHSFT	15985	GAGAATGGGCATTCTTTTACG	30308	GAAAACGGACACAGCTTCACA
1663	ENGRTEI	15986	GAGAATGGGCGTACGGAGATT	30309	GAAAACGGAAGAACAGAAATC
1664	ENKPGSP	15987	GAGAATAAGCCGGGGTCTCCT	30310	GAAAACAAACCAGGAAGCCCA
1665	ENMAYLS	15988	GAGAATATGGCTTATCTGAGT	30311	GAAAACATGGCATACCTCAGC
1666	ENPGSAS	15989	GAGAATCCGGGTAGTGCTTCT	30312	GAAAACCCAGGAAGCGCAAGC
1667	ENPPREP	15990	GAGAATCCGCCTCGTGAGCCT	30313	GAAAACCCACCAAGAGAACCA
1668	ENPRGSV	15991	GAGAATCCGCGTGGTAGTGTT	30314	GAAAACCCAAGAGGAAGCGTC
1669	ENPTMYS	15992	GAGAATCCTACGATGTATAGT	30315	GAAAACCCAACAATGTACAGC
1670	ENQYQDS	15993	GAGAATCAGTATCAGGATAGT	30316	GAAAACCAATACCAAGACAGC
1671	ENRLKNF	15994	GAGAATCGTCTGAAGAATTTT	30317	GAAAACAGACTCAAAAACTTC
1672	ENRSGED	15995	GAGAATAGGTCGGGTGAGGAT	30318	GAAAACAGAAGCGGAGAAGAC
1673	ENSSLVD	15996	GAGAATAGTTCGCTGGTTGAT	30319	GAAAACAGCAGCCTCGTCGAC
1674	ENTFSSR	15997	GAGAATACGTTTAGTTCTCGG	30320	GAAAACACATTCAGCAGCAGA
1675	ENTITSL	15998	GAGAATACTATTACGAGTCTT	30321	GAAAACACAATCACAAGCCTC
1676	ENTLRLD	15999	GAGAATACTTTGCGTCTGGAT	30322	GAAAACACACTCAGACTCGAC
1677	ENVKPGW	16000	GAGAATGTTAAGCCTGGGTGG	30323	GAAAACGTCAAACCAGGATGG
1678	EPAARAV	16001	GAGCCTGCTGCGCGTGCTGTT	30324	GAACCAGCAGCAAGAGCAGTC
1679	EPADRTQ	16002	GAGCCGGCTGATCGTACTCAG	30325	GAACCAGCAGACAGAACACAA
1680	EPAGPRL	16003	GAGCCGGCGGGGCCTCGGCTT	30326	GAACCAGCAGGACCAAGACTC
1681	EPALPYA	16004	GAGCCTGCGCTGCCGTATGCT	30327	GAACCAGCACTCCCATACGCA
1682	EPATGSS	16005	GAGCCGGCGACGGGGTCGTCT	30328	GAACCAGCAACAGGAAGCAGC
1683	EPDSAYS	16006	GAGCCGGATTCGGCTTATTCG	30329	GAACCAGACAGCGCATACAGC
1684	EPFDAKT	16007	GAGCCGTTTGATGCTAAGACT	30330	GAACCATTCGACGCAAAAACA
1685	EPFSNSP	16008	GAGCCTTTTTCGAATAGTCCT	30331	GAACCATTCAGCAACAGCCCA
1686	EPGGNHL	16009	GAGCCGGGTGGGAATCATCTT	30332	GAACCAGGAGGAAACCACCTC
1687	EPGHARA	16010	GAGCCTGGGCATGCTCGGGCG	30333	GAACCAGGACACGCAAGAGCA
1688	EPGRTGF	16011	GAGCCTGGTCGGACTGGGTTT	30334	GAACCAGGAAGAACAGGATTC
1689	EPGVVGC	16012	GAGCCGGGTGTGGTTGGGTGT	30335	GAACCAGGAGTCGTCGGATGC
1690	EPHAPER	16013	GAGCCGCATGCTCCTGAGCGT	30336	GAACCACACGCACCAGAAAGA
1691	EPHVPGA	16014	GAGCCGCATGTTCCGGGGGCT	30337	GAACCACACGTCCCAGGAGCA
1692	EPKHQFS	16015	GAGCCTAAGCATCAGTTTTCG	30338	GAACCAAAACACCAATTCAGC
1693	EPKRGWS	16016	GAGCCTAAGAGGGGGTGGTCT	30339	GAACCAAAAAGAGGATGGAGC
1694	EPKSASI	16017	GAGCCTAAGTCTGCTTCTATT	30340	GAACCAAAAAGCGCAAGCATC
1695	EPLNSSG	16018	GAGCCTCTTAATAGTAGTGGT	30341	GAACCACTCAACAGCAGCGGA
1696	EPLSANR	16019	GAGCCGCTGTCGGCTAATAGG	30342	GAACCACTCAGCGCAAACAGA
1697	EPNATSV	16020	GAGCCGAATGCTACTAGTGTT	30343	GAACCAAACGCAACAAGCGTC
1698	EPNHPVS	16021	GAGCCTAATCATCCGGTGTCG	30344	GAACCAAACCACCCAGTCAGC
1699	EPPSSLK	16022	GAGCCTCCGTCGTCTCTGAAG	30345	GAACCACCAAGCAGCCTCAAA

1700	EPQRPLR	16023	GAGCCTCAGCGTCCTTTGCGT	30346	GAACCACAAAGACCACTCAGA
1701	EPSNESA	16024	GAGCCTTCTAATGAGTCGGCT	30347	GAACCAAGCAACGAAAGCGCA
1702	EPSNSHA	16025	GAGCCGAGTAATTCGCATGCG	30348	GAACCAAGCAACAGCCACGCA
1703	EPSYLPS	16026	GAGCCGTCTTATCTGCCGTCG	30349	GAACCAAGCTACCTCCCAAGC
1704	EPTERIS	16027	GAGCCTACTGAGCGGATTAGT	30350	GAACCAACAGAAAGAATCAGC
1705	EPTIYLT	16028	GAGCCTACGATTTATTTGACT	30351	GAACCAACAATCTACCTCACA
1706	EPTMRSI	16029	GAGCCGACTATGAGGAGTATT	30352	GAACCAACAATGAGAAGCATC
1707	EPTRPAT	16030	GAGCCTACTAGGCCGGCGACG	30353	GAACCAACAAGACCAGCAACA
1708	EPTRSSS	16031	GAGCCGACTAGGTCTAGTAGT	30354	GAACCAACAAGAAGCAGCAGC
1709	EPTRTKM	16032	GAGCCTACTCGGACTAAGATG	30355	GAACCAACAAGAACAAAAATG
1710	EPVIGFP	16033	GAGCCGGTTATTGGGTTTCCT	30356	GAACCAGTCATCGGATTCCCA
1711	EPVSTAA	16034	GAGCCTGTGTCGACTGCGGCG	30357	GAACCAGTCAGCACAGCAGCA
1712	EPYLSAK	16035	GAGCCTTATCTGAGTGCGAAG	30358	GAACCATACCTCAGCGCAAAA
1713	EPYSPAI	16036	GAGCCTTATTCGCCGGCTATT	30359	GAACCATACAGCCCAGCAATC
1714	EQAALSF	16037	GAGCAGGCTGCTCTTTCGTTT	30360	GAACAAGCAGCACTCAGCTTC
1715	EQALKPE	16038	GAGCAGGCTCTGAAGCCGGAG	30361	GAACAAGCACTCAAACCAGAA
1716	EQARLDV	16039	GAGCAGGCGCGTCTGGATGTG	30362	GAACAAGCAAGACTCGACGTC
1717	EQASFKI	16040	GAGCAGGCTTCTTTTAAGATT	30363	GAACAAGCAAGCTTCAAAATC
1718	EQFAAPV	16041	GAGCAGTTTGCGGCGCCGGTG	30364	GAACAATTCGCAGCACCAGTC
1719	EQGTPSA	16042	GAGCAGGGTACGCCTAGTGCG	30365	GAACAAGGAACACCAAGCGCA
1720	EQKPLTR	16043	GAGCAGAAGCCGCTGACTCGT	30366	GAACAAAAACCACTCACAAGA
1721	EQLKDYE	16044	GAGCAGTTGAAGGATTATGAG	30367	GAACAACTCAAAGACTACGAA
1722	EQNSRGL	16045	GAGCAGAATTCGAGGGGTCTT	30368	GAACAAAACAGCAGAGGACTC
1723	EQPKYSK	16046	GAGCAGCCTAAGTATAGTAAG	30369	GAACAACCAAAATACAGCAAA
1724	EQQCPRS	16047	GAGCAGCAGTGTCCTCGGTCT	30370	GAACAACAATGCCCAAGAAGC
1725	EQRDRNG	16048	GAGCAGAGGGATCGTAATGGT	30371	GAACAAAGAGACAGAAACGGA
1726	EQRGTIL	16049	GAGCAGCGTGGTACGATTCTG	30372	GAACAAAGAGGAACAATCCTC
1727	EQRLSQS	16050	GAGCAGAGGTTGTCTCAGTCT	30373	GAACAAAGACTCAGCCAAAGC
1728	EQRRSET	16051	GAGCAGAGGCGTTCGGAGACT	30374	GAACAAAGAAGAAGCGAAACA
1729	EQSYRDS	16052	GAGCAGTCTTATCGGGATTCT	30375	GAACAAAGCTACAGAGACAGC
1730	EQTGHRA	16053	GAGCAGACTGGTCATCGTGCT	30376	GAACAAACAGGACACAGAGCA
1731	EQYRDNS	16054	GAGCAGTATCGTGATAATAGT	30377	GAACAATACAGAGACAACAGC
1732	ERAAGLR	16055	GAGCGTGCTGCTGGGCTGCGT	30378	GAAAGAGCAGCAGGACTCAGA
1733	ERAGPHD	16056	GAGCGTGCGGGGCCTCATGAT	30379	GAAAGAGCAGGACCACACGAC
1734	ERAPPGL	16057	GAGCGGGCGCCTCCGGGTCTT	30380	GAAAGAGCACCACCAGGACTC
1735	ERDSRKA	16058	GAGCGGGATTCGAGGAAGGCT	30381	GAAAGAGACAGCAGAAAAGCA
1736	ERFEGLR	16059	GAGCGGTTTGAGGGTTTGCGG	30382	GAAAGATTCGAAGGACTCAGA
1737	ERFLPEL	16060	GAGCGGTTTTTGCCGGAGCTT	30383	GAAAGATTCCTCCCAGAACTC
1738	ERFTSVP	16061	GAGCGTTTTACGTCTGTTCCT	30384	GAAAGATTCACAAGCGTCCCA
1739	ERGMTTP	16062	GAGCGTGGGATGACTACTCCG	30385	GAAAGAGGAATGACAACACCA
1740	ERGVIHP	16063	GAGCGTGGTGTGATTCATCCG	30386	GAAAGAGGAGTCATCCACCCA
1741	ERHADMT	16064	GAGCGTCATGCTGATATGACT	30387	GAAAGACACGCAGACATGACA
1742	ERHDLPR	16065	GAGCGTCATGATCTTCCGCGG	30388	GAAAGACACGACCTCCCAAGA
1743	ERHDVGP	16066	GAGCGGCATGATGTGGGTCCG	30389	GAAAGACACGACGTCGGACCA
1744	ERHIRME	16067	GAGCGGCATATTAGGATGGAG	30390	GAAAGACACATCAGAATGGAA

1745	ERHRVID	16068	GAGCGGCATAGGGTTATTGAT	30391	GAAAGACACAGAGTCATCGAC
1746	ERIRTPE	16069	GAGCGGATTAGGACTCCTGAG	30392	GAAAGAATCAGAACACCAGAA
1747	ERISPSI	16070	GAGCGGATTTCGCCTTCGATT	30393	GAAAGAATCAGCCCAAGCATC
1748	ERKGLGL	16071	GAGCGGAAGGGGCTTGGGTTG	30394	GAAAGAAAAGGACTCGGACTC
1749	ERKNQSP	16072	GAGCGTAAGAATCAGAGTCCT	30395	GAAAGAAAAAACCAAAGCCCA
1750	ERKTPSD	16073	GAGAGGAAGACTCCGTCGGAT	30396	GAAAGAAAAACACCAAGCGAC
1751	ERLESSL	16074	GAGAGGCTTGAGAGTTCTCTG	30397	GAAAGACTCGAAAGCAGCCTC
1752	ERLSPVA	16075	GAGCGTTTGTCGCCTGTGGCG	30398	GAAAGACTCAGCCCAGTCGCA
1753	ERLSSEP	16076	GAGCGTTTGAGTTCGGAGCCG	30399	GAAAGACTCAGCAGCGAACCA
1754	ERMAAPF	16077	GAGCGGATGGCTGCGCCTTTT	30400	GAAAGAATGGCAGCACCATTC
1755	ERNFESG	16078	GAGAGGAATTTTGAGTCGGGG	30401	GAAAGAAACTTCGAAAGCGGA
1756	ERNGLPA	16079	GAGCGGAATGGTCTTCCGGCG	30402	GAAAGAAACGGACTCCCAGCA
1757	ERNRVDS	16080	GAGAGGAATCGGGTGGATTCT	30403	GAAAGAAACAGAGTCGACAGC
1758	ERNSPVA	16081	GAGCGTAATTCTCCTGTTGCG	30404	GAAAGAAACAGCCCAGTCGCA
1759	ERPDGPS	16082	GAGCGTCCTGATGGTCCTTCG	30405	GAAAGACCAGACGGACCAAGC
1760	ERPPLVM	16083	GAGCGGCCTCCTCTTGTGATG	30406	GAAAGACCACCACTCGTCATG
1761	ERPYATV	16084	GAGAGGCCTTATGCTACGGTG	30407	GAAAGACCATACGCAACAGTC
1762	ERQAFHE	16085	GAGCGGCAGGCGTTTCATGAG	30408	GAAAGACAAGCATTCCACGAA
1763	ERQPMIK	16086	GAGCGGCAGCCGATGATTAAG	30409	GAAAGACAACCAATGATCAAA
1764	ERQRDSA	16087	GAGCGGCAGCGTGATTCTGCT	30410	GAAAGACAAAGAGACAGCGCA
1765	ERQTTLA	16088	GAGCGGCAGACTACGTTGGCT	30411	GAAAGACAAACAACACTCGCA
1766	ERRIGAS	16089	GAGCGTCGTATTGGGGCGTCT	30412	GAAAGAAGAATCGGAGCAAGC
1767	ERRPGTS	16090	GAGAGGAGGCCGGGTACGTCT	30413	GAAAGAAGACCAGGAACAAGC
1768	ERSKPVA	16091	GAGCGGTCGAAGCCGGTTGCG	30414	GAAAGAAGCAAACCAGTCGCA
1769	ERSRGQQ	16092	GAGAGGTCTCGTGGTCAGCAG	30415	GAAAGAAGCAGAGGACAACAA
1770	ERSSPQP	16093	GAGAGGTCGTCTCCTCAGCCT	30416	GAAAGAAGCAGCCCACAACCA
1771	ERSSRET	16094	GAGCGTTCTTCTCGGGAGACG	30417	GAAAGAAGCAGCAGAGAAACA
1772	ERTAVGV	16095	GAGCGGACGGCTGTGGGTGTG	30418	GAAAGAACAGCAGTCGGAGTC
1773	ERTKPPT	16096	GAGAGGACTAAGCCTCCTACT	30419	GAAAGAACAAAACCACCAACA
1774	ERYPSIS	16097	GAGCGGTATCCGTCTATTTCG	30420	GAAAGATACCCAAGCATCAGC
1775	ESAFKRC	16098	GAGTCTGCTTTTAAGCGTTGT	30421	GAAAGCGCATTCAAAAGATGC
1776	ESAWMQD	16099	GAGTCGGCGTGGATGCAGGAT	30422	GAAAGCGCATGGATGCAAGAC
1777	ESFTGVH	16100	GAGTCGTTTACTGGGGTGCAT	30423	GAAAGCTTCACAGGAGTCCAC
1778	ESGDKLR	16101	GAGTCTGGTGATAAGTTGAGG	30424	GAAAGCGGAGACAAACTCAGA
1779	ESGILQL	16102	GAGTCTGGGATTTTGCAGCTT	30425	GAAAGCGGAATCCTCCAACTC
1780	ESGLTQT	16103	GAGTCTGGTCTTACTCAGACT	30426	GAAAGCGGACTCACACAAACA
1781	ESGRPMV	16104	GAGAGTGGTCGGCCTATGGTT	30427	GAAAGCGGAAGACCAATGGTC
1782	ESITRSV	16105	GAGTCGATTACGCGGTCTGTT	30428	GAAAGCATCACAAGAAGCGTC
1783	ESIVGRR	16106	GAGTCGATTGTGGGTAGGAGG	30429	GAAAGCATCGTCGGAAGAAGA
1784	ESKELTS	16107	GAGTCGAAGGAGCTGACTTCT	30430	GAAAGCAAAGAACTCACAAGC
1785	ESKGAHA	16108	GAGTCTAAGGGTGCGCATGCG	30431	GAAAGCAAAGGAGCACACGCA
1786	ESKHFSP	16109	GAGTCGAAGCATTTTAGTCCG	30432	GAAAGCAAACACTTCAGCCCA
1787	ESKIGRP	16110	GAGTCTAAGATTGGTCGGCCT	30433	GAAAGCAAAATCGGAAGACCA
1788	ESKPNSR	16111	GAGTCGAAGCCTAATTCGCGT	30434	GAAAGCAAACCAAACAGCAGA
1789	ESPDRST	16112	GAGTCGCCTGATCGGTCTACT	30435	GAAAGCCCAGACAGAAGCACA

1790	ESPFSVP	16113	GAGTCGCCGTTTTCTGTGCCG	30436	GAAAGCCCATTCAGCGTCCCA
1791	ESPKADP	16114	GAGTCTCCTAAGGCGGATCCG	30437	GAAAGCCCAAAAGCAGACCCA
1792	ESPMVSP	16115	GAGAGTCCGATGGTTAGTCCG	30438	GAAAGCCCAATGGTCAGCCCA
1793	ESQVLVY	16116	GAGTCTCAGGTGCTGGTTTAT	30439	GAAAGCCAAGTCCTCGTCTAC
1794	ESRQAFP	16117	GAGTCGCGGCAGGCGTTTCCT	30440	GAAAGCAGACAAGCATTCCCA
1795	ESRSAAY	16118	GAGTCTCGTTCGGCGGCTTAT	30441	GAAAGCAGAAGCGCAGCATAC
1796	ESRSALP	16119	GAGTCTCGTTCGGCTTTGCCG	30442	GAAAGCAGAAGCGCACTCCCA
1797	ESRVGYI	16120	GAGAGTCGTGTTGGGTATATT	30443	GAAAGCAGAGTCGGATACATC
1798	ESRVSLG	16121	GAGTCGCGGGTGTCGTTGGGG	30444	GAAAGCAGAGTCAGCCTCGGA
1799	ESSQHLD	16122	GAGTCTTCTCAGCATTTGGAT	30445	GAAAGCAGCCAACACCTCGAC
1800	ESSREFH	16123	GAGTCGTCTCGTGAGTTTCAT	30446	GAAAGCAGCAGAGAATTCCAC
1801	ESSRELH	16124	GAGTCGTCTCGTGAGTTGCAT	30447	GAAAGCAGCAGAGAACTCCAC
1802	ESSSELH	16125	GAGTCGTCTAGTGAGTTGCAT	30448	GAAAGCAGCAGCGAACTCCAC
1803	ESSSRML	16126	GAGTCTAGTTCGCGGATGTTG	30449	GAAAGCAGCAGCAGAATGCTC
1804	ESTALKR	16127	GAGTCGACTGCTCTTAAGAGG	30450	GAAAGCACAGCACTCAAAAGA
1805	ESTSSRS	16128	GAGTCGACGTCGAGTAGGTCT	30451	GAAAGCACAAGCAGCAGAAGC
1806	ESVENDS	16129	GAGTCGGTTGAGAATGATAGT	30452	GAAAGCGTCGAAAACGACAGC
1807	ESVFKAA	16130	GAGTCTGTTTTTAAGGCGGCT	30453	GAAAGCGTCTTCAAAGCAGCA
1808	ESVGYAD	16131	GAGTCGGTGGGTTATGCTGAT	30454	GAAAGCGTCGGATACGCAGAC
1809	ESVRLQN	16132	GAGTCTGTGAGGCTTCAGAAT	30455	GAAAGCGTCAGACTCCAAAAC
1810	ESYTESL	16133	GAGAGTTATACTGAGAGTCTT	30456	GAAAGCTACACAGAAAGCCTC
1811	ETAKSGQ	16134	GAGACTGCTAAGTCTGGTCAG	30457	GAAACAGCAAAAAGCGGACAA
1812	ETDRKLS	16135	GAGACGGATCGGAAGTTGTCG	30458	GAAACAGACAGAAAACTCAGC
1813	ETDRNAS	16136	GAGACTGATCGTAATGCTAGT	30459	GAAACAGACAGAAACGCAAGC
1814	ETEHTVV	16137	GAGACGGAGCATACGGTGGTG	30460	GAAACAGAACACACAGTCGTC
1815	ETFTRSV	16138	GAGACGTTTACGCGTTCTGTT	30461	GAAACATTCACAAGAAGCGTC
1816	ETGKDRM	16139	GAGACGGGTAAGGATCGGATG	30462	GAAACAGGAAAAGACAGAATG
1817	ETGSHTT	16140	GAGACGGGGTCTCATACGACT	30463	GAAACAGGAAGCCACACAACA
1818	ETGSRAV	16141	GAGACTGGTTCGCGGGCGGTT	30464	GAAACAGGAAGCAGAGCAGTC
1819	ETKFSMG	16142	GAGACGAAGTTTTCTATGGGG	30465	GAAACAAAATTCAGCATGGGA
1820	ETKGSVA	16143	GAGACTAAGGGTTCTGTTGCG	30466	GAAACAAAAGGAAGCGTCGCA
1821	ETKKDYS	16144	GAGACTAAGAAGGATTATAGT	30467	GAAACAAAAAAAGACTACAGC
1822	ETLEVSL	16145	GAGACGCTTGAGGTTAGTTTG	30468	GAAACACTCGAAGTCAGCCTC
1823	ETLSGNE	16146	GAGACGTTGTCTGGTAATGAG	30469	GAAACACTCAGCGGAAACGAA
1824	ETMRKDP	16147	GAGACGATGCGTAAGGATCCT	30470	GAAACAATGAGAAAAGACCCA
1825	ETNFSGA	16148	GAGACGAATTTTTCGGGTGCT	30471	GAAACAAACTTCAGCGGAGCA
1826	ETNPRCS	16149	GAGACTAATCCGCGTTGTTCG	30472	GAAACAAACCCAAGATGCAGC
1827	ETPFKPS	16150	GAGACGCCTTTTAAGCCGTCT	30473	GAAACACCATTCAAACCAAGC
1828	ETPIDSD	16151	GAGACGCCTATTGATTCTGAT	30474	GAAACACCAATCGACAGCGAC
1829	ETPNHSR	16152	GAGACTCCGAATCATTCGCGG	30475	GAAACACCAAACCACAGCAGA
1830	ETRGHLI	16153	GAGACTCGTGGTCATCTGATT	30476	GAAACAAGAGGACACCTCATC
1831	ETRLVPT	16154	GAGACTCGGCTGGTGCCTACG	30477	GAAACAAGACTCGTCCCAACA
1832	ETRNLHG	16155	GAGACGCGTAATCTGCATGGG	30478	GAAACAAGAAACCTCCACGGA
1833	ETRNQFG	16156	GAGACTAGGAATCAGTTTGGG	30479	GAAACAAGAAACCAATTCGGA
1834	ETRSTRE	16157	GAGACTCGTAGTACTCGTGAG	30480	GAAACAAGAAGCACAAGAGAA

1835	ETRYPDM	16158	GAGACGCGGTATCCGGATATG	30481	GAAACAAGATACCCAGACATG
1836	ETSHSVS	16159	GAGACGTCTCATTCGGTGTCT	30482	GAAACAAGCCACAGCGTCAGC
1837	ETSRAST	16160	GAGACTAGTCGGGCGAGTACT	30483	GAAACAAGCAGAGCAAGCACA
1838	ETSRPTV	16161	GAGACGTCGAGGCCTACTGTT	30484	GAAACAAGCAGACCAACAGTC
1839	ETSSAYL	16162	GAGACGTCTTCGGCTTATTTG	30485	GAAACAAGCAGCGCATACCTC
1840	ETTQNYI	16163	GAGACGACTCAGAATTATATT	30486	GAAACAACACAAAACTACATC
1841	ETTSLPR	16164	GAGACGACGTCTCTTCCTCGG	30487	GAAACAACAAGCCTCCCAAGA
1842	ETTVQAS	16165	GAGACTACTGTTCAGGCTTCT	30488	GAAACAACAGTCCAAGCAAGC
1843	ETVFHVA	16166	GAGACGGTGTTTCATGTGGCT	30489	GAAACAGTCTTCCACGTCGCA
1844	EVAVQPM	16167	GAGGTGGCTGTGCAGCCGATG	30490	GAAGTCGCAGTCCAACCAATG
1845	EVGRNST	16168	GAGGTGGGGAGGAATTCTACT	30491	GAAGTCGGAAGAAACAGCACA
1846	EVHPGQA	16169	GAGGTTCATCCGGGTCAGGCT	30492	GAAGTCCACCCAGGACAAGCA
1847	EVKEQTV	16170	GAGGTTAAGGAGCAGACTGTG	30493	GAAGTCAAAGAACAAACAGTC
1848	EVKSFSS	16171	GAGGTTAAGAGTTTTAGTAGT	30494	GAAGTCAAAAGCTTCAGCAGC
1849	EVPAARS	16172	GAGGTGCCGGCGGCGAGGTCG	30495	GAAGTCCCAGCAGCAAGAAGC
1850	EVPNSSA	16173	GAGGTTCCGAATAGTAGTGCT	30496	GAAGTCCCAAACAGCAGCGCA
1851	EVQLPAR	16174	GAGGTTCAGCTGCCTGCGCGG	30497	GAAGTCCAACTCCCAGCAAGA
1852	EVRKGAQ	16175	GAGGTTCGTAAGGGTGCGCAG	30498	GAAGTCAGAAAAGGAGCACAA
1853	EVRLSNA	16176	GAGGTGCGTCTGTCTAATGCT	30499	GAAGTCAGACTCAGCAACGCA
1854	EVSFLPP	16177	GAGGTTTCGTTTTTGCCTCCT	30500	GAAGTCAGCTTCCTCCCACCA
1855	EVSLSTR	16178	GAGGTGAGTCTGTCGACGCGT	30501	GAAGTCAGCCTCAGCACAAGA
1856	EVSMLSK	16179	GAGGTGAGTATGCTGAGTAAG	30502	GAAGTCAGCATGCTCAGCAAA
1857	EVTGRAG	16180	GAGGTGACTGGGAGGGCGGGT	30503	GAAGTCACAGGAAGAGCAGGA
1858	EVTMKHT	16181	GAGGTGACGATGAAGCATACG	30504	GAAGTCACAATGAAACACACA
1859	EVTNPSA	16182	GAGGTGACTAATCCTTCTGCT	30505	GAAGTCACAAACCCAAGCGCA
1860	EVTVGLP	16183	GAGGTTACTGTGGGTTTGCCT	30506	GAAGTCACAGTCGGACTCCCA
1861	EWADSSG	16184	GAGTGGGCGGATTCTTCGGGT	30507	GAATGGGCAGACAGCAGCGGA
1862	EWNRQAN	16185	GAGTGGAATCGTCAGGCTAAT	30508	GAATGGAACAGACAAGCAAAC
1863	EYASLGL	16186	GAGTATGCGTCGCTGGGGCTT	30509	GAATACGCAAGCCTCGGACTC
1864	EYDHSML	16187	GAGTATGATCATTCGATGCTG	30510	GAATACGACCACAGCATGCTC
1865	EYIRGKE	16188	GAGTATATTCGTGGTAAGGAG	30511	GAATACATCAGAGGAAAAGAA
1866	EYLDESG	16189	GAGTATTTGGATGAGTCTGGT	30512	GAATACCTCGACGAAAGCGGA
1867	EYLPNSA	16190	GAGTATCTGCCGAATTCGGCT	30513	GAATACCTCCCAAACAGCGCA
1868	EYPAHLT	16191	GAGTATCCGGCGCATCTGACT	30514	GAATACCCAGCACACCTCACA
1869	EYPLNTG	16192	GAGTATCCGCTTAATACTGGG	30515	GAATACCCACTCAACACAGGA
1870	EYQRPDP	16193	GAGTATCAGCGGCCGGATCCG	30516	GAATACCAAAGACCAGACCCA
1871	EYSFPKE	16194	GAGTATTCTTTTCCGAAGGAG	30517	GAATACAGCTTCCCAAAAGAA
1872	EYTPISG	16195	GAGTATACTCCGATTTCTGGT	30518	GAATACACACCAATCAGCGGA
1873	EYVGVQR	16196	GAGTATGTTGGGGTTCAGAGG	30519	GAATACGTCGGAGTCCAAAGA
1874	FAAKDVT	16197	TTTGCTGCGAAGGATGTTACT	30520	TTCGCAGCAAAAGACGTCACA
1875	FAAKMPS	16198	TTTGCTGCGAAGATGCCTTCG	30521	TTCGCAGCAAAAATGCCAAGC
1876	FAALRVD	16199	TTTGCTGCGCTGCGGGTTGAT	30522	TTCGCAGCACTCAGAGTCGAC
1877	FAAQVED	16200	TTTGCGGCTCAGGTTGAGGAT	30523	TTCGCAGCACAAGTCGAAGAC
1878	FAASSQD	16201	TTTGCGGCTTCTTCTCAGGAT	30524	TTCGCAGCAAGCAGCCAAGAC
1879	FADAMVM	16202	TTTGCTGATGCTATGGTTATG	30525	TTCGCAGACGCAATGGTCATG

1880	FAEKSRG	16203	TTTGCTGAGAAGTCTCGGGGG	30526	TTCGCAGAAAAAAGCAGAGGA
1881	FAGIAQY	16204	TTTGCGGGGATTGCGCAGTAT	30527	TTCGCAGGAATCGCACAATAC
1882	FAGKHQN	16205	TTTGCGGGGAAGCATCAGAAT	30528	TTCGCAGGAAAACACCAAAAC
1883	FAGLTPV	16206	TTTGCGGGGCTGACTCCTGTT	30529	TTCGCAGGACTCACACCAGTC
1884	FAGNSPS	16207	TTTGCGGGGAATTCTCCGTCG	30530	TTCGCAGGAAACAGCCCAAGC
1885	FAHTARP	16208	TTTGCTCATACTGCGAGGCCG	30531	TTCGCACACACAGCAAGACCA
1886	FAKHGGP	16209	TTTGCTAAGCATGGTGGGCCG	30532	TTCGCAAAACACGGAGGACCA
1887	FAKPASL	16210	TTTGCGAAGCCGGCTAGTCTT	30533	TTCGCAAAACCAGCAAGCCTC
1888	FALEGRS	16211	TTTGCTCTGGAGGGTCGTTCT	30534	TTCGCACTCGAAGGAAGAAGC
1889	FALSASL	16212	TTTGCTCTGTCGGCTTCTCTT	30535	TTCGCACTCAGCGCAAGCCTC
1890	FAMANDK	16213	TTTGCGATGGCGAATGATAAG	30536	TTCGCAATGGCAAACGACAAA
1891	FANRATI	16214	TTTGCGAATCGGGCTACGATT	30537	TTCGCAAACAGAGCAACAATC
1892	FANSAVE	16215	TTTGCTAATTCTGCGGTTGAG	30538	TTCGCAAACAGCGCAGTCGAA
1893	FAPGHAI	16216	TTTGCGCCGGGTCATGCGATT	30539	TTCGCACCAGGACACGCAATC
1894	FAPLSPH	16217	TTTGCTCCGCTGAGTCCTCAT	30540	TTCGCACCACTCAGCCCACAC
1895	FAPPPAF	16218	TTTGCTCCGCCGCCGGCTTTT	30541	TTCGCACCACCACCAGCATTC
1896	FAPSRND	16219	TTTGCTCCGTCTCGGAATGAT	30542	TTCGCACCAAGCAGAAACGAC
1897	FAQKLSP	16220	TTTGCGCAGAAGTTGAGTCCT	30543	TTCGCACAAAAACTCAGCCCA
1898	FAQKNLS	16221	TTTGCGCAGAAGAATCTGTCG	30544	TTCGCACAAAAAAACCTCAGC
1899	FARNPDA	16222	TTTGCGAGGAATCCTGATGCT	30545	TTCGCAAGAAACCCAGACGCA
1900	FARPDSM	16223	TTTGCTCGTCCTGATTCGATG	30546	TTCGCAAGACCAGACAGCATG
1901	FARSSIP	16224	TTTGCGCGGAGTAGTATTCCT	30547	TTCGCAAGAAGCAGCATCCCA
1902	FASAAPR	16225	TTTGCGAGTGCTGCGCCGAGG	30548	TTCGCAAGCGCAGCACCAAGA
1903	FASARAQ	16226	TTTGCGAGTGCGCGTGCTCAG	30549	TTCGCAAGCGCAAGAGCACAA
1904	FASGHFN	16227	TTTGCGTCGGGGCATTTTAAT	30550	TTCGCAAGCGGACACTTCAAC
1905	FASLVTN	16228	TTTGCGTCTCTTGTTACGAAT	30551	TTCGCAAGCCTCGTCACAAAC
1906	FASSRNN	16229	TTTGCGAGTTCGCGTAATAAT	30552	TTCGCAAGCAGCAGAAACAAC
1907	FASSSSH	16230	TTTGCTTCTTCGAGTTCGCAT	30553	TTCGCAAGCAGCAGCAGCCAC
1908	FASVRTV	16231	TTTGCTTCTGTTCGTACGGTT	30554	TTCGCAAGCGTCAGAACAGTC
1909	FASYGSP	16232	TTTGCGTCGTATGGTTCGCCG	30555	TTCGCAAGCTACGGAAGCCCA
1910	FATSGYA	16233	TTTGCGACGTCGGGGTATGCT	30556	TTCGCAACAAGCGGATACGCA
1911	FATSTIP	16234	TTTGCTACTTCGACTACTCCG	30557	TTCGCAACAAGCACAACACCA
1912	FATTKLD	16235	TTTGCTACTACTAAGCTTGAT	30558	TTCGCAACAACAAAACTCGAC
1913	FCSEQHS	16236	TTTTGTTCTGAGCAGCATAGT	30559	TTCTGCAGCGAACAACACAGC
1914	FDAPQTR	16237	TTTGATGCGCCGCAGACTAGG	30560	TTCGACGCACCACAAACAAGA
1915	FDAYHRL	16238	TTTGATGCGTATCATAGGCTT	30561	TTCGACGCATACCACAGACTC
1916	FDDFALD	16239	TTTGATGATTTTGCTCTTGAT	30562	TTCGACGACTTCGCACTCGAC
1917	FDEAHAP	16240	TTTGATGAGGCTCATGCGCCT	30563	TTCGACGAAGCACACGCACCA
1918	FDEDDLA	16241	TTTGATGAGGATGATCTTGCT	30564	TTCGACGAAGACGACCTCGCA
1919	FDGARSE	16242	TTTGATGGTGCTAGGAGTGAG	30565	TTCGACGGAGCAAGAAGCGAA
1920	FDGIRPT	16243	TTTGATGGGATTCGGCCGACG	30566	TTCGACGGAATCAGACCAACA
1921	FDHPSFP	16244	TTTGATCATCCGTCGTTTCCG	30567	TTCGACCACCCAAGCTTCCCA
1922	FDHPVRM	16245	TTTGATCATCCTGTTCGTATG	30568	TTCGACCACCCAGTCAGAATG
1923	FDHTKAW	16246	TTTGATCATACGAAGGCGTGG	30569	TTCGACCACACAAAAGCATGG
1924	FDKSTKY	16247	TTTGATAAGAGTACTAAGTAT	30570	TTCGACAAAAGCACAAAATAC

1925	FDQHTRS	16248	TTTGATCAGCATACGCGGTCT	30571	TTCGACCAACACACAAGAAGC
1926	FDRAMQR	16249	TTTGATCGGGCGATGCAGCGT	30572	TTCGACAGAGCAATGCAAAGA
1927	FDRQTQI	16250	TTTGATCGTCAGACGCAGATT	30573	TTCGACAGACAAACACAAATC
1928	FDSVRLS	16251	TTTGATTCGGTGAGGCTGTCT	30574	TTCGACAGCGTCAGACTCAGC
1929	FDTAVNA	16252	TTTGATACGGCTGTGAATGCT	30575	TTCGACACAGCAGTCAACGCA
1930	FDTGKFA	16253	TTTGATACGGGTAAGTTTGCG	30576	TTCGACACAGGAAAATTCGCA
1931	FDYGPMD	16254	TTTGATTATGGTCCTATGGAT	30577	TTCGACTACGGACCAATGGAC
1932	FEAKSSL	16255	TTTGAGGCGAAGTCGTCGCTT	30578	TTCGAAGCAAAAAGCAGCCTC
1933	FEAKVTR	16256	TTTGAGGCGAAGGTTACGCGT	30579	TTCGAAGCAAAAGTCACAAGA
1934	FEARLGT	16257	TTTGAGGCGCGGTTGGGTACG	30580	TTCGAAGCAAGACTCGGAACA
1935	FEDGSLA	16258	TTTGAGGATGGTTCGCTGGCT	30581	TTCGAAGACGGAAGCCTCGCA
1936	FEGSQPP	16259	TTTGAGGGGTCGCAGCCGCCG	30582	TTCGAAGGAAGCCAACCACCA
1937	FEGVQSS	16260	TTTGAGGGGGTGCAGTCGTCG	30583	TTCGAAGGAGTCCAAAGCAGC
1938	FEHHYTP	16261	TTTGAGCATCATTATACGCCT	30584	TTCGAACACCACTACACACCA
1939	FEKRLTI	16262	TTTGAGAAGAGGCTTACGATT	30585	TTCGAAAAAAGACTCACAATC
1940	FEKSLPD	16263	TTTGAGAAGAGTCTTCCTGAT	30586	TTCGAAAAAAGCCTCCCAGAC
1941	FEMVSSL	16264	TTTGAGATGGTGAGTTCTCTT	30587	TTCGAAATGGTCAGCAGCCTC
1942	FENKYHV	16265	TTTGAGAATAAGTATCATGTG	30588	TTCGAAAACAAATACCACGTC
1943	FEPAHAS	16266	TTTGAGCCGGCTCATGCTAGT	30589	TTCGAACCAGCACACGCAAGC
1944	FEPSQLR	16267	TTTGAGCCTTCGCAGCTTCGG	30590	TTCGAACCAAGCCAACTCAGA
1945	FEPVQNT	16268	TTTGAGCCTGTGCAGAATACT	30591	TTCGAACCAGTCCAAAACACA
1946	FEQLLDF	16269	TTTGAGCAGCTGTTGGATTTT	30592	TTCGAACAACTCCTCGACTTC
1947	FERNRTS	16270	TTTGAGCGGAATCGTACTTCT	30593	TTCGAAAGAAACAGAACAAGC
1948	FERPTVI	16271	TTTGAGAGGCCGACGGTGATT	30594	TTCGAAAGACCAACAGTCATC
1949	FERSSGT	16272	TTTGAGCGGTCTTCTGGTACG	30595	TTCGAAAGAAGCAGCGGAACA
1950	FERVPLD	16273	TTTGAGCGTGTGCCTTTGGAT	30596	TTCGAAAGAGTCCCACTCGAC
1951	FESNSVL	16274	TTTGAGTCTAATTCGGTTTTG	30597	TTCGAAAGCAACAGCGTCCTC
1952	FESTTSV	16275	TTTGAGTCTACTACGAGTGTG	30598	TTCGAAAGCACAACAAGCGTC
1953	FETRYEA	16276	TTTGAGACGCGTTATGAGGCG	30599	TTCGAAACAAGATACGAAGCA
1954	FETTIRL	16277	TTTGAGACTACTATTCGTCTG	30600	TTCGAAACAACAATCAGACTC
1955	FEVPSTR	16278	TTTGAGGTTCCGTCGACTCGG	30601	TTCGAAGTCCCAAGCACAAGA
1956	FEYHASG	16279	TTTGAGTATCATGCGTCGGGT	30602	TTCGAATACCACGCAAGCGGA
1957	FFGPGPT	16280	TTTTTTGGGCCGGGGCCTACG	30603	TTCTTCGGACCAGGACCAACA
1958	FFPITSA	16281	TTTTTTCCGATTACTTCTGCT	30604	TTCTTCCCAATCACAAGCGCA
1959	FFSDGRV	16282	TTTTTTTCTGATGGGCGTGTT	30605	TTCTTCAGCGACGGAAGAGTC
1960	FGACRVS	16283	TTTGGTGCTTGTCGGGTTTCG	30606	TTCGGAGCATGCAGAGTCAGC
1961	FGAEPDA	16284	TTTGGGGCGGAGCCTGATGCG	30607	TTCGGAGCAGAACCAGACGCA
1962	FGDRPFP	16285	TTTGGTGATAGGCCGTTTCCG	30608	TTCGGAGACAGACCATTCCCA
1963	FGGGRPE	16286	TTTGGTGGGGGGCGTCCGGAG	30609	TTCGGAGGAGGAAGACCAGAA
1964	FGGQGGQ	16287	TTTGGTGGGCAGGGTGGTCAG	30610	TTCGGAGGACAAGGAGGACAA
1965	FGGTGQF	16288	TTTGGTGGGACTGGTCAGTTT	30611	TTCGGAGGAACAGGACAATTC
1966	FGHMKTP	16289	TTTGGTCATATGAAGACTCCT	30612	TTCGGACACATGAAAACACCA
1967	FGHPIAS	16290	TTTGGGCATCCTATTGCTTCG	30613	TTCGGACACCCAATCGCAAGC
1968	FGHVHLN	16291	TTTGGGCATGTGCATCTGAAT	30614	TTCGGACACGTCCACCTCAAC
1969	FGIAGSP	16292	TTTGGTATTGCTGGTTCTCCT	30615	TTCGGAATCGCAGGAAGCCCA

1970	FGKISMT	16293	TTTGGGAAGATTTCTATGACT	30616	TTCGGAAAAATCAGCATGACA
1971	FGLSPLP	16294	TTTGGGCTTTCGCCTCTTCCT	30617	TTCGGACTCAGCCCACTCCCA
1972	FGLSSAA	16295	TTTGGGCTGAGTTCGGCTGCT	30618	TTCGGACTCAGCAGCGCAGCA
1973	FGLTRPE	16296	TTTGGGCTGACTCGTCCTGAG	30619	TTCGGACTCACAAGACCAGAA
1974	FGNRLSN	16297	TTTGGGAATAGGCTGTCGAAT	30620	TTCGGAAACAGACTCAGCAAC
1975	FGPMLLG	16298	TTTGGTCCGATGCTTCTGGGT	30621	TTCGGACCAATGCTCCTCGGA
1976	FGPNKAD	16299	TTTGGGCCTAATAAGGCGGAT	30622	TTCGGACCAAACAAAGCAGAC
1977	FGPPSGF	16300	TTTGGGCCGCCGTCGGGTTTT	30623	TTCGGACCACCAAGCGGATTC
1978	FGQHAVL	16301	TTTGGTCAGCATGCTGTGCTG	30624	TTCGGACAACACGCAGTCCTC
1979	FGQKHTE	16302	TTTGGTCAGAAGCATACTGAG	30625	TTCGGACAAAAACACACAGAA
1980	FGQNRVT	16303	TTTGGGCAGAATCGGGTGACT	30626	TTCGGACAAAACAGAGTCACA
1981	FGQTALG	16304	TTTGGTCAGACGGCTCTTGGG	30627	TTCGGACAAACAGCACTCGGA
1982	FGRFPTE	16305	TTTGGGCGTTTTCCGACTGAG	30628	TTCGGAAGATTCCCAACAGAA
1983	FGRTPYS	16306	TTTGGTCGGACGCCTTATAGT	30629	TTCGGAAGAACACCATACAGC
1984	FGSDTLI	16307	TTTGGTTCTGATACTCTGATT	30630	TTCGGAAGCGACACACTCATC
1985	FGSHGER	16308	TTTGGTTCGCATGGTGAGAGG	30631	TTCGGAAGCCACGGAGAAAGA
1986	FGTGYAG	16309	TTTGGGACGGGGTATGCGGGT	30632	TTCGGAACAGGATACGCAGGA
1987	FGTRMEP	16310	TTTGGTACGCGTATGGAGCCG	30633	TTCGGAACAAGAATGGAACCA
1988	FGTSEDV	16311	TTTGGGACGTCGGAGGATGTG	30634	TTCGGAACAAGCGAAGACGTC
1989	FGTTRMA	16312	TTTGGGACTACTAGGATGGCT	30635	TTCGGAACAACAAGAATGGCA
1990	FGTVRPS	16313	TTTGGGACGGTGCGTCCGTCT	30636	TTCGGAACAGTCAGACCAAGC
1991	FGVQKIT	16314	TTTGGGGTGCAGAAGATTACG	30637	TTCGGAGTCCAAAAAATCACA
1992	FHASHLG	16315	TTTCATGCTTCTCATTTGGGG	30638	TTCCACGCAAGCCACCTCGGA
1993	FHDPYIW	16316	TTTCATGATCCTTATATTTGG	30639	TTCCACGACCCATACATCTGG
1994	FHGLTVA	16317	TTTCATGGGTTGACTGTTGCG	30640	TTCCACGGACTCACAGTCGCA
1995	FHGTSLG	16318	TTTCATGGGACTTCGCTGGGG	30641	TTCCACGGAACAAGCCTCGGA
1996	FHLPPEL	16319	TTTCATCTTCCTCCTGAGCTT	30642	TTCCACCTCCCACCAGAACTC
1997	FHLSSAS	16320	TTTCATCTGTCGAGTGCGTCT	30643	TTCCACCTCAGCAGCGCAAGC
1998	FHPASVN	16321	TTTCATCCGGCGTCTGTGAAT	30644	TTCCACCCAGCAAGCGTCAAC
1999	FHPHSPP	16322	TTTCATCCGCATAGTCCGCCG	30645	TTCCACCCACACAGCCCACCA
2000	FHQRSQS	16323	TTTCATCAGAGGAGTCAGTCG	30646	TTCCACCAAAGAAGCCAAAGC
2001	FHRNVAN	16324	TTTCATCGGAATGTGGCGAAT	30647	TTCCACAGAAACGTCGCAAAC
2002	FHTANTE	16325	TTTCATACTGCGAATACTGAG	30648	TTCCACACAGCAAACACAGAA
2003	FIDHSIA	16326	TTTATTGATCATAGTATTGCT	30649	TTCATCGACCACAGCATCGCA
2004	FIGNATQ	16327	TTTATTGGGAATGCGACGCAG	30650	TTCATCGGAAACGCAACACAA
2005	FIGTASQ	16328	TTTATTGGTACTGCTTCTCAG	30651	TTCATCGGAACAGCAAGCCAA
2006	FIGYPQG	16329	TTTATTGGTTATCCTCAGGGT	30652	TTCATCGGATACCCACAAGGA
2007	FIPSVSV	16330	TTTATTCCTTCGGTTTCTGTT	30653	TTCATCCCAAGCGTCAGCGTC
2008	FIQDKHV	16331	TTTATTCAGGATAAGCATGTT	30654	TTCATCCAAGACAAACACGTC
2009	FIRHESV	16332	TTTATTAGGCATGAGTCTGTT	30655	TTCATCAGACACGAAAGCGTC
2010	FIRPDLD	16333	TTTATTAGGCCGGATCTTGAT	30656	TTCATCAGACCAGACCTCGAC
2011	FITGALG	16334	TTTATTACTGGGGCGCTGGGG	30657	TTCATCACAGGAGCACTCGGA
2012	FKAYDNI	16335	TTTAAGGCGTATGATAATATT	30658	TTCAAAGCATACGACAACATC
2013	FKDWFED	16336	TTTAAGGATTGGTTTGAGGAT	30659	TTCAAAGACTGGTTCGAAGAC
2014	FKESWPA	16337	TTTAAGGAGTCTTGGCCTGCG	30660	TTCAAAGAAAGCTGGCCAGCA

2015	FKETSNH	16338	TTTAAGGAGACTAGTAATCAT	30661	TTCAAAGAAACAAGCAACCAC
2016	FKGMGVG	16339	TTTAAGGGTATGGGGGTGGGT	30662	TTCAAAGGAATGGGAGTCGGA
2017	FKHPMDG	16340	TTTAAGCATCCTATGGATGGT	30663	TTCAAACACCCAATGGACGGA
2018	FKLGPPE	16341	TTTAAGCTTGGTCCTCCTGAG	30664	TTCAAACTCGGACCACCAGAA
2019	FKLVTRE	16342	TTTAAGCTTGTGACGCGTGAG	30665	TTCAAACTCGTCACAAGAGAA
2020	FKNGTPP	16343	TTTAAGAATGGTACGCCGCCT	30666	TTCAAAAACGGAACACCACCA
2021	FKNVLGT	16344	TTTAAGAATGTTCTGGGGACT	30667	TTCAAAAACGTCCTCGGAACA
2022	FKPANNV	16345	TTTAAGCCGGCTAATAATGTT	30668	TTCAAACCAGCAAACAACGTC
2023	FKPPPMS	16346	TTTAAGCCGCCTCCGATGTCG	30669	TTCAAACCACCACCAATGAGC
2024	FKQPPYV	16347	TTTAAGCAGCCTCCTTATGTG	30670	TTCAAACAACCACCATACGTC
2025	FKQPYAR	16348	TTTAAGCAGCCGTATGCTAGG	30671	TTCAAACAACCATACGCAAGA
2026	FKSVGTI	16349	TTTAAGAGTGTGGGGACTATT	30672	TTCAAAAGCGTCGGAACAATC
2027	FKTMERL	16350	TTTAAGACTATGGAGCGTCTG	30673	TTCAAAACAATGGAAAGACTC
2028	FKVHASS	16351	TTTAAGGTGCATGCGTCTAGT	30674	TTCAAAGTCCACGCAAGCAGC
2029	FLAKLQP	16352	TTTCTGGCGAAGCTGCAGCCG	30675	TTCCTCGCAAAACTCCAACCA
2030	FLALERQ	16353	TTTCTGGCGTTGGAGCGGCAG	30676	TTCCTCGCACTCGAAAGACAA
2031	FLASLND	16354	TTTCTTGCTAGTCTTAATGAT	30677	TTCCTCGCAAGCCTCAACGAC
2032	FLDNRAV	16355	TTTTTGGATAATAGGGCTGTG	30678	TTCCTCGACAACAGAGCAGTC
2033	FLGAAGQ	16356	TTTCTTGGTGCTGCGGGGCAG	30679	TTCCTCGGAGCAGCAGGACAA
2034	FLGAHSA	16357	TTTCTTGGTGCGCATTCGGCT	30680	TTCCTCGGAGCACACAGCGCA
2035	FLHAMDL	16358	TTTTTGCATGCTATGGATCTG	30681	TTCCTCCACGCAATGGACCTC
2036	FLHGETG	16359	TTTCTTCATGGGGAGACTGGG	30682	TTCCTCCACGGAGAAACAGGA
2037	FLKSNIA	16360	TTTCTGAAGTCGAATATTGCT	30683	TTCCTCAAAAGCAACATCGCA
2038	FLKTAVP	16361	TTTCTGAAGACTGCTGTTCCT	30684	TTCCTCAAAACAGCAGTCCCA
2039	FLKTDTG	16362	TTTCTGAAGACTGATACGGGG	30685	TTCCTCAAAACAGACACAGGA
2040	FLPERGS	16363	TTTCTGCCTGAGCGTGGTTCT	30686	TTCCTCCCAGAAAGAGGAAGC
2041	FLPQHSP	16364	TTTCTTCCGCAGCATTCTCCT	30687	TTCCTCCCACAACACAGCCCA
2042	FLPSGGA	16365	TTTCTGCCGAGTGGGGGTGCG	30688	TTCCTCCCAAGCGGAGGAGCA
2043	FLRENAS	16366	TTTCTGCGTGAGAATGCTTCT	30689	TTCCTCAGAGAAAACGCAAGC
2044	FLRIPDD	16367	TTTCTGCGTATTCCGGATGAT	30690	TTCCTCAGAATCCCAGACGAC
2045	FLSKPLS	16368	TTTTTGTCTAAGCCTCTGTCT	30691	TTCCTCAGCAAACCACTCAGC
2046	FLSNSNA	16369	TTTCTGTCTAATTCTAATGCT	30692	TTCCTCAGCAACAGCAACGCA
2047	FLSPNLI	16370	TTTCTTTCGCCGAATCTGATT	30693	TTCCTCAGCCCAAACCTCATC
2048	FLSSDGR	16371	TTTTTGAGTTCGGATGGTCGT	30694	TTCCTCAGCAGCGACGGAAGA
2049	FLSVPET	16372	TTTCTGAGTGTTCCGGAGACT	30695	TTCCTCAGCGTCCCAGAAACA
2050	FLTAGMP	16373	TTTCTGACGGCGGGGATGCCT	30696	TTCCTCACAGCAGGAATGCCA
2051	FLTSAKS	16374	TTTCTGACTTCGGCTAAGTCT	30697	TTCCTCACAAGCGCAAAAAGC
2052	FLTTGVD	16375	TTTCTGACGACTGGGGTGGAT	30698	TTCCTCACAACAGGAGTCGAC
2053	FMFNDSP	16376	TTTATGTTTAATGATAGTCCG	30699	TTCATGTTCAACGACAGCCCA
2054	FMGTVVN	16377	TTTATGGGGACTGTGGTTAAT	30700	TTCATGGGAACAGTCGTCAAC
2055	FMHQQGL	16378	TTTATGCATCAGCAGGGTCTG	30701	TTCATGCACCAACAAGGACTC
2056	FMLRDAT	16379	TTTATGCTTAGGGATGCTACT	30702	TTCATGCTCAGAGACGCAACA
2057	FMMTGTA	16380	TTTATGATGACTGGTACGGCT	30703	TTCATGATGACAGGAACAGCA
2058	FMPKTSP	16381	TTTATGCCTAAGACTTCTCCG	30704	TTCATGCCAAAAACAAGCCCA
2059	FMRSTQS	16382	TTTATGCGGAGTACTCAGTCG	30705	TTCATGAGAAGCACACAAAGC

2060	FMSRGLA	16383	TTTATGTCTAGGGGGCTGGCG	30706	TTCATGAGCAGAGGACTCGCA
2061	FMTERAA	16384	TTTATGACTGAGCGTGCGGCT	30707	TTCATGACAGAAAGAGCAGCA
2062	FMTNLSG	16385	TTTATGACTAATCTTTCTGGG	30708	TTCATGACAAACCTCAGCGGA
2063	FMTSGDL	16386	TTTATGACGTCTGGGGATTTG	30709	TTCATGACAAGCGGAGACCTC
2064	FMVDPVN	16387	TTTATGGTTGATCCGGTGAAT	30710	TTCATGGTCGACCCAGTCAAC
2065	FMVSAPL	16388	TTTATGGTTTCTGCGCCGCTT	30711	TTCATGGTCAGCGCACCACTC
2066	FMYGNGV	16389	TTTATGTATGGGAATGGTGTT	30712	TTCATGTACGGAAACGGAGTC
2067	FNAIHVS	16390	TTTAATGCTATTCATGTGAGT	30713	TTCAACGCAATCCACGTCAGC
2068	FNELSGL	16391	TTTAATGAGCTTAGTGGTTTG	30714	TTCAACGAACTCAGCGGACTC
2069	FNFNKMD	16392	TTTAATTTTAATAAGATGGAT	30715	TTCAACTTCAACAAAATGGAC
2070	FNGDSPA	16393	TTTAATGGTGATAGTCCTGCT	30716	TTCAACGGAGACAGCCCAGCA
2071	FNGPYEL	16394	TTTAATGGTCCTTATGAGCTG	30717	TTCAACGGACCATACGAACTC
2072	FNLSTSA	16395	TTTAATTTGTCTACGTCTGCG	30718	TTCAACCTCAGCACAAGCGCA
2073	FNPTVRE	16396	TTTAATCCGACGGTTAGGGAG	30719	TTCAACCCAACAGTCAGAGAA
2074	FNRPVTT	16397	TTTAATAGGCCTGTGACTACG	30720	TTCAACAGACCAGTCACAACA
2075	FNSDSNS	16398	TTTAATTCTGATTCTAATAGT	30721	TTCAACAGCGACAGCAACAGC
2076	FNSSPDL	16399	TTTAATTCTAGTCCGGATCTT	30722	TTCAACAGCAGCCCAGACCTC
2077	FNTPTKV	16400	TTTAATACGCCTACGAAGGTT	30723	TTCAACACACCAACAAAAGTC
2078	FNVMQER	16401	TTTAATGTTATGCAGGAGAGG	30724	TTCAACGTCATGCAAGAAAGA
2079	FPALSGG	16402	TTTCCGGCTTTGTCTGGTGGG	30725	TTCCCAGCACTCAGCGGAGGA
2080	FPAVNVP	16403	TTTCCGGCTGTTAATGTTCCG	30726	TTCCCAGCAGTCAACGTCCCA
2081	FPERGMV	16404	TTTCCTGAGCGTGGTATGGTT	30727	TTCCCAGAAAGAGGAATGGTC
2082	FPFNSGS	16405	TTTCCGTTTAATAGTGGTTCT	30728	TTCCCATTCAACAGCGGAAGC
2083	FPGFPSK	16406	TTTCCTGGTTTTCCTTCGAAG	30729	TTCCCAGGATTCCCAAGCAAA
2084	FPGSDSL	16407	TTTCCGGGTAGTGATTCGCTG	30730	TTCCCAGGAAGCGACAGCCTC
2085	FPHTLSE	16408	TTTCCTCATACGTTGTCTGAG	30731	TTCCCACACACACTCAGCGAA
2086	FPKGSTP	16409	TTTCCTAAGGGGTCTACGCCG	30732	TTCCCAAAAGGAAGCACACCA
2087	FPKTDDT	16410	TTTCCTAAGACTGATGATACG	30733	TTCCCAAAAACAGACGACACA
2088	FPKYAIA	16411	TTTCCGAAGTATGCTATTGCG	30734	TTCCCAAAATACGCAATCGCA
2089	FPLMSSN	16412	TTTCCTTTGATGTCTTCGAAT	30735	TTCCCACTCATGAGCAGCAAC
2090	FPLSDPY	16413	TTTCCTCTTTCGGATCCGTAT	30736	TTCCCACTCAGCGACCCATAC
2091	FPLSQQA	16414	TTTCCGTTGTCGCAGCAGGCT	30737	TTCCCACTCAGCCAACAAGCA
2092	FPMAKPY	16415	TTTCCGATGGCGAAGCCGTAT	30738	TTCCCAATGGCAAAACCATAC
2093	FPMRGAP	16416	TTTCCGATGCGTGGTGCTCCT	30739	TTCCCAATGAGAGGAGCACCA
2094	FPMTNPA	16417	TTTCCTATGACGAATCCTGCG	30740	TTCCCAATGACAAACCCAGCA
2095	FPNAQLV	16418	TTTCCTAATGCGCAGCTGGTT	30741	TTCCCAAACGCACAACTCGTC
2096	FPNDLPL	16419	TTTCCGAATGATCTTCCTCTT	30742	TTCCCAAACGACCTCCCACTC
2097	FPNMSSV	16420	TTTCCTAATATGAGTTCGGTT	30743	TTCCCAAACATGAGCAGCGTC
2098	FPNRFEA	16421	TTTCCTAATCGGTTTGAGGCT	30744	TTCCCAAACAGATTCGAAGCA
2099	FPPGVRP	16422	TTTCCGCCTGGTGTTCGTCCT	30745	TTCCCACCAGGAGTCAGACCA
2100	FPPRDTP	16423	TTTCCTCCGAGGGATACGCCG	30746	TTCCCACCAAGAGACACACCA
2101	FPPSCAN	16424	TTTCCGCCTAGTTGTGCGAAT	30747	TTCCCACCAAGCTGCGCAAAC
2102	FPPSLSA	16425	TTTCCGCCTTCGCTGTCTGCT	30748	TTCCCACCAAGCCTCAGCGCA
2103	FPPSSLP	16426	TTTCCGCCGAGTTCTTTGCCT	30749	TTCCCACCAAGCAGCCTCCCA
2104	FPPTNSF	16427	TTTCCGCCGACTAATTCGTTT	30750	TTCCCACCAACAAACAGCTTC

2105	FPQITLN	16428	TTTCCTCAGATTACTTTGAAT	30751	TTCCCACAAATCACACTCAAC
2106	FPQKEGT	16429	TTTCCGCAGAAGGAGGGGACG	30752	TTCCCACAAAAAGAAGGAACA
2107	FPQPADM	16430	TTTCCTCAGCCGGCTGATATG	30753	TTCCCACAACCAGCAGACATG
2108	FPRAIDA	16431	TTTCCTAGGGCTATTGATGCG	30754	TTCCCAAGAGCAATCGACGCA
2109	FPRGAVL	16432	TTTCCGCGGGGGGCTGTGCTT	30755	TTCCCAAGAGGAGCAGTCCTC
2110	FPRPQLG	16433	TTTCCGAGGCCGCAGCTTGGT	30756	TTCCCAAGACCACAACTCGGA
2111	FPSNPAH	16434	TTTCCGTCGAATCCTGCGCAT	30757	TTCCCAAGCAACCCAGCACAC
2112	FPSSQQT	16435	TTTCCTAGTTCTCAGCAGACT	30758	TTCCCAAGCAGCCAACAAACA
2113	FPSSRLS	16436	TTTCCTTCGTCTCGTCTTTCG	30759	TTCCCAAGCAGCAGACTCAGC
2114	FPSTTLP	16437	TTTCCTAGTACGACTCTGCCG	30760	TTCCCAAGCACAACACTCCCA
2115	FPTDYVP	16438	TTTCCGACTGATTATGTGCCT	30761	TTCCCAACAGACTACGTCCCA
2116	FPTKGFV	16439	TTTCCGACGAAGGGTTTTGTG	30762	TTCCCAACAAAAGGATTCGTC
2117	FPTSTSS	16440	TTTCCGACTTCGACGAGTAGT	30763	TTCCCAACAAGCACAAGCAGC
2118	FPTSTTP	16441	TTTCCGACTTCTACTACGCCG	30764	TTCCCAACAAGCACAACACCA
2119	FPVAQHD	16442	TTTCCTGTTGCGCAGCATGAT	30765	TTCCCAGTCGCACAACACGAC
2120	FPVDGRQ	16443	TTTCCGGTGGATGGGCGGCAG	30766	TTCCCAGTCGACGGAAGACAA
2121	FPVGNRL	16444	TTTCCTGTTGGTAATCGGCTG	30767	TTCCCAGTCGGAAACAGACTC
2122	FPVGQLA	16445	TTTCCTGTGGGGCAGCTTGCT	30768	TTCCCAGTCGGACAACTCGCA
2123	FPVKTMV	16446	TTTCCGGTTAAGACGATGGTT	30769	TTCCCAGTCAAAACAATGGTC
2124	FPVSARD	16447	TTTCCTGTTTCGGCGCGGGAT	30770	TTCCCAGTCAGCGCAAGAGAC
2125	FQAAPDH	16448	TTTCAGGCTGCTCCGGATCAT	30771	TTCCAAGCAGCACCAGACCAC
2126	FQAGKAV	16449	TTTCAGGCTGGGAAGGCGGTT	30772	TTCCAAGCAGGAAAAGCAGTC
2127	FQGAISR	16450	TTTCAGGGGGCGATTTCGCGG	30773	TTCCAAGGAGCAATCAGCAGA
2128	FQGLRLG	16451	TTTCAGGGGTTGCGGTTGGGT	30774	TTCCAAGGACTCAGACTCGGA
2129	FQGSVPE	16452	TTTCAGGGTAGTGTGCCGGAG	30775	TTCCAAGGAAGCGTCCCAGAA
2130	FQITAQG	16453	TTTCAGATTACTGCGCAGGGG	30776	TTCCAAATCACAGCACAAGGA
2131	FQKSHAG	16454	TTTCAGAAGTCGCATGCTGGG	30777	TTCCAAAAAAGCCACGCAGGA
2132	FQNPQSS	16455	TTTCAGAATCCTCAGTCTTCT	30778	TTCCAAAACCCACAAAGCAGC
2133	FQNQGPL	16456	TTTCAGAATCAGGGGCCTCTT	30779	TTCCAAAACCAAGGACCACTC
2134	FQQTGPR	16457	TTTCAGCAGACTGGGCCTCGT	30780	TTCCAACAAACAGGACCAAGA
2135	FQRATLQ	16458	TTTCAGAGGGCTACGCTGCAG	30781	TTCCAAAGAGCAACACTCCAA
2136	FQSATVA	16459	TTTCAGTCTGCGACGGTGGCT	30782	TTCCAAAGCGCAACAGTCGCA
2137	FQTPSGD	16460	TTTCAGACTCCGAGTGGGGAT	30783	TTCCAAACACCAAGCGGAGAC
2138	FQVVGSP	16461	TTTCAGGTGGTTGGGTCGCCT	30784	TTCCAAGTCGTCGGAAGCCCA
2139	FQYEPAI	16462	TTTCAGTATGAGCCTGCGATT	30785	TTCCAATACGAACCAGCAATC
2140	FRADLLN	16463	TTTAGGGCGGATCTTTTGAAT	30786	TTCAGAGCAGACCTCCTCAAC
2141	FRAIGSG	16464	TTTCGGGCTATTGGGTCGGGG	30787	TTCAGAGCAATCGGAAGCGGA
2142	FRALVEP	16465	TTTAGGGCTCTTGTGGAGCCT	30788	TTCAGAGCACTCGTCGAACCA
2143	FRDEQPS	16466	TTTAGGGATGAGCAGCCGTCG	30789	TTCAGAGACGAACAACCAAGC
2144	FRDQADG	16467	TTTAGGGATCAGGCTGATGGT	30790	TTCAGAGACCAAGCAGACGGA
2145	FRDSPPS	16468	TTTCGGGATAGTCCTCCTTCG	30791	TTCAGAGACAGCCCACCAAGC
2146	FREEPQT	16469	TTTCGGGAGGAGCCTCAGACT	30792	TTCAGAGAAGAACCACAAACA
2147	FRGPSSS	16470	TTTCGGGGTCCGAGTTCTTCG	30793	TTCAGAGGACCAAGCAGCAGC
2148	FRHADAV	16471	TTTCGTCATGCTGATGCGGTG	30794	TTCAGACACGCAGACGCAGTC
2149	FRHDHSV	16472	TTTCGGCATGATCATTCGGTT	30795	TTCAGACACGACCACAGCGTC

2150	FRLHSTS	16473	TTTAGGCTGCATTCTACGTCG	30796	TTCAGACTCCACAGCACAAGC
2151	FRLPHET	16474	TTTAGGCTGCCGCATGAGACT	30797	TTCAGACTCCCACACGAAACA
2152	FRMGEAP	16475	TTTAGGATGGGGGAGGCTCCT	30798	TTCAGAATGGGAGAAGCACCA
2153	FRMQNAA	16476	TTTCGGATGCAGAATGCTGCG	30799	TTCAGAATGCAAAACGCAGCA
2154	FRNGPEP	16477	TTTAGGAATGGGCCTGAGCCG	30800	TTCAGAAACGGACCAGAACCA
2155	FRNNVSL	16478	TTTCGGAATAATGTTAGTCTT	30801	TTCAGAAACAACGTCAGCCTC
2156	FRPLALE	16479	TTTAGGCCGTTGGCGCTGGAG	30802	TTCAGACCACTCGCACTCGAA
2157	FRPLSTP	16480	TTTCGTCCGTTGAGTACGCCG	30803	TTCAGACCACTCAGCACACCA
2158	FRPPALS	16481	TTTCGTCCTCCTGCTCTTTCT	30804	TTCAGACCACCAGCACTCAGC
2159	FRPQDTM	16482	TTTCGTCCGCAGGATACGATG	30805	TTCAGACCACAAGACACAATG
2160	FRQTPNH	16483	TTTCGGCAGACGCCGAATCAT	30806	TTCAGACAAACACCAAACCAC
2161	FRSDSHN	16484	TTTCGTTCTGATTCTCATAAT	30807	TTCAGAAGCGACAGCCACAAC
2162	FRSGLAI	16485	TTTAGGTCTGGGCTTGCGATT	30808	TTCAGAAGCGGACTCGCAATC
2163	FRSGLEY	16486	TTTCGTTCTGGGTTGGAGTAT	30809	TTCAGAAGCGGACTCGAATAC
2164	FRSGMVA	16487	TTTCGGTCGGGTATGGTTGCG	30810	TTCAGAAGCGGAATGGTCGCA
2165	FRSKIDA	16488	TTTCGTTCGAAGATTGATGCT	30811	TTCAGAAGCAAAATCGACGCA
2166	FRSPAGL	16489	TTTCGGTCGCCTGCGGGTCTG	30812	TTCAGAAGCCCAGCAGGACTC
2167	FRSTENN	16490	TTTCGGAGTACGGAGAATAAT	30813	TTCAGAAGCACAGAAAACAAC
2168	FRTPHSE	16491	TTTCGGACGCCTCATTCGGAG	30814	TTCAGAACACCACACAGCGAA
2169	FRTSTEG	16492	TTTAGGACGAGTACGGAGGGT	30815	TTCAGAACAAGCACAGAAGGA
2170	FRVPDAD	16493	TTTCGGGTTCCTGATGCTGAT	30816	TTCAGAGTCCCAGACGCAGAC
2171	FSADVDG	16494	TTTTCGGCGGATGTTGATGGG	30817	TTCAGCGCAGACGTCGACGGA
2172	FSARGSG	16495	TTTAGTGCTCGGGGTTCTGGG	30818	TTCAGCGCAAGAGGAAGCGGA
2173	FSDGESL	16496	TTTTCGGATGGTGAGAGTCTT	30819	TTCAGCGACGGAGAAAGCCTC
2174	FSDHTAH	16497	TTTTCGGATCATACTGCTCAT	30820	TTCAGCGACCACACAGCACAC
2175	FSDNALD	16498	TTTTCGGATAATGCGCTGGAT	30821	TTCAGCGACAACGCACTCGAC
2176	FSDRPGD	16499	TTTTCGGATAGGCCTGGTGAT	30822	TTCAGCGACAGACCAGGAGAC
2177	FSEHVSK	16500	TTTTCGGAGCATGTTTCTAAG	30823	TTCAGCGAACACGTCAGCAAA
2178	FSERHSE	16501	TTTTCGGAGCGTCATTCTGAG	30824	TTCAGCGAAAGACACAGCGAA
2179	FSESKTP	16502	TTTTCTGAGTCGAAGACGCCG	30825	TTCAGCGAAAGCAAAACACCA
2180	FSETSNM	16503	TTTTCTGAGACGAGTAATATG	30826	TTCAGCGAAACAAGCAACATG
2181	FSGEPLS	16504	TTTTCTGGTGAGCCTCTGAGT	30827	TTCAGCGGAGAACCACTCAGC
2182	FSGHNTI	16505	TTTTCTGGTCATAATACTATT	30828	TTCAGCGGACACAACACAATC
2183	FSHPGAA	16506	TTTTCGCATCCTGGGGCGGCT	30829	TTCAGCCACCCAGGAGCAGCA
2184	FSHPHPA	16507	TTTAGTCATCCGCATCCTGCT	30830	TTCAGCCACCCACACCCAGCA
2185	FSHSQST	16508	TTTTCTCATAGTCAGTCTACG	30831	TTCAGCCACAGCCAAAGCACA
2186	FSHSSGK	16509	TTTTCGCATTCTTCGGGTAAG	30832	TTCAGCCACAGCAGCGGAAAA
2187	FSITPIK	16510	TTTTCTATTACTCCGATTAAG	30833	TTCAGCATCACACCAATCAAA
2188	FSLMPRE	16511	TTTAGTCTTATGCCTCGGGAG	30834	TTCAGCCTCATGCCAAGAGAA
2189	FSLTADK	16512	TTTTCTTTGACTGCGGATAAG	30835	TTCAGCCTCACAGCAGACAAA
2190	FSMTAQD	16513	TTTTCTATGACTGCTCAGGAT	30836	TTCAGCATGACAGCACAAGAC
2191	FSMTVHH	16514	TTTTCTATGACGGTGCATCAT	30837	TTCAGCATGACAGTCCACCAC
2192	FSNQMPI	16515	TTTAGTAATCAGATGCCTATT	30838	TTCAGCAACCAAATGCCAATC
2193	FSNSGPF	16516	TTTTCGAATTCTGGGCCTTTT	30839	TTCAGCAACAGCGGACCATTC
2194	FSNTTSL	16517	TTTTCTAATACTACGTCTCTG	30840	TTCAGCAACACAACAAGCCTC

2195	FSNTTTT	16518	TTTTCTAATACTACTACTACG	30841	TTCAGCAACACAACAACAACA
2196	FSPGSLA	16519	TTTTCTCCTGGGTCGTTGGCT	30842	TTCAGCCCAGGAAGCCTCGCA
2197	FSPHTLP	16520	TTTAGTCCGCATACGCTGCCT	30843	TTCAGCCCACACACACTCCCA
2198	FSPMEAS	16521	TTTTCTCCTATGGAGGCTTCG	30844	TTCAGCCCAATGGAAGCAAGC
2199	FSPNIMR	16522	TTTAGTCCGAATATTATGCGG	30845	TTCAGCCCAAACATCATGAGA
2200	FSPRSIG	16523	TTTAGTCCGAGGTCGATTGGG	30846	TTCAGCCCAAGAAGCATCGGA
2201	FSPYADE	16524	TTTAGTCCGTATGCGGATGAG	30847	TTCAGCCCATACGCAGACGAA
2202	FSQPLRN	16525	TTTAGTCAGCCGCTGAGGAAT	30848	TTCAGCCAACCACTCAGAAAC
2203	FSQSLPT	16526	TTTTCGCAGAGTCTTCCTACT	30849	TTCAGCCAAAGCCTCCCAACA
2204	FSRGSGP	16527	TTTTCTCGTGGTTCGGGTCCG	30850	TTCAGCAGAGGAAGCGGACCA
2205	FSRLNPS	16528	TTTTCGCGGTTGAATCCTAGT	30851	TTCAGCAGACTCAACCCAAGC
2206	FSRSHIP	16529	TTTTCTCGGAGTCATATTCCT	30852	TTCAGCAGAAGCCACATCCCA
2207	FSRTLTS	16530	TTTTCTCGTACGCTGACTTCG	30853	TTCAGCAGAACACTCACAAGC
2208	FSSHESS	16531	TTTTCTTCGCATGAGAGTTCT	30854	TTCAGCAGCCACGAAAGCAGC
2209	FSSHGES	16532	TTTTCTAGTCATGGTGAGTCT	30855	TTCAGCAGCCACGGAGAAAGC
2210	FSSNTEL	16533	TTTTCTAGTAATACGGAGTTG	30856	TTCAGCAGCAACACAGAACTC
2211	FSSNTFD	16534	TTTTCGTCTAATACTTTTGAT	30857	TTCAGCAGCAACACATTCGAC
2212	FSSNTSA	16535	TTTTCGTCGAATACGAGTGCG	30858	TTCAGCAGCAACACAAGCGCA
2213	FSSNTSE	16536	TTTTCGTCGAATACGAGTGAG	30859	TTCAGCAGCAACACAAGCGAA
2214	FSSPSGY	16537	TTTTCTTCTCCGAGTGGGTAT	30860	TTCAGCAGCCCAAGCGGATAC
2215	FSSRTQA	16538	TTTTCGTCGCGGACTCAGGCG	30861	TTCAGCAGCAGAACACAAGCA
2216	FSSSMAA	16539	TTTAGTAGTTCGATGGCGGCT	30862	TTCAGCAGCAGCATGGCAGCA
2217	FSSSTLK	16540	TTTAGTAGTTCGACGCTTAAG	30863	TTCAGCAGCAGCACACTCAAA
2218	FSSSVTS	16541	TTTTCGAGTAGTGTGACGTCG	30864	TTCAGCAGCAGCGTCACAAGC
2219	FSSTNLA	16542	TTTAGTTCTACGAATCTTGCG	30865	TTCAGCAGCACAAACCTCGCA
2220	FSSTPGH	16543	TTTTCTAGTACTCCGGGGCAT	30866	TTCAGCAGCACACCAGGACAC
2221	FSSTSPD	16544	TTTAGTTCGACGTCTCCGGAT	30867	TTCAGCAGCACAAGCCCAGAC
2222	FSSTSPM	16545	TTTTCTTCTACGAGTCCTATG	30868	TTCAGCAGCACAAGCCCAATG
2223	FSSTSSA	16546	TTTTCGTCGACGTCTTCGGCT	30869	TTCAGCAGCACAAGCAGCGCA
2224	FSSVIPS	16547	TTTTCGTCGGTGATTCCGAGT	30870	TTCAGCAGCGTCATCCCAAGC
2225	FSSVRNE	16548	TTTTCGTCGGTTCGTAATGAG	30871	TTCAGCAGCGTCAGAAACGAA
2226	FSSVSTT	16549	TTTTCTTCGGTTAGTACGACG	30872	TTCAGCAGCGTCAGCACAACA
2227	FSSYASM	16550	TTTTCGTCTTATGCTTCTATG	30873	TTCAGCAGCTACGCAAGCATG
2228	FSSYNNA	16551	TTTAGTTCTTATAATAATGCG	30874	TTCAGCAGCTACAACAACGCA
2229	FSTLSIP	16552	TTTTCTACTCTTAGTATTCCT	30875	TTCAGCACACTCAGCATCCCA
2230	FSTMPAK	16553	TTTAGTACGATGCCGGCGAAG	30876	TTCAGCACAATGCCAGCAAAA
2231	FSTMPRD	16554	TTTTCGACGATGCCTCGTGAT	30877	TTCAGCACAATGCCAAGAGAC
2232	FSTRTQP	16555	TTTTCGACTCGTACGCAGCCG	30878	TTCAGCACAAGAACACAACCA
2233	FSTSGQE	16556	TTTTCGACTAGTGGTCAGGAG	30879	TTCAGCACAAGCGGACAAGAA
2234	FSTVHQA	16557	TTTTCTACGGTTCATCAGGCT	30880	TTCAGCACAGTCCACCAAGCA
2235	FSTVKAD	16558	TTTTCTACTGTTAAGGCTGAT	30881	TTCAGCACAGTCAAAGCAGAC
2236	FSTYSHH	16559	TTTTCTACGTATAGTCATCAT	30882	TTCAGCACATACAGCCACCAC
2237	FSVARIG	16560	TTTTCGGTTGCGCGTATTGGT	30883	TTCAGCGTCGCAAGAATCGGA
2238	FSVPSAG	16561	TTTTCGGTGCCTTCGGCGGGT	30884	TTCAGCGTCCCAAGCGCAGGA
2239	FTAKGIT	16562	TTTACTGCGAAGGGTATTACT	30885	TTCACAGCAAAAGGAATCACA

2240	FTARTTA	16563	TTTACGGCTCGTACTACGGCT	30886	TTCACAGCAAGAACAACAGCA
2241	FTASGVS	16564	TTTACTGCGTCGGGTGTTTCG	30887	TTCACAGCAAGCGGAGTCAGC
2242	FTATVAI	16565	TTTACGGCGACTGTGGCTATT	30888	TTCACAGCAACAGTCGCAATC
2243	FTCPAVS	16566	TTTACGTGTCCGGCGGTGTCT	30889	TTCACATGCCCAGCAGTCAGC
2244	FTDIDDR	16567	TTTACTGATATTGATGATCGG	30890	TTCACAGACATCGACGACAGA
2245	FTDRQGY	16568	TTTACTGATCGGCAGGGTTAT	30891	TTCACAGACAGACAAGGATAC
2246	FTDSSPY	16569	TTTACGGATTCGTCGCCTTAT	30892	TTCACAGACAGCAGCCCATAC
2247	FTEHGYS	16570	TTTACTGAGCATGGGTATAGT	30893	TTCACAGAACACGGATACAGC
2248	FTEPSTS	16571	TTTACGGAGCCTTCTACGTCT	30894	TTCACAGAACCAAGCACAAGC
2249	FTGKGDV	16572	TTTACTGGGAAGGGGGATGTT	30895	TTCACAGGAAAAGGAGACGTC
2250	FTGTHSA	16573	TTTACGGGTACTCATAGTGCG	30896	TTCACAGGAACACACAGCGCA
2251	FTHRVPD	16574	TTTACTCATCGTGTGCCTGAT	30897	TTCACACACAGAGTCCCAGAC
2252	FTIKTIL	16575	TTTACTATTAAGACGATTCTT	30898	TTCACAATCAAAACAATCCTC
2253	FTKMQLS	16576	TTTACTAAGATGCAGCTTTCT	30899	TTCACAAAAATGCAACTCAGC
2254	FTKPSTT	16577	TTTACGAAGCCGAGTACGACG	30900	TTCACAAAACCAAGCACAACA
2255	FTKSKAD	16578	TTTACTAAGTCTAAGGCTGAT	30901	TTCACAAAAAGCAAAGCAGAC
2256	FTLESKL	16579	TTTACTTTGGAGTCTAAGCTT	30902	TTCACACTCGAAAGCAAACTC
2257	FTLVTLE	16580	TTTACTCTTGTTACTCTGGAG	30903	TTCACACTCGTCACACTCGAA
2258	FTMAPIV	16581	TTTACTATGGCTCCTATTGTG	30904	TTCACAATGGCACCAATCGTC
2259	FTNDPSS	16582	TTTACGAATGATCCGTCTTCT	30905	TTCACAAACGACCCAAGCAGC
2260	FTNRDVA	16583	TTTACTAATCGTGATGTGGCT	30906	TTCACAAACAGAGACGTCGCA
2261	FTNSSSP	16584	TTTACTAATTCGAGTAGTCCG	30907	TTCACAAACAGCAGCAGCCCA
2262	FTPLISH	16585	TTTACTCCGCTGATTTCTCAT	30908	TTCACACCACTCATCAGCCAC
2263	FTQALFP	16586	TTTACTCAGGCGCTGTTTCCT	30909	TTCACACAAGCACTCTTCCCA
2264	FTQLPSL	16587	TTTACTCAGTTGCCTAGTCTT	30910	TTCACACAACTCCCAAGCCTC
2265	FTQMSLS	16588	TTTACTCAGATGTCTCTGTCT	30911	TTCACACAAATGAGCCTCAGC
2266	FTQNKPM	16589	TTTACGCAGAATAAGCCGATG	30912	TTCACACAAAACAAACCAATG
2267	FTQSLPT	16590	TTTACGCAGTCGTTGCCGACT	30913	TTCACACAAAGCCTCCCAACA
2268	FTRLEPQ	16591	TTTACTAGGCTTGAGCCTCAG	30914	TTCACAAGACTCGAACCACAA
2269	FTRPSLA	16592	TTTACGCGTCCGAGTTTGGCT	30915	TTCACAAGACCAAGCCTCGCA
2270	FTRSVAA	16593	TTTACGCGGTCTGTGGCGGCG	30916	TTCACAAGAAGCGTCGCAGCA
2271	FTSAPLL	16594	TTTACGAGTGCGCCGCTGCTT	30917	TTCACAAGCGCACCACTCCTC
2272	FTSAPNM	16595	TTTACTTCTGCTCCTAATATG	30918	TTCACAAGCGCACCAAACATG
2273	FTSDGTE	16596	TTTACGAGTGATGGTACGGAG	30919	TTCACAAGCGACGGAACAGAA
2274	FTSKGPF	16597	TTTACGTCGAAGGGGCCGTTT	30920	TTCACAAGCAAAGGACCATTC
2275	FTSKHLG	16598	TTTACTTCGAAGCATCTTGGG	30921	TTCACAAGCAAACACCTCGGA
2276	FTSREDA	16599	TTTACGAGTAGGGAGGATGCG	30922	TTCACAAGCAGAGAAGACGCA
2277	FTSTFPS	16600	TTTACTTCGACGTTTCCTAGT	30923	TTCACAAGCACATTCCCAAGC
2278	FTTAPIL	16601	TTTACGACTGCGCCGATTCTG	30924	TTCACAACAGCACCAATCCTC
2279	FTTDRVS	16602	TTTACGACTGATAGGGTGTCG	30925	TTCACAACAGACAGAGTCAGC
2280	FTTKAAF	16603	TTTACGACGAAGGCGGCGTTT	30926	TTCACAACAAAAGCAGCATTC
2281	FTVNLLG	16604	TTTACGGTTAATCTTCTTGGG	30927	TTCACAGTCAACCTCCTCGGA
2282	FVANVRP	16605	TTTGTTGCGAATGTTAGGCCT	30928	TTCGTCGCAAACGTCAGACCA
2283	FVASASH	16606	TTTGTTGCTAGTGCGTCTCAT	30929	TTCGTCGCAAGCGCAAGCCAC
2284	FVDNNLS	16607	TTTGTGGATAATAATCTTTCT	30930	TTCGTCGACAACAACCTCAGC

2285	FVDPYYE	16608	TTTGTGGATCCGTATTATGAG	30931	TTCGTCGACCCATACTACGAA
2286	FVERSSS	16609	TTTGTTGAGCGGTCGTCGAGT	30932	TTCGTCGAAAGAAGCAGCAGC
2287	FVGATMS	16610	TTTGTTGGTGCGACTATGAGT	30933	TTCGTCGGAGCAACAATGAGC
2288	FVGKPES	16611	TTTGTGGGGAAGCCGGAGTCT	30934	TTCGTCGGAAAACCAGAAAGC
2289	FVGNSRL	16612	TTTGTTGGGAATTCTCGTTTG	30935	TTCGTCGGAAACAGCAGACTC
2290	FVHSGRQ	16613	TTTGTGCATAGTGGGCGGCAG	30936	TTCGTCCACAGCGGAAGACAA
2291	FVMHTRD	16614	TTTGTTATGCATACGCGTGAT	30937	TTCGTCATGCACACAAGAGAC
2292	FVNARVP	16615	TTTGTTAATGCGCGGGTGCCG	30938	TTCGTCAACGCAAGAGTCCCA
2293	FVNPHPS	16616	TTTGTTAATCCGCATCCTTCT	30939	TTCGTCAACCCACACCCAAGC
2294	FVNQTTV	16617	TTTGTGAATCAGACGACTGTG	30940	TTCGTCAACCAAACAACAGTC
2295	FVPHANQ	16618	TTTGTGCCGCATGCTAATCAG	30941	TTCGTCCCACACGCAAACCAA
2296	FVQQSKP	16619	TTTGTGCAGCAGTCTAAGCCT	30942	TTCGTCCAACAAAGCAAACCA
2297	FVSHSQS	16620	TTTGTTTCGCATAGTCAGTCT	30943	TTCGTCAGCCACAGCCAAAGC
2298	FVSRDRA	16621	TTTGTTAGTCGGGATCGGGCG	30944	TTCGTCAGCAGAGACAGAGCA
2299	FVSSIHA	16622	TTTGTTTCTTCGATTCATGCG	30945	TTCGTCAGCAGCATCCACGCA
2300	FVSTPGM	16623	TTTGTTAGTACGCCGGGGATG	30946	TTCGTCAGCACACCAGGAATG
2301	FVSTTSP	16624	TTTGTTTCGACTACTAGTCCT	30947	TTCGTCAGCACAACAAGCCCA
2302	FVSTVAP	16625	TTTGTTAGTACTGTTGCTCCT	30948	TTCGTCAGCACAGTCGCACCA
2303	FVTATLP	16626	TTTGTTACTGCTACTTTGCCT	30949	TTCGTCACAGCAACACTCCCA
2304	FVTESML	16627	TTTGTTACGGAGTCTATGCTG	30950	TTCGTCACAGAAAGCATGCTC
2305	FVVGSDG	16628	TTTGTGGTTGGGTCTGATGGT	30951	TTCGTCGTCGGAAGCGACGGA
2306	FWKEGSP	16629	TTTTGGAAGGAGGGTTCGCCG	30952	TTCTGGAAAGAAGGAAGCCCA
2307	FYPGPKI	16630	TTTTATCCGGGTCCGAAGATT	30953	TTCTACCCAGGACCAAAAATC
2308	FYPSMKD	16631	TTTTATCCGTCGATGAAGGAT	30954	TTCTACCCAAGCATGAAAGAC
2309	FYPTELK	16632	TTTTATCCGACTGAGCTGAAG	30955	TTCTACCCAACAGAACTCAAA
2310	FYSATMP	16633	TTTTATTCGGCTACTATGCCT	30956	TTCTACAGCGCAACAATGCCA
2311	GAAAQYT	16634	GGGGCGGCTGCGCAGTATACG	30957	GGAGCAGCAGCACAATACACA
2312	GAAPQSI	16635	GGGGCGGCTCCGCAGTCTATT	30958	GGAGCAGCACCACAAAGCATC
2313	GAASGLG	16636	GGGGCGGCTAGTGGTCTTGGT	30959	GGAGCAGCAAGCGGACTCGGA
2314	GAATLIS	16637	GGGGCTGCTACTCTTATTTCG	30960	GGAGCAGCAACACTCATCAGC
2315	GAATRNP	16638	GGTGCTGCGACGCGGAATCCG	30961	GGAGCAGCAACAAGAAACCCA
2316	GADEPGG	16639	GGTGCTGATGAGCCTGGGGGT	30962	GGAGCAGACGAACCAGGAGGA
2317	GADLSGR	16640	GGTGCTGATCTGAGTGGGCGG	30963	GGAGCAGACCTCAGCGGAAGA
2318	GADRNVP	16641	GGGGCGGATCGTAATGTTCCG	30964	GGAGCAGACAGAAACGTCCCA
2319	GADSSRY	16642	GGGGCTGATTCGAGTCGGTAT	30965	GGAGCAGACAGCAGCAGATAC
2320	GAEGGGN	16643	GGGGCTGAGGGGGGTGGTAAT	30966	GGAGCAGAAGGAGGAGGAAAC
2321	GAEKHLP	16644	GGTGCTGAGAAGCATTTGCCT	30967	GGAGCAGAAAAACACCTCCCA
2322	GAEPMLA	16645	GGGGCTGAGCCGATGTTGGCG	30968	GGAGCAGAACCAATGCTCGCA
2323	GAESLSV	16646	GGTGCTGAGTCGCTGTCTGTG	30969	GGAGCAGAAAGCCTCAGCGTC
2324	GAFALSG	16647	GGGGCTTTTGCTTTGAGTGGT	30970	GGAGCATTCGCACTCAGCGGA
2325	GAFGPTS	16648	GGTGCTTTTGGTCCTACGTCG	30971	GGAGCATTCGGACCAACAAGC
2326	GAGAGSR	16649	GGTGCGGGTGCTGGGTCGCGT	30972	GGAGCAGGAGCAGGAAGCAGA
2327	GAGELPP	16650	GGTGCTGGTGAGCTGCCTCCG	30973	GGAGCAGGAGAACTCCCACCA
2328	GAGLKGS	16651	GGTGCTGGTCTTAAGGGTAGT	30974	GGAGCAGGACTCAAAGGAAGC
2329	GAGLPVT	16652	GGTGCGGGGTTGCCGGTGACT	30975	GGAGCAGGACTCCCAGTCACA

2330	GAGMNTA	16653	GGGGCGGGTATGAATACTGCT	30976	GGAGCAGGAATGAACACAGCA
2331	GAGTAML	16654	GGGGCTGGTACTGCTATGCTT	30977	GGAGCAGGAACAGCAATGCTC
2332	GAHDTVT	16655	GGGGCGCATGATACTGTGACT	30978	GGAGCACACGACACAGTCACA
2333	GAHECLS	16656	GGGGCTCATGAGTGTCTTAGT	30979	GGAGCACACGAATGCCTCAGC
2334	GAHGAYQ	16657	GGGGCGCATGGTGCTTATCAG	30980	GGAGCACACGGAGCATACCAA
2335	GAHSYNV	16658	GGGGCTCATTCTTATAATGTG	30981	GGAGCACACAGCTACAACGTC
2336	GAHTGLS	16659	GGTGCGCATACTGGGTTGTCT	30982	GGAGCACACACAGGACTCAGC
2337	GAHTVRL	16660	GGTGCGCATACTGTTCGGCTT	30983	GGAGCACACACAGTCAGACTC
2338	GAHVAPV	16661	GGGGCGCATGTGGCGCCGGTT	30984	GGAGCACACGTCGCACCAGTC
2339	GALATAT	16662	GGGGCTTTGGCTACTGCTACG	30985	GGAGCACTCGCAACAGCAACA
2340	GALDGTA	16663	GGGGCTTTGGATGGTACTGCT	30986	GGAGCACTCGACGGAACAGCA
2341	GALGFPQ	16664	GGTGCTCTTGGGTTTCCTCAG	30987	GGAGCACTCGGATTCCCACAA
2342	GALGVAH	16665	GGTGCGCTGGGGGTGGCTCAT	30988	GGAGCACTCGGAGTCGCACAC
2343	GALMQKN	16666	GGTGCGCTGATGCAGAAGAAT	30989	GGAGCACTCATGCAAAAAAAC
2344	GALMVSR	16667	GGTGCGCTGATGGTGTCGCGG	30990	GGAGCACTCATGGTCAGCAGA
2345	GALSANQ	16668	GGGGCGCTTAGTGCTAATCAG	30991	GGAGCACTCAGCGCAAACCAA
2346	GALVITS	16669	GGGGCTCTTGTTATTACGTCT	30992	GGAGCACTCGTCATCACAAGC
2347	GAMSINA	16670	GGTGCGATGTCTATTAATGCG	30993	GGAGCAATGAGCATCAACGCA
2348	GANGALR	16671	GGGGCTAATGGTGCGCTGAGG	30994	GGAGCAAACGGAGCACTCAGA
2349	GANIRIA	16672	GGTGCTAATATTCGTATTGCT	30995	GGAGCAAACATCAGAATCGCA
2350	GANRLDN	16673	GGTGCGAATCGGTTGGATAAT	30996	GGAGCAAACAGACTCGACAAC
2351	GAPPLPR	16674	GGTGCTCCTCCTCTGCCGCGT	30997	GGAGCACCACCACTCCCAAGA
2352	GAQLTRM	16675	GGGGCGCAGTTGACGCGTATG	30998	GGAGCACAACTCACAAGAATG
2353	GAQRQLN	16676	GGTGCGCAGCGTCAGCTTAAT	30999	GGAGCACAAAGACAACTCAAC
2354	GARALGL	16677	GGGGCTCGGGCGCTTGGTCTT	31000	GGAGCAAGAGCACTCGGACTC
2355	GARANGG	16678	GGTGCTCGTGCGAATGGTGGT	31001	GGAGCAAGAGCAAACGGAGGA
2356	GAREIPS	16679	GGGGCGAGGGAGATTCCGAGT	31002	GGAGCAAGAGAAATCCCAAGC
2357	GARPDLG	16680	GGTGCTCGTCCTGATCTGGGT	31003	GGAGCAAGACCAGACCTCGGA
2358	GARVLGS	16681	GGTGCTCGGGTTCTTGGTTCT	31004	GGAGCAAGAGTCCTCGGAAGC
2359	GASDTDW	16682	GGGGCGTCGGATACTGATTGG	31005	GGAGCAAGCGACACAGACTGG
2360	GASGTST	16683	GGTGCTTCTGGGACTAGTACT	31006	GGAGCAAGCGGAACAAGCACA
2361	GASIKSS	16684	GGGGCTAGTATTAAGTCTTCT	31007	GGAGCAAGCATCAAAAGCAGC
2362	GASKNPT	16685	GGTGCTAGTAAGAATCCTACG	31008	GGAGCAAGCAAAAACCCAACA
2363	GASLADD	16686	GGTGCTTCTTTGGCTGATGAT	31009	GGAGCAAGCCTCGCAGACGAC
2364	GASLKPV	16687	GGTGCGTCGTTGAAGCCGGTG	31010	GGAGCAAGCCTCAAACCAGTC
2365	GASSASG	16688	GGTGCGTCGAGTGCTAGTGGT	31011	GGAGCAAGCAGCGCAAGCGGA
2366	GASSLKP	16689	GGTGCGTCGAGTTTGAAGCCG	31012	GGAGCAAGCAGCCTCAAACCA
2367	GASSRPV	16690	GGGGCTTCTAGTCGTCCTGTT	31013	GGAGCAAGCAGCAGACCAGTC
2368	GASTRNI	16691	GGGGCTAGTACGCGTAATATT	31014	GGAGCAAGCACAAGAAACATC
2369	GASVNPT	16692	GGTGCTTCGGTGAATCCTACG	31015	GGAGCAAGCGTCAACCCAACA
2370	GATPKTL	16693	GGTGCTACTCCGAAGACTTTG	31016	GGAGCAACACCAAAAACACTC
2371	GATPPST	16694	GGGGCTACGCCGCCTTCGACG	31017	GGAGCAACACCACCAAGCACA
2372	GATQFRE	16695	GGGGCTACGCAGTTTAGGGAG	31018	GGAGCAACACAATTCAGAGAA
2373	GATSQIM	16696	GGGGCGACTAGTCAGATTATG	31019	GGAGCAACAAGCCAAATCATG
2374	GAVRPLM	16697	GGGGCTGTTAGGCCGCTGATG	31020	GGAGCAGTCAGACCACTCATG

2375	GAWKAET	16698	GGGGCTTGGAAGGCTGAGACT	31021	GGAGCATGGAAAGCAGAAACA
2376	GAWLPNA	16699	GGGGCTTGGCTGCCGAATGCT	31022	GGAGCATGGCTCCCAAACGCA
2377	GAWSLPD	16700	GGTGCTTGGTCTTTGCCGGAT	31023	GGAGCATGGAGCCTCCCAGAC
2378	GAYARAT	16701	GGGGCTTATGCGAGGGCTACG	31024	GGAGCATACGCAAGAGCAACA
2379	GAYAYNG	16702	GGGGCGTATGCTTATAATGGG	31025	GGAGCATACGCATACAACGGA
2380	GAYGMSE	16703	GGTGCGTATGGTATGTCTGAG	31026	GGAGCATACGGAATGAGCGAA
2381	GAYRPDL	16704	GGTGCTTATCGGCCGGATCTG	31027	GGAGCATACAGACCAGACCTC
2382	GCSGQQS	16705	GGTTGTTCGGGGCAGCAGTCG	31028	GGATGCAGCGGACAACAAAGC
2383	GCSSLPE	16706	GGTTGTTCGTCTCTTCCGGAG	31029	GGATGCAGCAGCCTCCCAGAA
2384	GCTGYQA	16707	GGGTGTACGGGGTATCAGGCG	31030	GGATGCACAGGATACCAAGCA
2385	GCVGPFS	16708	GGGTGTGTTGGTCCTTTTAGT	31031	GGATGCGTCGGACCATTCAGC
2386	GDAAYKN	16709	GGTGATGCGGCGTATAAGAAT	31032	GGAGACGCAGCATACAAAAAC
2387	GDAFVVG	16710	GGTGATGCGTTTGTGGTGGGT	31033	GGAGACGCATTCGTCGTCGGA
2388	GDATDRM	16711	GGGGATGCTACTGATCGGATG	31034	GGAGACGCAACAGACAGAATG
2389	GDFGMKL	16712	GGTGATTTTGGTATGAAGTTG	31035	GGAGACTTCGGAATGAAACTC
2390	GDGTRGA	16713	GGTGATGGTACGCGGGGTGCG	31036	GGAGACGGAACAAGAGGAGCA
2391	GDGVYPA	16714	GGTGATGGTGTTTATCCGGCT	31037	GGAGACGGAGTCTACCCAGCA
2392	GDHKSGA	16715	GGTGATCATAAGAGTGGTGCG	31038	GGAGACCACAAAAGCGGAGCA
2393	GDKVRTL	16716	GGGGATAAGGTTAGGACGCTT	31039	GGAGACAAAGTCAGAACACTC
2394	GDLHIPV	16717	GGTGATCTTCATATTCCGGTG	31040	GGAGACCTCCACATCCCAGTC
2395	GDLNPVP	16718	GGGGATTTGAATCCGGTGCCG	31041	GGAGACCTCAACCCAGTCCCA
2396	GDLYYKA	16719	GGTGATCTTTATTATAAGGCG	31042	GGAGACCTCTACTACAAAGCA
2397	GDMLNVI	16720	GGTGATATGCTTAATGTGATT	31043	GGAGACATGCTCAACGTCATC
2398	GDPNPAE	16721	GGGGATCCGAATCCTGCTGAG	31044	GGAGACCCAAACCCAGCAGAA
2399	GDPVHQS	16722	GGTGATCCTGTTCATCAGTCG	31045	GGAGACCCAGTCCACCAAAGC
2400	GDRDGSW	16723	GGTGATCGTGATGGTTCTTGG	31046	GGAGACAGAGACGGAAGCTGG
2401	GDRMPRS	16724	GGTGATAGGATGCCGAGGTCG	31047	GGAGACAGAATGCCAAGAAGC
2402	GDRSTSH	16725	GGGGATAGGAGTACTTCGCAT	31048	GGAGACAGAAGCACAAGCCAC
2403	GDRTSLR	16726	GGGGATCGTACGTCGCTGCGT	31049	GGAGACAGAACAAGCCTCAGA
2404	GDRVVGV	16727	GGTGATCGGGTTGTTGGTGTG	31050	GGAGACAGAGTCGTCGGAGTC
2405	GDSFPMS	16728	GGGGATTCTTTTCCGATGAGT	31051	GGAGACAGCTTCCCAATGAGC
2406	GDSQLYY	16729	GGTGATTCTCAGCTGTATTAT	31052	GGAGACAGCCAACTCTACTAC
2407	GDSSLHS	16730	GGTGATTCGTCGCTTCATAGT	31053	GGAGACAGCAGCCTCCACAGC
2408	GDTHLIG	16731	GGTGATACGCATCTGATTGGT	31054	GGAGACACACACCTCATCGGA
2409	GDTLKAP	16732	GGTGATACGCTGAAGGCTCCT	31055	GGAGACACACTCAAAGCACCA
2410	GDTRPSL	16733	GGGGATACTCGTCCTAGTTTG	31056	GGAGACACAAGACCAAGCCTC
2411	GDVITTH	16734	GGGGATGTGATTACGACTCAT	31057	GGAGACGTCATCACAACACAC
2412	GDVSVYD	16735	GGTGATGTGTCGGTTTATGAT	31058	GGAGACGTCAGCGTCTACGAC
2413	GEDAFLR	16736	GGTGAGGATGCTTTTTTGCGT	31059	GGAGAAGACGCATTCCTCAGA
2414	GEDGFSY	16737	GGTGAGGATGGTTTTTCTTAT	31060	GGAGAAGACGGATTCAGCTAC
2415	GEDHSPH	16738	GGGGAGGATCATTCGCCGCAT	31061	GGAGAAGACCACAGCCCACAC
2416	GEGSYPR	16739	GGGGAGGGGTCTTATCCTCGG	31062	GGAGAAGGAAGCTACCCAAGA
2417	GEGTYQA	16740	GGTGAGGGTACTTATCAGGCG	31063	GGAGAAGGAACATACCAAGCA
2418	GEHKANS	16741	GGTGAGCATAAGGCGAATTCT	31064	GGAGAACACAAAGCAAACAGC
2419	GEKLRAY	16742	GGGGAGAAGCTTCGTGCGTAT	31065	GGAGAAAAACTCAGAGCATAC

2420	GEKSIPP	16743	GGGGAGAAGTCTATTCCGCCT	31066	GGAGAAAAAAGCATCCCACCA
2421	GEKSLVV	16744	GGTGAGAAGAGTCTGGTTGTT	31067	GGAGAAAAAAGCCTCGTCGTC
2422	GELFLSS	16745	GGTGAGCTGTTTCTGTCGTCG	31068	GGAGAACTCTTCCTCAGCAGC
2423	GENPLPV	16746	GGTGAGAATCCGCTGCCGGTT	31069	GGAGAAAACCCACTCCCAGTC
2424	GEPFMRA	16747	GGGGAGCCGTTTATGCGGGCG	31070	GGAGAACCATTCATGAGAGCA
2425	GEPKHHS	16748	GGGGAGCCTAAGCATCATTCT	31071	GGAGAACCAAAACACCACAGC
2426	GEPVDTW	16749	GGGGAGCCTGTGGATACTTGG	31072	GGAGAACCAGTCGACACATGG
2427	GEPVLGA	16750	GGTGAGCCGGTGCTGGGGGCG	31073	GGAGAACCAGTCCTCGGAGCA
2428	GERFREW	16751	GGGGAGCGTTTTCGTGAGTGG	31074	GGAGAAAGATTCAGAGAATGG
2429	GERMKID	16752	GGTGAGCGGATGAAGATTGAT	31075	GGAGAAAGAATGAAAATCGAC
2430	GERSLNM	16753	GGGGAGAGGTCGTTGAATATG	31076	GGAGAAAGAAGCCTCAACATG
2431	GERSPPE	16754	GGGGAGCGGTCGCCTCCTGAG	31077	GGAGAAAGAAGCCCACCAGAA
2432	GESPANL	16755	GGGGAGTCGCCTGCGAATCTG	31078	GGAGAAAGCCCAGCAAACCTC
2433	GETPAHA	16756	GGGGAGACGCCTGCTCATGCT	31079	GGAGAAACACCAGCACACGCA
2434	GETRHVG	16757	GGGGAGACTAGGCATGTGGGG	31080	GGAGAAACAAGACACGTCGGA
2435	GETSAMQ	16758	GGTGAGACTAGTGCGATGCAG	31081	GGAGAAACAAGCGCAATGCAA
2436	GETTKMR	16759	GGGGAGACGACGAAGATGCGT	31082	GGAGAAACAACAAAAATGAGA
2437	GEVAMLY	16760	GGTGAGGTTGCGATGCTGTAT	31083	GGAGAAGTCGCAATGCTCTAC
2438	GEVTIMS	16761	GGTGAGGTGACGATTATGTCT	31084	GGAGAAGTCACAATCATGAGC
2439	GEVVNTM	16762	GGTGAGGTTGTTAATACGATG	31085	GGAGAAGTCGTCAACACAATG
2440	GFDAGKS	16763	GGTTTTGATGCTGGTAAGTCG	31086	GGATTCGACGCAGGAAAAAGC
2441	GFDIASG	16764	GGGTTTGATATTGCGAGTGGG	31087	GGATTCGACATCGCAAGCGGA
2442	GFDVKMS	16765	GGGTTTGATGTGAAGATGAGT	31088	GGATTCGACGTCAAAATGAGC
2443	GFEVQLI	16766	GGGTTTGAGGTGCAGTTGATT	31089	GGATTCGAAGTCCAACTCATC
2444	GFFAQVP	16767	GGTTTTTTTGCGCAGGTGCCG	31090	GGATTCTTCGCACAAGTCCCA
2445	GFHNAAP	16768	GGGTTTCATAATGCGGCGCCT	31091	GGATTCCACAACGCAGCACCA
2446	GFISPSA	16769	GGTTTTATTAGTCCTTCTGCT	31092	GGATTCATCAGCCCAAGCGCA
2447	GFKNALP	16770	GGGTTTAAGAATGCTCTTCCG	31093	GGATTCAAAAACGCACTCCCA
2448	GFNALTG	16771	GGGTTTAATGCGTTGACTGGT	31094	GGATTCAACGCACTCACAGGA
2449	GFNPSLV	16772	GGGTTTAATCCTAGTTTGGTT	31095	GGATTCAACCCAAGCCTCGTC
2450	GFNVASG	16773	GGGTTTAATGTGGCTAGTGGG	31096	GGATTCAACGTCGCAAGCGGA
2451	GFNVGGP	16774	GGTTTTAATGTGGGTGGGCCT	31097	GGATTCAACGTCGGAGGACCA
2452	GFPGPQF	16775	GGGTTTCCTGGTCCTCAGTTT	31098	GGATTCCCAGGACCACAATTC
2453	GFSGTPY	16776	GGTTTTAGTGGGACTCCGTAT	31099	GGATTCAGCGGAACACCATAC
2454	GFSHISL	16777	GGGTTTTCGCATATTTCGTTG	31100	GGATTCAGCCACATCAGCCTC
2455	GFSIRST	16778	GGTTTTTCTATTCGTTCGACG	31101	GGATTCAGCATCAGAAGCACA
2456	GFSSLSS	16779	GGTTTTTCTTCGCTTAGTAGT	31102	GGATTCAGCAGCCTCAGCAGC
2457	GFTQSQM	16780	GGTTTTACTCAGTCGCAGATG	31103	GGATTCACACAAAGCCAAATG
2458	GGAAREL	16781	GGGGGTGCGGCTCGGGAGCTG	31104	GGAGGAGCAGCAAGAGAACTC
2459	GGAATSV	16782	GGGGGTGCGGCTACTTCGGTG	31105	GGAGGAGCAGCAACAAGCGTC
2460	GGAGART	16783	GGGGGTGCTGGTGCTCGTACT	31106	GGAGGAGCAGGAGCAAGAACA
2461	GGARSSM	16784	GGTGGTGCTCGGTCTAGTATG	31107	GGAGGAGCAAGAAGCAGCATG
2462	GGAVHTV	16785	GGTGGGGCTGTTCATACGGTT	31108	GGAGGAGCAGTCCACACAGTC
2463	GGDSGAE	16786	GGGGGTGATAGTGGTGCGGAG	31109	GGAGGAGACAGCGGAGCAGAA
2464	GGENVYI	16787	GGTGGGGAGAATGTGTATATT	31110	GGAGGAGAAAACGTCTACATC

2465	GGFAHQS	16788	GGGGGTTTTGCTCATCAGTCT	31111	GGAGGATTCGCACACCAAAGC
2466	GGFNGAN	16789	GGTGGGTTTAATGGGGCGAAT	31112	GGAGGATTCAACGGAGCAAAC
2467	GGGLTMT	16790	GGTGGTGGGCTTACTATGACG	31113	GGAGGAGGACTCACAATGACA
2468	GGGPALP	16791	GGGGGTGGTCCTGCTTTGCCT	31114	GGAGGAGGACCAGCACTCCCA
2469	GGGVNKP	16792	GGTGGTGGTGTGAATAAGCCG	31115	GGAGGAGGAGTCAACAAACCA
2470	GGHMRDG	16793	GGTGGGCATATGAGGGATGGT	31116	GGAGGACACATGAGAGACGGA
2471	GGIESAV	16794	GGGGGTATTGAGAGTGCTGTG	31117	GGAGGAATCGAAAGCGCAGTC
2472	GGIQSTG	16795	GGTGGGATTCAGTCGACGGGT	31118	GGAGGAATCCAAAGCACAGGA
2473	GGKDRPE	16796	GGTGGTAAGGATCGGCCTGAG	31119	GGAGGAAAAGACAGACCAGAA
2474	GGKQPQA	16797	GGTGGGAAGCAGCCTCAGGCT	31120	GGAGGAAAACAACCACAAGCA
2475	GGKVATG	16798	GGTGGGAAGGTTGCTACGGGG	31121	GGAGGAAAAGTCGCAACAGGA
2476	GGLNRNP	16799	GGGGGTCTGAATCGGAATCCG	31122	GGAGGACTCAACAGAAACCCA
2477	GGLPSPA	16800	GGGGGGTTGCCGAGTCCTGCG	31123	GGAGGACTCCCAAGCCCAGCA
2478	GGLSKSL	16801	GGTGGTCTTTCTAAGTCTTTG	31124	GGAGGACTCAGCAAAAGCCTC
2479	GGMAPGP	16802	GGTGGTATGGCGCCTGGGCCT	31125	GGAGGAATGGCACCAGGACCA
2480	GGPAYVG	16803	GGTGGGCCTGCTTATGTGGGG	31126	GGAGGACCAGCATACGTCGGA
2481	GGPGNNP	16804	GGTGGTCCGGGTAATAATCCG	31127	GGAGGACCAGGAAACAACCCA
2482	GGPLPKS	16805	GGTGGGCCGTTGCCTAAGTCT	31128	GGAGGACCACTCCCAAAAAGC
2483	GGPLTGP	16806	GGGGGTCCGCTTACTGGTCCG	31129	GGAGGACCACTCACAGGACCA
2484	GGPRVAP	16807	GGTGGTCCGAGGGTTGCTCCT	31130	GGAGGACCAAGAGTCGCACCA
2485	GGPYGPA	16808	GGTGGTCCGTATGGTCCGGCG	31131	GGAGGACCATACGGACCAGCA
2486	GGQAGKT	16809	GGTGGGCAGGCTGGTAAGACG	31132	GGAGGACAAGCAGGAAAAACA
2487	GGQHLAP	16810	GGGGGTCAGCATCTGGCGCCG	31133	GGAGGACAACACCTCGCACCA
2488	GGQSCRE	16811	GGGGGGCAGTCGTGTAGGGAG	31134	GGAGGACAAAGCTGCAGAGAA
2489	GGRLAVE	16812	GGTGGTCGTTTGGCGGTTGAG	31135	GGAGGAAGACTCGCAGTCGAA
2490	GGRLQQG	16813	GGGGGGCGGTTGCAGCAGGGT	31136	GGAGGAAGACTCCAACAAGGA
2491	GGRPDPE	16814	GGTGGTCGGCCGGATCCTGAG	31137	GGAGGAAGACCAGACCCAGAA
2492	GGRPTIT	16815	GGTGGTAGGCCTACGATTACT	31138	GGAGGAAGACCAACAATCACA
2493	GGRVVYS	16816	GGTGGTCGGGTGGTGTATTCG	31139	GGAGGAAGAGTCGTCTACAGC
2494	GGRYSEL	16817	GGTGGTCGTTATAGTGAGCTG	31140	GGAGGAAGATACAGCGAACTC
2495	GGSGLAG	16818	GGTGGTTCGGGGTTGGCGGGG	31141	GGAGGAAGCGGACTCGCAGGA
2496	GGSMDSL	16819	GGGGGTTCGATGGATTCGCTT	31142	GGAGGAAGCATGGACAGCCTC
2497	GGSVRTL	16820	GGTGGTTCGGTGAGGACTCTG	31143	GGAGGAAGCGTCAGAACACTC
2498	GGTSRSP	16821	GGTGGGACGAGTCGGAGTCCG	31144	GGAGGAACAAGCAGAAGCCCA
2499	GGTTNLF	16822	GGTGGGACTACGAATCTGTTT	31145	GGAGGAACAACAAACCTCTTC
2500	GGVAYIA	16823	GGGGGTGTTGCGTATATTGCG	31146	GGAGGAGTCGCATACATCGCA
2501	GGVGKPA	16824	GGGGGGGTTGGTAAGCCTGCG	31147	GGAGGAGTCGGAAAACCAGCA
2502	GGVNAMR	16825	GGTGGTGTTAATGCTATGAGG	31148	GGAGGAGTCAACGCAATGAGA
2503	GGWSSAP	16826	GGGGGTTGGAGTTCTGCGCCG	31149	GGAGGATGGAGCAGCGCACCA
2504	GGYESNN	16827	GGGGGTTATGAGTCTAATAAT	31150	GGAGGATACGAAAGCAACAAC
2505	GGYSMGH	16828	GGTGGTTATTCGATGGGTCAT	31151	GGAGGATACAGCATGGGACAC
2506	GHAIQLL	16829	GGGCATGCTATTCAGCTGCTG	31152	GGACACGCAATCCAACTCCTC
2507	GHAKHNV	16830	GGTCATGCGAAGCATAATGTG	31153	GGACACGCAAAACACAACGTC
2508	GHAPHMI	16831	GGTCATGCTCCGCATATGATT	31154	GGACACGCACCACACATGATC
2509	GHCTSKN	16832	GGGCATTGTACGAGTAAGAAT	31155	GGACACTGCACAAGCAAAAAC

2510	GHDLKPV	16833	GGTCATGATCTTAAGCCGGTG	31156	GGACACGACCTCAAACCAGTC
2511	GHETRQE	16834	GGTCATGAGACTCGTCAGGAG	31157	GGACACGAAACAAGACAAGAA
2512	GHGLPRL	16835	GGGCATGGGCTTCCTAGGCTG	31158	GGACACGGACTCCCAAGACTC
2513	GHGPFVG	16836	GGGCATGGGCCTTTTGTTGGG	31159	GGACACGGACCATTCGTCGGA
2514	GHGQNPG	16837	GGGCATGGTCAGAATCCTGGG	31160	GGACACGGACAAAACCCAGGA
2515	GHHQPDQ	16838	GGTCATCATCAGCCGGATCAG	31161	GGACACCACCAACCAGACCAA
2516	GHKARPD	16839	GGTCATAAGGCTAGGCCTGAT	31162	GGACACAAAGCAAGACCAGAC
2517	GHKDESL	16840	GGTCATAAGGATGAGTCTCTG	31163	GGACACAAAGACGAAAGCCTC
2518	GHLALHS	16841	GGGCATTTGGCTCTGCATTCT	31164	GGACACCTCGCACTCCACAGC
2519	GHLQVNT	16842	GGTCATTTGCAGGTGAATACT	31165	GGACACCTCCAAGTCAACACA
2520	GHLSPSM	16843	GGGCATCTTTCGCCTAGTATG	31166	GGACACCTCAGCCCAAGCATG
2521	GHMAPVH	16844	GGTCATATGGCTCCTGTGCAT	31167	GGACACATGGCACCAGTCCAC
2522	GHMSKTA	16845	GGGCATATGTCTAAGACGGCG	31168	GGACACATGAGCAAAACAGCA
2523	GHQGSDH	16846	GGGCATCAGGGGTCTGATCAT	31169	GGACACCAAGGAAGCGACCAC
2524	GHQGVLL	16847	GGGCATCAGGGGGTTCTTCTG	31170	GGACACCAAGGAGTCCTCCTC
2525	GHQTYPS	16848	GGGCATCAGACGTATCCTTCT	31171	GGACACCAAACATACCCAAGC
2526	GHRSDQS	16849	GGGCATCGTTCGGATCAGTCT	31172	GGACACAGAAGCGACCAAAGC
2527	GHSAGAS	16850	GGTCATTCGGCTGGGGCGTCT	31173	GGACACAGCGCAGGAGCAAGC
2528	GHSGDRA	16851	GGTCATTCGGGGGATCGGGCT	31174	GGACACAGCGGAGACAGAGCA
2529	GHSHNAY	16852	GGTCATTCTCATAATGCGTAT	31175	GGACACAGCCACAACGCATAC
2530	GHSSASN	16853	GGTCATAGTTCTGCTTCTAAT	31176	GGACACAGCAGCGCAAGCAAC
2531	GHSVTHP	16854	GGGCATTCGGTTACTCATCCG	31177	GGACACAGCGTCACACACCCA
2532	GHSVVKS	16855	GGTCATTCTGTTGTGAAGTCG	31178	GGACACAGCGTCGTCAAAAGC
2533	GHSYPQA	16856	GGTCATTCGTATCCGCAGGCG	31179	GGACACAGCTACCCACAAGCA
2534	GHTLKPP	16857	GGTCATACTCTGAAGCCTCCT	31180	GGACACACACTCAAACCACCA
2535	GHVEPRY	16858	GGTCATGTTGAGCCTCGGTAT	31181	GGACACGTCGAACCAAGATAC
2536	GHVGSRV	16859	GGTCATGTGGGTAGTCGTGTT	31182	GGACACGTCGGAAGCAGAGTC
2537	GHVLVTP	16860	GGTCATGTTCTTGTTACTCCG	31183	GGACACGTCCTCGTCACACCA
2538	GHVSVNT	16861	GGGCATGTTTCTGTTAATACT	31184	GGACACGTCAGCGTCAACACA
2539	GIADLAV	16862	GGTATTGCGGATTTGGCTGTT	31185	GGAATCGCAGACCTCGCAGTC
2540	GIAGGRP	16863	GGTATTGCTGGGGGGAGGCCT	31186	GGAATCGCAGGAGGAAGACCA
2541	GIAGRAT	16864	GGGATTGCTGGGCGTGCGACG	31187	GGAATCGCAGGAAGAGCAACA
2542	GIASELP	16865	GGGATTGCTAGTGAGCTGCCG	31188	GGAATCGCAAGCGAACTCCCA
2543	GIAYMTP	16866	GGTATTGCTTATATGACGCCT	31189	GGAATCGCATACATGACACCA
2544	GIDLHTA	16867	GGTATTGATCTTCATACTGCG	31190	GGAATCGACCTCCACACAGCA
2545	GIDNGTV	16868	GGTATTGATAATGGGACTGTT	31191	GGAATCGACAACGGAACAGTC
2546	GIEIDTQ	16869	GGGATTGAGATTGATACGCAG	31192	GGAATCGAAATCGACACACAA
2547	GIERNSI	16870	GGTATTGAGAGGAATTCTATT	31193	GGAATCGAAAGAAACAGCATC
2548	GIFAATS	16871	GGGATTTTTGCTGCTACTTCT	31194	GGAATCTTCGCAGCAACAAGC
2549	GIGSDRD	16872	GGTATTGGTTCGGATCGTGAT	31195	GGAATCGGAAGCGACAGAGAC
2550	GIGTHNP	16873	GGTATTGGTACGCATAATCCG	31196	GGAATCGGAACACACAACCCA
2551	GIHIKYA	16874	GGTATTCATATTAAGTATGCG	31197	GGAATCCACATCAAATACGCA
2552	GIKMTIS	16875	GGGATTAAGATGACTATTAGT	31198	GGAATCAAAATGACAATCAGC
2553	GINWQSP	16876	GGTATTAATTGGCAGTCTCCT	31199	GGAATCAACTGGCAAAGCCCA
2554	GIPRGAT	16877	GGTATTCCTAGGGGGGCGACT	31200	GGAATCCCAAGAGGAGCAACA

2555	GIPSNSR	16878	GGGATTCCTTCTAATTCTCGT	31201	GGAATCCCAAGCAACAGCAGA
2556	GIPVRGE	16879	GGGATTCCGGTTAGGGGGGAG	31202	GGAATCCCAGTCAGAGGAGAA
2557	GIQTFAP	16880	GGGATTCAGACGTTTGCGCCT	31203	GGAATCCAAACATTCGCACCA
2558	GIQTVMS	16881	GGTATTCAGACTGTGATGTCG	31204	GGAATCCAAACAGTCATGAGC
2559	GIREHPY	16882	GGTATTCGTGAGCATCCGTAT	31205	GGAATCAGAGAACACCCATAC
2560	GIRILEA	16883	GGTATTCGGATTCTGGAGGCG	31206	GGAATCAGAATCCTCGAAGCA
2561	GIRMPAN	16884	GGTATTCGTATGCCGGCTAAT	31207	GGAATCAGAATGCCAGCAAAC
2562	GISAGIL	16885	GGGATTTCTGCTGGTATTCTG	31208	GGAATCAGCGCAGGAATCCTC
2563	GISGSTV	16886	GGGATTTCTGGGTCGACGGTG	31209	GGAATCAGCGGAAGCACAGTC
2564	GISLSSA	16887	GGGATTTCTTTGTCGAGTGCT	31210	GGAATCAGCCTCAGCAGCGCA
2565	GISRTVD	16888	GGGATTTCTCGGACGGTTGAT	31211	GGAATCAGCAGAACAGTCGAC
2566	GISVDAL	16889	GGTATTTCTGTTGATGCGCTT	31212	GGAATCAGCGTCGACGCACTC
2567	GITTSQR	16890	GGGATTACTACGAGTCAGCGT	31213	GGAATCACAACAAGCCAAAGA
2568	GIVTNNT	16891	GGTATTGTGACTAATAATACT	31214	GGAATCGTCACAAACAACACA
2569	GIVVTGP	16892	GGTATTGTGGTTACGGGTCCG	31215	GGAATCGTCGTCACAGGACCA
2570	GKDRLLA	16893	GGGAAGGATAGGTTGTTGGCT	31216	GGAAAAGACAGACTCCTCGCA
2571	GKEFSYT	16894	GGTAAGGAGTTTTCTTATACG	31217	GGAAAAGAATTCAGCTACACA
2572	GKFLPQT	16895	GGTAAGTTTTTGCCTCAGACT	31218	GGAAAATTCCTCCCACAAACA
2573	GKGFDSP	16896	GGTAAGGGGTTTGATAGTCCG	31219	GGAAAAGGATTCGACAGCCCA
2574	GKGLTAT	16897	GGGAAGGGTCTGACTGCTACT	31220	GGAAAAGGACTCACAGCAACA
2575	GKHVKEM	16898	GGGAAGCATGTGAAGGAGATG	31221	GGAAAACACGTCAAAGAAATG
2576	GKISSSL	16899	GGTAAGATTTCGTCGAGTCTG	31222	GGAAAAATCAGCAGCAGCCTC
2577	GKLELAP	16900	GGTAAGCTTGAGCTTGCGCCG	31223	GGAAAACTCGAACTCGCACCA
2578	GKLLMPQ	16901	GGGAAGCTGCTTATGCCTCAG	31224	GGAAAACTCCTCATGCCACAA
2579	GKLTSTL	16902	GGGAAGCTGACGTCGACTCTT	31225	GGAAAACTCACAAGCACACTC
2580	GKLVSYD	16903	GGGAAGTTGGTTTCTTATGAT	31226	GGAAAACTCGTCAGCTACGAC
2581	GKMSVGN	16904	GGGAAGATGTCGGTTGGGAAT	31227	GGAAAAATGAGCGTCGGAAAC
2582	GKNATFP	16905	GGTAAGAATGCGACTTTTCCT	31228	GGAAAAAACGCAACATTCCCA
2583	GKNGDRT	16906	GGTAAGAATGGGGATCGTACT	31229	GGAAAAAACGGAGACAGAACA
2584	GKPAGAI	16907	GGTAAGCCTGCTGGTGCTATT	31230	GGAAAACCAGCAGGAGCAATC
2585	GKPASPY	16908	GGTAAGCCTGCTTCTCCTTAT	31231	GGAAAACCAGCAAGCCCATAC
2586	GKQNQYT	16909	GGTAAGCAGAATCAGTATACT	31232	GGAAAACAAAACCAATACACA
2587	GKQTPPS	16910	GGTAAGCAGACGCCTCCGTCT	31233	GGAAAACAAACACCACCAAGC
2588	GKRAPVD	16911	GGGAAGCGTGCTCCTGTTGAT	31234	GGAAAAAGAGCACCAGTCGAC
2589	GKSPGPL	16912	GGTAAGTCGCCTGGGCCGTTG	31235	GGAAAAAGCCCAGGACCACTC
2590	GKSQSGL	16913	GGGAAGTCTCAGTCTGGTCTG	31236	GGAAAAAGCCAAAGCGGACTC
2591	GKSVTVS	16914	GGTAAGTCTGTTACGGTGTCG	31237	GGAAAAAGCGTCACAGTCAGC
2592	GKTEERP	16915	GGGAAGACTGAGGAGCGTCCG	31238	GGAAAAACAGAAGAAAGACCA
2593	GKTKPDY	16916	GGGAAGACTAAGCCGGATTAT	31239	GGAAAAACAAAACCAGACTAC
2594	GKTVDWG	16917	GGGAAGACTGTTGATTGGGGT	31240	GGAAAAACAGTCGACTGGGGA
2595	GKTVNIV	16918	GGTAAGACTGTGAATATTGTT	31241	GGAAAAACAGTCAACATCGTC
2596	GKTVVSV	16919	GGTAAGACGGTGGTGAGTGTG	31242	GGAAAAACAGTCGTCAGCGTC
2597	GKVEFAI	16920	GGTAAGGTTGAGTTTGCGATT	31243	GGAAAAGTCGAATTCGCAATC
2598	GKVHEGM	16921	GGTAAGGTGCATGAGGGTATG	31244	GGAAAAGTCCACGAAGGAATG
2599	GKVPTIS	16922	GGGAAGGTGCCGACGATTAGT	31245	GGAAAAGTCCCAACAATCAGC

2600	GKVVQTP	16923	GGTAAGGTTGTTCAGACGCCG	31246	GGAAAAGTCGTCCAAACACCA
2601	GLAAKAD	16924	GGTCTTGCGGCTAAGGCGGAT	31247	GGACTCGCAGCAAAAGCAGAC
2602	GLAATVP	16925	GGGTTGGCTGCGACTGTTCCG	31248	GGACTCGCAGCAACAGTCCCA
2603	GLAHQGT	16926	GGGCTTGCTCATCAGGGTACT	31249	GGACTCGCACACCAAGGAACA
2604	GLAKYAE	16927	GGTTTGGCTAAGTATGCGGAG	31250	GGACTCGCAAAATACGCAGAA
2605	GLALSSP	16928	GGGCTTGCTCTTTCTTCTCCG	31251	GGACTCGCACTCAGCAGCCCA
2606	GLANSPS	16929	GGTCTGGCGAATTCTCCGTCT	31252	GGACTCGCAAACAGCCCAAGC
2607	GLAVGTR	16930	GGGTTGGCGGTTGGTACGCGT	31253	GGACTCGCAGTCGGAACAAGA
2608	GLEHHVT	16931	GGTCTTGAGCATCATGTTACG	31254	GGACTCGAACACCACGTCACA
2609	GLGAPER	16932	GGTTTGGGTGCTCCTGAGCGT	31255	GGACTCGGAGCACCAGAAAGA
2610	GLGLVTG	16933	GGGCTGGGTCTTGTGACGGGG	31256	GGACTCGGACTCGTCACAGGA
2611	GLGMPQS	16934	GGTTTGGGTATGCCGCAGTCT	31257	GGACTCGGAATGCCACAAAGC
2612	GLGSTLG	16935	GGGTTGGGTTCTACTCTGGGT	31258	GGACTCGGAAGCACACTCGGA
2613	GLGTASA	16936	GGGTTGGGTACGGCTTCGGCG	31259	GGACTCGGAACAGCAAGCGCA
2614	GLGTMVI	16937	GGTCTGGGGACTATGGTTATT	31260	GGACTCGGAACAATGGTCATC
2615	GLGTPSP	16938	GGTTTGGGTACGCCGAGTCCG	31261	GGACTCGGAACACCAAGCCCA
2616	GLGTTGR	16939	GGGCTGGGGACGACGGGTCGG	31262	GGACTCGGAACAACAGGAAGA
2617	GLHDPPV	16940	GGTCTTCATGATCCGCCTGTG	31263	GGACTCCACGACCCACCAGTC
2618	GLHLMDV	16941	GGTCTTCATCTGATGGATGTG	31264	GGACTCCACCTCATGGACGTC
2619	GLISQTD	16942	GGTCTTATTTCGCAGACTGAT	31265	GGACTCATCAGCCAAACAGAC
2620	GLKAVDG	16943	GGTCTTAAGGCTGTTGATGGG	31266	GGACTCAAAGCAGTCGACGGA
2621	GLKITTE	16944	GGGCTGAAGATTACTACGGAG	31267	GGACTCAAAATCACAACAGAA
2622	GLKNPQM	16945	GGGTTGAAGAATCCTCAGATG	31268	GGACTCAAAAACCCACAAATG
2623	GLKSTIN	16946	GGTCTGAAGAGTACTATTAAT	31269	GGACTCAAAAGCACAATCAAC
2624	GLLGEKS	16947	GGTTTGCTGGGTGAGAAGTCT	31270	GGACTCCTCGGAGAAAAAAGC
2625	GLLGRYE	16948	GGGCTGCTTGGTAGGTATGAG	31271	GGACTCCTCGGAAGATACGAA
2626	GLLGTKL	16949	GGGCTTCTTGGGACGAAGCTG	31272	GGACTCCTCGGAACAAAACTC
2627	GLLSRAE	16950	GGGTTGCTGTCGCGGGCGGAG	31273	GGACTCCTCAGCAGAGCAGAA
2628	GLLVLYP	16951	GGTCTTTTGGTTCTTTATCCT	31274	GGACTCCTCGTCCTCTACCCA
2629	GLMAHRN	16952	GGTTTGATGGCTCATCGTAAT	31275	GGACTCATGGCACACAGAAAC
2630	GLMLMNG	16953	GGGCTTATGCTGATGAATGGT	31276	GGACTCATGCTCATGAACGGA
2631	GLNPGTH	16954	GGGCTTAATCCGGGGACGCAT	31277	GGACTCAACCCAGGAACACAC
2632	GLNRFSG	16955	GGGTTGAATCGGTTTTCTGGT	31278	GGACTCAACAGATTCAGCGGA
2633	GLNVTKF	16956	GGGTTGAATGTTACGAAGTTT	31279	GGACTCAACGTCACAAAATTC
2634	GLPGELA	16957	GGTCTTCCTGGGGAGCTTGCG	31280	GGACTCCCAGGAGAACTCGCA
2635	GLPGGRS	16958	GGGCTGCCGGGTGGGCGGTCG	31281	GGACTCCCAGGAGGAAGAAGC
2636	GLPGRHA	16959	GGTTTGCCTGGGCGGCATGCG	31282	GGACTCCCAGGAAGACACGCA
2637	GLPHRYE	16960	GGTTTGCCTCATAGGTATGAG	31283	GGACTCCCACACAGATACGAA
2638	GLPIPSL	16961	GGGTTGCCTATTCCGAGTCTT	31284	GGACTCCCAATCCCAAGCCTC
2639	GLPKHPP	16962	GGGTTGCCGAAGCATCCTCCT	31285	GGACTCCCAAAACACCCACCA
2640	GLPMATA	16963	GGGTTGCCGATGGCTACGGCG	31286	GGACTCCCAATGGCAACAGCA
2641	GLPNREP	16964	GGTTTGCCTAATCGGGAGCCG	31287	GGACTCCCAAACAGAGAACCA
2642	GLPPASK	16965	GGGTTGCCTCCTGCGTCTAAG	31288	GGACTCCCACCAGCAAGCAAA
2643	GLPQASH	16966	GGTCTTCCGCAGGCGTCTCAT	31289	GGACTCCCACAAGCAAGCCAC
2644	GLPQHKQ	16967	GGTTTGCCGCAGCATAAGCAG	31290	GGACTCCCACAACACAAACAA

2645	GLPSNLT	16968	GGTCTGCCGAGTAATTTGACG	31291	GGACTCCCAAGCAACCTCACA
2646	GLPTEDR	16969	GGGTTGCCGACTGAGGATCGG	31292	GGACTCCCAACAGAAGACAGA
2647	GLPYGNS	16970	GGGCTTCCTTATGGGAATAGT	31293	GGACTCCCATACGGAAACAGC
2648	GLQQEVR	16971	GGTTTGCAGCAGGAGGTTCGT	31294	GGACTCCAACAAGAAGTCAGA
2649	GLQSTGL	16972	GGGCTGCAGTCTACGGGGCTT	31295	GGACTCCAAAGCACAGGACTC
2650	GLREPVA	16973	GGTTTGAGGGAGCCGGTTGCT	31296	GGACTCAGAGAACCAGTCGCA
2651	GLRFTVE	16974	GGTCTGAGGTTTACTGTTGAG	31297	GGACTCAGATTCACAGTCGAA
2652	GLRNLGS	16975	GGGTTGCGTAATTTGGGGTCT	31298	GGACTCAGAAACCTCGGAAGC
2653	GLRNQEL	16976	GGGTTGAGGAATCAGGAGTTG	31299	GGACTCAGAAACCAAGAACTC
2654	GLRPGQD	16977	GGTCTGCGTCCTGGTCAGGAT	31300	GGACTCAGACCAGGACAAGAC
2655	GLRSLSA	16978	GGGCTTCGTTCTCTGTCGGCG	31301	GGACTCAGAAGCCTCAGCGCA
2656	GLRSMPE	16979	GGGCTTCGTTCGATGCCGGAG	31302	GGACTCAGAAGCATGCCAGAA
2657	GLRSSYA	16980	GGTTTGCGGTCGAGTTATGCT	31303	GGACTCAGAAGCAGCTACGCA
2658	GLRTASN	16981	GGGTTGCGGACTGCGTCGAAT	31304	GGACTCAGAACAGCAAGCAAC
2659	GLRTDML	16982	GGGTTGCGGACGGATATGCTT	31305	GGACTCAGAACAGACATGCTC
2660	GLSAAAT	16983	GGGCTTAGTGCTGCGGCGACG	31306	GGACTCAGCGCAGCAGCAACA
2661	GLSALAS	16984	GGGCTGTCGGCGTTGGCGTCG	31307	GGACTCAGCGCACTCGCAAGC
2662	GLSAYIP	16985	GGGCTTTCGGCGTATATTCCT	31308	GGACTCAGCGCATACATCCCA
2663	GLSHSAL	16986	GGGCTTTCGCATTCTGCGTTG	31309	GGACTCAGCCACAGCGCACTC
2664	GLSLDDY	16987	GGGTTGTCTCTTGATGATTAT	31310	GGACTCAGCCTCGACGACTAC
2665	GLSLKYG	16988	GGGCTGTCTCTTAAGTATGGG	31311	GGACTCAGCCTCAAATACGGA
2666	GLSLLRN	16989	GGTCTTTCGCTGCTGCGTAAT	31312	GGACTCAGCCTCCTCAGAAAC
2667	GLSMPLP	16990	GGGCTGTCTATGCCGCTGCCT	31313	GGACTCAGCATGCCACTCCCA
2668	GLSPRQT	16991	GGTCTTAGTCCTCGTCAGACG	31314	GGACTCAGCCCAAGACAAACA
2669	GLSRAPP	16992	GGTCTTTCGCGTGCTCCTCCT	31315	GGACTCAGCAGAGCACCACCA
2670	GLSSHHP	16993	GGTTTGAGTTCGCATCATCCT	31316	GGACTCAGCAGCCACCACCCA
2671	GLSTKTS	16994	GGGCTTTCTACGAAGACGTCG	31317	GGACTCAGCACAAAAACAAGC
2672	GLSTVLM	16995	GGTTTGTCTACGGTGCTTATG	31318	GGACTCAGCACAGTCCTCATG
2673	GLSVTRV	16996	GGTCTGTCTGTTACGCGTGTT	31319	GGACTCAGCGTCACAAGAGTC
2674	GLTHVVQ	16997	GGTTTGACTCATGTTGTGCAG	31320	GGACTCACACACGTCGTCCAA
2675	GLTLDLR	16998	GGGCTGACTTTGGATTTGAGG	31321	GGACTCACACTCGACCTCAGA
2676	GLTLVPA	16999	GGTTTGACTTTGGTTCCGGCT	31322	GGACTCACACTCGTCCCAGCA
2677	GLTNTGS	17000	GGTCTTACTAATACGGGGAGT	31323	GGACTCACAAACACAGGAAGC
2678	GLTPDHG	17001	GGTCTGACTCCGGATCATGGG	31324	GGACTCACACCAGACCACGGA
2679	GLTQPGP	17002	GGGCTTACTCAGCCTGGGCCT	31325	GGACTCACACAACCAGGACCA
2680	GLTSHPI	17003	GGTTTGACGTCGCATCCTATT	31326	GGACTCACAAGCCACCCAATC
2681	GLTYALT	17004	GGTCTGACTTATGCTTTGACG	31327	GGACTCACATACGCACTCACA
2682	GLVAHTI	17005	GGTCTGGTTGCGCATACTATT	31328	GGACTCGTCGCACACACAATC
2683	GLVGRVQ	17006	GGTCTGGTGGGTAGGGTGCAG	31329	GGACTCGTCGGAAGAGTCCAA
2684	GLVIGVA	17007	GGTTTGGTTATTGGTGTGGCT	31330	GGACTCGTCATCGGAGTCGCA
2685	GLVPTDA	17008	GGGTTGGTGCCTACGGATGCG	31331	GGACTCGTCCCAACAGACGCA
2686	GLVSTHD	17009	GGGCTTGTTTCTACTCATGAT	31332	GGACTCGTCAGCACACACGAC
2687	GLYDTRS	17010	GGTTTGTATGATACTCGGTCG	31333	GGACTCTACGACACAAGAAGC
2688	GLYHLNA	17011	GGGTTGTATCATCTTAATGCG	31334	GGACTCTACCACCTCAACGCA
2689	GLYNTST	17012	GGGCTTTATAATACGAGTACT	31335	GGACTCTACAACACAAGCACA

2690	GLYPNFT	17013	GGTCTTTATCCGAATTTTACT	31336	GGACTCTACCCAAACTTCACA
2691	GMAAGHS	17014	GGTATGGCTGCGGGTCATTCT	31337	GGAATGGCAGCAGGACACAGC
2692	GMAATAS	17015	GGGATGGCGGCTACTGCTAGT	31338	GGAATGGCAGCAACAGCAAGC
2693	GMAGIRD	17016	GGGATGGCTGGTATTCGTGAT	31339	GGAATGGCAGGAATCAGAGAC
2694	GMAMTLS	17017	GGGATGGCTATGACTTTGTCT	31340	GGAATGGCAATGACACTCAGC
2695	GMATGVD	17018	GGGATGGCGACTGGTGTTGAT	31341	GGAATGGCAACAGGAGTCGAC
2696	GMDQVLR	17019	GGTATGGATCAGGTTTTGAGG	31342	GGAATGGACCAAGTCCTCAGA
2697	GMGTAYG	17020	GGGATGGGTACTGCTTATGGT	31343	GGAATGGGAACAGCATACGGA
2698	GMKPPVD	17021	GGTATGAAGCCTCCTGTTGAT	31344	GGAATGAAACCACCAGTCGAC
2699	GMLRAVS	17022	GGGATGCTTCGGGCGGTTTCG	31345	GGAATGCTCAGAGCAGTCAGC
2700	GMNNTVR	17023	GGTATGAATAATACTGTGCGT	31346	GGAATGAACAACACAGTCAGA
2701	GMNSSLV	17024	GGTATGAATTCGTCGTTGGTT	31347	GGAATGAACAGCAGCCTCGTC
2702	GMPHLPP	17025	GGGATGCCGCATCTGCCTCCT	31348	GGAATGCCACACCTCCCACCA
2703	GMPIPSN	17026	GGGATGCCTATTCCTAGTAAT	31349	GGAATGCCAATCCCAAGCAAC
2704	GMRDLQP	17027	GGTATGAGGGATCTGCAGCCT	31350	GGAATGAGAGACCTCCAACCA
2705	GMRQTQA	17028	GGTATGAGGCAGACTCAGGCG	31351	GGAATGAGACAAACACAAGCA
2706	GMSMITR	17029	GGTATGTCTATGATTACGCGG	31352	GGAATGAGCATGATCACAAGA
2707	GMSQGSY	17030	GGGATGTCTCAGGGTTCTTAT	31353	GGAATGAGCCAAGGAAGCTAC
2708	GMSRSFS	17031	GGGATGTCTAGGTCGTTTAGT	31354	GGAATGAGCAGAAGCTTCAGC
2709	GMSSALS	17032	GGTATGAGTTCGGCGCTGTCG	31355	GGAATGAGCAGCGCACTCAGC
2710	GMSVPMD	17033	GGTATGTCGGTTCCGATGGAT	31356	GGAATGAGCGTCCCAATGGAC
2711	GMTRPQV	17034	GGGATGACTCGTCCTCAGGTT	31357	GGAATGACAAGACCACAAGTC
2712	GNAATLR	17035	GGGAATGCTGCTACTCTTAGG	31358	GGAAACGCAGCAACACTCAGA
2713	GNARPIT	17036	GGGAATGCGCGGCCTATTACT	31359	GGAAACGCAAGACCAATCACA
2714	GNASPQM	17037	GGTAATGCTAGTCCTCAGATG	31360	GGAAACGCAAGCCCACAAATG
2715	GNAVGGD	17038	GGGAATGCTGTTGGGGGTGAT	31361	GGAAACGCAGTCGGAGGAGAC
2716	GNDDSKY	17039	GGTAATGATGATTCTAAGTAT	31362	GGAAACGACGACAGCAAATAC
2717	GNFQKNA	17040	GGGAATTTTCAGAAGAATGCG	31363	GGAAACTTCCAAAAAAACGCA
2718	GNGRGFQ	17041	GGGAATGGGCGTGGTTTTCAG	31364	GGAAACGGAAGAGGATTCCAA
2719	GNGTPEH	17042	GGTAATGGGACTCCTGAGCAT	31365	GGAAACGGAACACCAGAACAC
2720	GNHAFHA	17043	GGTAATCATGCTTTTCATGCT	31366	GGAAACCACGCATTCCACGCA
2721	GNHLHLC	17044	GGGAATCATCTTCATCTGTGT	31367	GGAAACCACCTCCACCTCTGC
2722	GNHVLQP	17045	GGGAATCATGTGCTTCAGCCG	31368	GGAAACCACGTCCTCCAACCA
2723	GNLLTIS	17046	GGGAATCTTCTTACTATTTCG	31369	GGAAACCTCCTCACAATCAGC
2724	GNLSQRF	17047	GGTAATCTTTCGCAGCGTTTT	31370	GGAAACCTCAGCCAAAGATTC
2725	GNMHTLT	17048	GGTAATATGCATACGTTGACT	31371	GGAAACATGCACACACTCACA
2726	GNPLKPQ	17049	GGGAATCCTTTGAAGCCTCAG	31372	GGAAACCCACTCAAACCACAA
2727	GNREALA	17050	GGTAATAGGGAGGCTCTTGCG	31373	GGAAACAGAGAAGCACTCGCA
2728	GNRNSNV	17051	GGTAATCGGAATTCTAATGTT	31374	GGAAACAGAAACAGCAACGTC
2729	GNSAMNS	17052	GGGAATAGTGCGATGAATTCG	31375	GGAAACAGCGCAATGAACAGC
2730	GNSDQTR	17053	GGGAATTCTGATCAGACGCGT	31376	GGAAACAGCGACCAAACAAGA
2731	GNSLAPQ	17054	GGGAATTCTTTGGCTCCGCAG	31377	GGAAACAGCCTCGCACCACAA
2732	GNSSAGN	17055	GGTAATAGTTCGGCGGGGAAT	31378	GGAAACAGCAGCGCAGGAAAC
2733	GNSSHSD	17056	GGGAATTCGTCGCATAGTGAT	31379	GGAAACAGCAGCCACAGCGAC
2734	GNSTVDP	17057	GGGAATAGTACGGTGGATCCG	31380	GGAAACAGCACAGTCGACCCA

2735	GNSVPHN	17058	GGTAATTCGGTTCCTCATAAT	31381	GGAAACAGCGTCCCACACAAC
2736	GNSVQHR	17059	GGGAATTCTGTTCAGCATCGT	31382	GGAAACAGCGTCCAACACAGA
2737	GNTAPQS	17060	GGGAATACTGCGCCTCAGTCT	31383	GGAAACACAGCACCACAAAGC
2738	GNTHNMQ	17061	GGTAATACTCATAATATGCAG	31384	GGAAACACACACAACATGCAA
2739	GNTKSPG	17062	GGGAATACTAAGTCTCCTGGG	31385	GGAAACACAAAAAGCCCAGGA
2740	GNTNRNG	17063	GGGAATACTAATCGGAATGGT	31386	GGAAACACAAACAGAAACGGA
2741	GNTSSRA	17064	GGGAATACGTCGTCTCGGGCT	31387	GGAAACACAAGCAGCAGAGCA
2742	GNTVRIP	17065	GGTAATACTGTGCGGATTCCG	31388	GGAAACACAGTCAGAATCCCA
2743	GNVLRVV	17066	GGTAATGTTCTTAGGGTTGTT	31389	GGAAACGTCCTCAGAGTCGTC
2744	GNVTKGL	17067	GGGAATGTTACTAAGGGGCTT	31390	GGAAACGTCACAAAAGGACTC
2745	GNYILKP	17068	GGTAATTATATTTTGAAGCCT	31391	GGAAACTACATCCTCAAACCA
2746	GNYISAS	17069	GGTAATTATATTTCGGCTTCT	31392	GGAAACTACATCAGCGCAAGC
2747	GNYNLDL	17070	GGTAATTATAATTTGGATCTG	31393	GGAAACTACAACCTCGACCTC
2748	GNYSSEV	17071	GGGAATTATTCGTCGGAGGTG	31394	GGAAACTACAGCAGCGAAGTC
2749	GPAADVR	17072	GGTCCGGCTGCGGATGTGCGG	31395	GGACCAGCAGCAGACGTCAGA
2750	GPALLMD	17073	GGGCCGGCGCTTCTTATGGAT	31396	GGACCAGCACTCCTCATGGAC
2751	GPALPIA	17074	GGGCCTGCTTTGCCGATTGCG	31397	GGACCAGCACTCCCAATCGCA
2752	GPAMGSL	17075	GGGCCGGCGATGGGGAGTCTT	31398	GGACCAGCAATGGGAAGCCTC
2753	GPAPSIS	17076	GGGCCGGCGCCTTCTATTTCT	31399	GGACCAGCACCAAGCATCAGC
2754	GPAQRLQ	17077	GGGCCGGCTCAGCGTCTTCAG	31400	GGACCAGCACAAAGACTCCAA
2755	GPASIVS	17078	GGGCCTGCTTCTATTGTTTCT	31401	GGACCAGCAAGCATCGTCAGC
2756	GPATHLT	17079	GGGCCGGCGACGCATCTTACG	31402	GGACCAGCAACACACCTCACA
2757	GPDLTTG	17080	GGTCCTGATTTGACGACGGGT	31403	GGACCAGACCTCACAACAGGA
2758	GPDQEEH	17081	GGGCCTGATCAGGAGGAGCAT	31404	GGACCAGACCAAGAAGAACAC
2759	GPEAMYK	17082	GGTCCGGAGGCGATGTATAAG	31405	GGACCAGAAGCAATGTACAAA
2760	GPEQDIM	17083	GGTCCTGAGCAGGATATTATG	31406	GGACCAGAACAAGACATCATG
2761	GPEWVTG	17084	GGGCCGGAGTGGGTGACGGGT	31407	GGACCAGAATGGGTCACAGGA
2762	GPFEQTD	17085	GGGCCTTTTGAGCAGACGGAT	31408	GGACCATTCGAACAAACAGAC
2763	GPGAIHY	17086	GGTCCGGGGGCGATTCATTAT	31409	GGACCAGGAGCAATCCACTAC
2764	GPGIASF	17087	GGTCCGGGGATTGCTAGTTTT	31410	GGACCAGGAATCGCAAGCTTC
2765	GPGKETR	17088	GGGCCGGGGAAGGAGACGCGT	31411	GGACCAGGAAAAGAAACAAGA
2766	GPGMLCA	17089	GGTCCTGGTATGCTGTGTGCG	31412	GGACCAGGAATGCTCTGCGCA
2767	GPGPIGS	17090	GGTCCTGGTCCTATTGGGTCT	31413	GGACCAGGACCAATCGGAAGC
2768	GPGSFRP	17091	GGTCCGGGTTCGTTTCGTCCT	31414	GGACCAGGAAGCTTCAGACCA
2769	GPGSSSM	17092	GGGCCTGGGTCGTCGTCTATG	31415	GGACCAGGAAGCAGCAGCATG
2770	GPHIRIA	17093	GGTCCGCATATTCGGATTGCT	31416	GGACCACACATCAGAATCGCA
2771	GPHLVQH	17094	GGGCCTCATCTTGTGCAGCAT	31417	GGACCACACCTCGTCCAACAC
2772	GPHTSMI	17095	GGGCCGCATACTAGTATGATT	31418	GGACCACACACAAGCATGATC
2773	GPHYNDP	17096	GGGCCGCATTATAATGATCCT	31419	GGACCACACTACAACGACCCA
2774	GPIELTL	17097	GGGCCGATTGAGCTTACGTTG	31420	GGACCAATCGAACTCACACTC
2775	GPKLTPV	17098	GGGCCTAAGCTTACGCCGGTG	31421	GGACCAAAACTCACACCAGTC
2776	GPKMEPH	17099	GGGCCTAAGATGGAGCCGCAT	31422	GGACCAAAAATGGAACCACAC
2777	GPLLVRG	17100	GGTCCTTTGCTGGTGCGTGGT	31423	GGACCACTCCTCGTCAGAGGA
2778	GPLNSVM	17101	GGGCCGCTTAATTCTGTGATG	31424	GGACCACTCAACAGCGTCATG
2779	GPLPEGH	17102	GGGCCTTTGCCTGAGGGTCAT	31425	GGACCACTCCCAGAAGGACAC

2780	GPLPPTT	17103	GGTCCGCTTCCGCCTACGACG	31426	GGACCACTCCCACCAACAACA
2781	GPLPVAT	17104	GGTCCGCTGCCGGTGGCGACT	31427	GGACCACTCCCAGTCGCAACA
2782	GPLSAMP	17105	GGTCCGTTGTCTGCGATGCCT	31428	GGACCACTCAGCGCAATGCCA
2783	GPLSNVK	17106	GGGCCGTTGAGTAATGTGAAG	31429	GGACCACTCAGCAACGTCAAA
2784	GPLVYAD	17107	GGTCCTTTGGTTTATGCTGAT	31430	GGACCACTCGTCTACGCAGAC
2785	GPMQMPS	17108	GGGCCTATGCAGATGCCGAGT	31431	GGACCAATGCAAATGCCAAGC
2786	GPMREME	17109	GGGCCGATGCGGGAGATGGAG	31432	GGACCAATGAGAGAAATGGAA
2787	GPMYANP	17110	GGTCCTATGTATGCGAATCCT	31433	GGACCAATGTACGCAAACCCA
2788	GPNDVQK	17111	GGTCCGAATGATGTGCAGAAG	31434	GGACCAAACGACGTCCAAAAA
2789	GPNFLLP	17112	GGTCCTAATTTTCTTTTGCCT	31435	GGACCAAACTTCCTCCTCCCA
2790	GPNGAVG	17113	GGTCCGAATGGTGCTGTTGGG	31436	GGACCAAACGGAGCAGTCGGA
2791	GPNMRNG	17114	GGTCCGAATATGCGTAATGGT	31437	GGACCAAACATGAGAAACGGA
2792	GPNRGSL	17115	GGGCCGAATCGTGGGTCGTTG	31438	GGACCAAACAGAGGAAGCCTC
2793	GPNRLTV	17116	GGTCCGAATCGGCTGACTGTG	31439	GGACCAAACAGACTCACAGTC
2794	GPNVLSP	17117	GGTCCTAATGTTCTTTCGCCT	31440	GGACCAAACGTCCTCAGCCCA
2795	GPPAVKV	17118	GGGCCTCCGGCTGTTAAGGTG	31441	GGACCACCAGCAGTCAAAGTC
2796	GPPHGHS	17119	GGGCCTCCTCATGGTCATTCG	31442	GGACCACCACACGGACACAGC
2797	GPPKANP	17120	GGTCCGCCTAAGGCTAATCCT	31443	GGACCACCAAAAGCAAACCCA
2798	GPPLLAP	17121	GGTCCTCCGCTTCTTGCGCCG	31444	GGACCACCACTCCTCGCACCA
2799	GPPMRPS	17122	GGGCCTCCTATGAGGCCTTCT	31445	GGACCACCAATGAGACCAAGC
2800	GPPPQPS	17123	GGGCCGCCGCCGCAGCCGTCT	31446	GGACCACCACCACAACCAAGC
2801	GPPPTNW	17124	GGTCCTCCTCCGACTAATTGG	31447	GGACCACCACCAACAAACTGG
2802	GPQTVTG	17125	GGGCCGCAGACGGTTACGGGT	31448	GGACCACAAACAGTCACAGGA
2803	GPRDPRN	17126	GGTCCTAGGGATCCTCGTAAT	31449	GGACCAAGAGACCCAAGAAAC
2804	GPRGFLN	17127	GGGCCTCGTGGGTTTTTGAAT	31450	GGACCAAGAGGATTCCTCAAC
2805	GPRPQHL	17128	GGTCCTCGGCCGCAGCATTTG	31451	GGACCAAGACCACAACACCTC
2806	GPRVTND	17129	GGGCCGAGGGTTACTAATGAT	31452	GGACCAAGAGTCACAAACGAC
2807	GPSDHGS	17130	GGTCCGAGTGATCATGGGTCG	31453	GGACCAAGCGACCACGGAAGC
2808	GPSKALA	17131	GGTCCGTCTAAGGCGTTGGCT	31454	GGACCAAGCAAAGCACTCGCA
2809	GPSLNTT	17132	GGTCCGAGTTTGAATACGACG	31455	GGACCAAGCCTCAACACAACA
2810	GPSPESS	17133	GGGCCTTCTCCTGAGTCTTCT	31456	GGACCAAGCCCAGAAAGCAGC
2811	GPSRNAP	17134	GGTCCTAGTCGGAATGCTCCG	31457	GGACCAAGCAGAAACGCACCA
2812	GPSSAKL	17135	GGGCCTAGTTCGGCGAAGCTG	31458	GGACCAAGCAGCGCAAAACTC
2813	GPSSSAY	17136	GGTCCTTCGAGTTCTGCGTAT	31459	GGACCAAGCAGCAGCGCATAC
2814	GPSSVPD	17137	GGTCCTTCTTCTGTGCCTGAT	31460	GGACCAAGCAGCGTCCCAGAC
2815	GPSTSLI	17138	GGGCCGAGTACTTCTCTGATT	31461	GGACCAAGCACAAGCCTCATC
2816	GPSVHPA	17139	GGTCCGAGTGTGCATCCGGCG	31462	GGACCAAGCGTCCACCCAGCA
2817	GPSVHTD	17140	GGTCCTAGTGTGCATACTGAT	31463	GGACCAAGCGTCCACACAGAC
2818	GPSYIDS	17141	GGTCCGTCTTATATTGATAGT	31464	GGACCAAGCTACATCGACAGC
2819	GPTETPL	17142	GGTCCTACGGAGACGCCTTTG	31465	GGACCAACAGAAACACCACTC
2820	GPTGDLV	17143	GGGCCGACTGGTGATCTTGTT	31466	GGACCAACAGGAGACCTCGTC
2821	GPTGSSE	17144	GGGCCGACGGGGTCGTCGGAG	31467	GGACCAACAGGAAGCAGCGAA
2822	GPTHPRI	17145	GGTCCGACGCATCCGCGGATT	31468	GGACCAACACACCCAAGAATC
2823	GPTMSMT	17146	GGGCCTACTATGTCTATGACG	31469	GGACCAACAATGAGCATGACA
2824	GPTSLAI	17147	GGGCCTACGAGTCTTGCTATT	31470	GGACCAACAAGCCTCGCAATC

2825	GPTYPHA	17148	GGGCCGACGTATCCGCATGCG	31471	GGACCAACATACCCACACGCA
2826	GPVKPRD	17149	GGGCCGGTTAAGCCTCGTGAT	31472	GGACCAGTCAAACCAAGAGAC
2827	GPVNAPD	17150	GGGCCGGTTAATGCGCCTGAT	31473	GGACCAGTCAACGCACCAGAC
2828	GPVSGVS	17151	GGGCCGGTTTCGGGTGTTTCG	31474	GGACCAGTCAGCGGAGTCAGC
2829	GPYNVDV	17152	GGGCCTTATAATGTTGATGTG	31475	GGACCATACAACGTCGACGTC
2830	GPYSAPG	17153	GGGCCGTATTCGGCTCCTGGT	31476	GGACCATACAGCGCACCAGGA
2831	GQAIGHP	17154	GGTCAGGCGATTGGGCATCCG	31477	GGACAAGCAATCGGACACCCA
2832	GQARNET	17155	GGGCAGGCTCGTAATGAGACT	31478	GGACAAGCAAGAAACGAAACA
2833	GQASAPF	17156	GGGCAGGCGTCGGCTCCTTTT	31479	GGACAAGCAAGCGCACCATTC
2834	GQASISS	17157	GGTCAGGCTAGTATTAGTTCT	31480	GGACAAGCAAGCATCAGCAGC
2835	GQASRQS	17158	GGGCAGGCGTCGCGTCAGTCT	31481	GGACAAGCAAGCAGACAAAGC
2836	GQAVKVN	17159	GGTCAGGCGGTGAAGGTTAAT	31482	GGACAAGCAGTCAAAGTCAAC
2837	GQDDVNI	17160	GGGCAGGATGATGTGAATATT	31483	GGACAAGACGACGTCAACATC
2838	GQDMHDS	17161	GGGCAGGATATGCATGATTCT	31484	GGACAAGACATGCACGACAGC
2839	GQEWQAG	17162	GGGCAGGAGTGGCAGGCTGGG	31485	GGACAAGAATGGCAAGCAGGA
2840	GQFVVRQ	17163	GGTCAGTTTGTGGTGCGGCAG	31486	GGACAATTCGTCGTCAGACAA
2841	GQGHPPN	17164	GGTCAGGGGCATCCGCCTAAT	31487	GGACAAGGACACCCACCAAAC
2842	GQGSTPL	17165	GGTCAGGGTTCGACTCCTTTG	31488	GGACAAGGAAGCACACCACTC
2843	GQHARLQ	17166	GGTCAGCATGCTCGGCTGCAG	31489	GGACAACACGCAAGACTCCAA
2844	GQHGKPA	17167	GGTCAGCATGGGAAGCCTGCT	31490	GGACAACACGGAAAACCAGCA
2845	GQHLSPN	17168	GGTCAGCATTTGTCTCCTAAT	31491	GGACAACACCTCAGCCCAAAC
2846	GQIVAPT	17169	GGTCAGATTGTGGCTCCTACT	31492	GGACAAATCGTCGCACCAACA
2847	GQIVTSG	17170	GGTCAGATTGTTACGTCGGGT	31493	GGACAAATCGTCACAAGCGGA
2848	GQLDMTT	17171	GGGCAGCTTGATATGACTACT	31494	GGACAACTCGACATGACAACA
2849	GQLNLRP	17172	GGGCAGCTGAATCTTAGGCCG	31495	GGACAACTCAACCTCAGACCA
2850	GQLQSGS	17173	GGGCAGCTGCAGAGTGGTTCG	31496	GGACAACTCCAAAGCGGAAGC
2851	GQMARPD	17174	GGGCAGATGGCGCGTCCTGAT	31497	GGACAAATGGCAAGACCAGAC
2852	GQMISAQ	17175	GGTCAGATGATTTCTGCTCAG	31498	GGACAAATGATCAGCGCACAA
2853	GQPSPWP	17176	GGTCAGCCTAGTCCGTGGCCG	31499	GGACAACCAAGCCCATGGCCA
2854	GQQDNRD	17177	GGTCAGCAGGATAATCGGGAT	31500	GGACAACAAGACAACAGAGAC
2855	GQQQGFI	17178	GGGCAGCAGCAGGGTTTTATT	31501	GGACAACAACAAGGATTCATC
2856	GQRKLEG	17179	GGTCAGAGGAAGCTTGAGGGG	31502	GGACAAAGAAAACTCGAAGGA
2857	GQRMSMT	17180	GGGCAGAGGATGTCGATGACG	31503	GGACAAAGAATGAGCATGACA
2858	GQRTTYV	17181	GGGCAGAGGACTACTTATGTT	31504	GGACAAAGAACAACATACGTC
2859	GQSFERT	17182	GGGCAGTCTTTTGAGCGGACG	31505	GGACAAAGCTTCGAAAGAACA
2860	GQSLAIR	17183	GGTCAGTCTCTTGCTATTCGG	31506	GGACAAAGCCTCGCAATCAGA
2861	GQSLTHP	17184	GGGCAGTCTTTGACGCATCCG	31507	GGACAAAGCCTCACACACCCA
2862	GQSTRQD	17185	GGTCAGTCTACTCGGCAGGAT	31508	GGACAAAGCACAAGACAAGAC
2863	GQTCTSL	17186	GGGCAGACTTGTACGTCGCTG	31509	GGACAAACATGCACAAGCCTC
2864	GQTLALD	17187	GGGCAGACGTTGGCTCTTGAT	31510	GGACAAACACTCGCACTCGAC
2865	GQTYPTL	17188	GGTCAGACGTATCCGACTCTG	31511	GGACAAACATACCCAACACTC
2866	GQVHLNP	17189	GGTCAGGTTCATCTTAATCCG	31512	GGACAAGTCCACCTCAACCCA
2867	GQYGRQP	17190	GGGCAGTATGGGCGTCAGCCT	31513	GGACAATACGGAAGACAACCA
2868	GQYHRDT	17191	GGGCAGTATCATAGGGATACT	31514	GGACAATACCACAGAGACACA
2869	GQYSAST	17192	GGTCAGTATTCTGCTTCTACT	31515	GGACAATACAGCGCAAGCACA

2870	GRAAPIS	17193	GGTCGTGCTGCTCCTATTTCG	31516	GGAAGAGCAGCACCAATCAGC
2871	GRANTGF	17194	GGGAGGGCTAATACTGGTTTT	31517	GGAAGAGCAAACACAGGATTC
2872	GRARPLP	17195	GGGCGTGCTCGTCCGCTGCCG	31518	GGAAGAGCAAGACCACTCCCA
2873	GRASTYV	17196	GGTCGGGCTTCTACTTATGTT	31519	GGAAGAGCAAGCACATACGTC
2874	GRDEVPL	17197	GGTCGGGATGAGGTTCCGCTG	31520	GGAAGAGACGAAGTCCCACTC
2875	GRDGMPS	17198	GGGAGGGATGGGATGCCTTCT	31521	GGAAGAGACGGAATGCCAAGC
2876	GRDPTPV	17199	GGGAGGGATCCGACTCCGGTT	31522	GGAAGAGACCCAACACCAGTC
2877	GRDPVRH	17200	GGGAGGGATCCTGTTCGTCAT	31523	GGAAGAGACCCAGTCAGACAC
2878	GREHMHT	17201	GGGCGTGAGCATATGCATACG	31524	GGAAGAGAACACATGCACACA
2879	GRELLHS	17202	GGGAGGGAGCTTTTGCATTCT	31525	GGAAGAGAACTCCTCCACAGC
2880	GRESQIP	17203	GGTCGTGAGTCGCAGATTCCG	31526	GGAAGAGAAAGCCAAATCCCA
2881	GRESVTS	17204	GGGCGTGAGTCTGTGACGTCT	31527	GGAAGAGAAAGCGTCACAAGC
2882	GREYVGN	17205	GGTCGTGAGTATGTTGGTAAT	31528	GGAAGAGAATACGTCGGAAAC
2883	GRFGTSD	17206	GGGCGTTTTGGGACTAGTGAT	31529	GGAAGATTCGGAACAAGCGAC
2884	GRGAQPG	17207	GGGCGGGGTGCTCAGCCTGGG	31530	GGAAGAGGAGCACAACCAGGA
2885	GRGDNPA	17208	GGTAGGGGTGATAATCCGGCT	31531	GGAAGAGGAGACAACCCAGCA
2886	GRGEAGL	17209	GGTCGGGGTGAGGCTGGTCTT	31532	GGAAGAGGAGAAGCAGGACTC
2887	GRGGESV	17210	GGTAGGGGGGGGGAGAGTGTG	31533	GGAAGAGGAGGAGAAAGCGTC
2888	GRGLPMS	17211	GGTCGTGGTCTGCCTATGAGT	31534	GGAAGAGGACTCCCAATGAGC
2889	GRGPPPP	17212	GGTCGGGGGCCTCCTCCGCCT	31535	GGAAGAGGACCACCACCACCA
2890	GRGQSAS	17213	GGGCGTGGGCAGTCTGCTTCT	31536	GGAAGAGGACAAAGCGCAAGC
2891	GRGTPPD	17214	GGGAGGGGTACTCCTCCGGAT	31537	GGAAGAGGAACACCACCAGAC
2892	GRIAPVP	17215	GGGCGTATTGCGCCTGTTCCT	31538	GGAAGAATCGCACCAGTCCCA
2893	GRIYTAE	17216	GGTCGTATTTATACGGCGGAG	31539	GGAAGAATCTACACAGCAGAA
2894	GRLLPEV	17217	GGTCGTTTGTTGCCGGAGGTG	31540	GGAAGACTCCTCCCAGAAGTC
2895	GRLPASL	17218	GGTAGGCTTCCTGCGTCGTTG	31541	GGAAGACTCCCAGCAAGCCTC
2896	GRMEGGG	17219	GGTAGGATGGAGGGTGGGGGT	31542	GGAAGAATGGAAGGAGGAGGA
2897	GRMENTV	17220	GGTCGTATGGAGAATACTGTT	31543	GGAAGAATGGAAAACACAGTC
2898	GRMMNSS	17221	GGGCGGATGATGAATAGTAGT	31544	GGAAGAATGATGAACAGCAGC
2899	GRMVTGE	17222	GGTAGGATGGTTACTGGTGAG	31545	GGAAGAATGGTCACAGGAGAA
2900	GRNDAYA	17223	GGTAGGAATGATGCTTATGCG	31546	GGAAGAAACGACGCATACGCA
2901	GRNEPWS	17224	GGTCGGAATGAGCCTTGGTCG	31547	GGAAGAAACGAACCATGGAGC
2902	GRNPPLY	17225	GGGCGGAATCCGCCTCTGTAT	31548	GGAAGAAACCCACCACTCTAC
2903	GRNPPSA	17226	GGTCGGAATCCGCCGAGTGCG	31549	GGAAGAAACCCACCAAGCGCA
2904	GRNSNYD	17227	GGGAGGAATTCGAATTATGAT	31550	GGAAGAAACAGCAACTACGAC
2905	GRNVAGL	17228	GGGAGGAATGTTGCGGGTCTT	31551	GGAAGAAACGTCGCAGGACTC
2906	GRPDTEH	17229	GGTCGGCCTGATACGGAGCAT	31552	GGAAGACCAGACACAGAACAC
2907	GRPLPTS	17230	GGGCGTCCTCTTCCTACGAGT	31553	GGAAGACCACTCCCAACAAGC
2908	GRPLQAP	17231	GGTAGGCCTTTGCAGGCTCCT	31554	GGAAGACCACTCCAAGCACCA
2909	GRPPLLP	17232	GGTAGGCCGCCTCTTCTTCCT	31555	GGAAGACCACCACTCCTCCCA
2910	GRPPSMS	17233	GGGAGGCCTCCTAGTATGTCG	31556	GGAAGACCACCAAGCATGAGC
2911	GRPPTDK	17234	GGTCGGCCGCCTACTGATAAG	31557	GGAAGACCACCAACAGACAAA
2912	GRQDHPG	17235	GGTAGGCAGGATCATCCGGGT	31558	GGAAGACAAGACCACCCAGGA
2913	GRQLACN	17236	GGTCGGCAGCTTGCGTGTAAT	31559	GGAAGACAACTCGCATGCAAC
2914	GRQMGIT	17237	GGTCGGCAGATGGGTATTACG	31560	GGAAGACAAATGGGAATCACA

2915	GRQPSGE	17238	GGGCGGCAGCCGAGTGGGGAG	31561	GGAAGACAACCAAGCGGAGAA
2916	GRQSVSN	17239	GGTAGGCAGAGTGTTTCGAAT	31562	GGAAGACAAAGCGTCAGCAAC
2917	GRQVDFV	17240	GGGCGTCAGGTTGATTTTGTT	31563	GGAAGACAAGTCGACTTCGTC
2918	GRSDLSN	17241	GGGCGTTCGGATTTGAGTAAT	31564	GGAAGAAGCGACCTCAGCAAC
2919	GRSEYNQ	17242	GGTAGGTCTGAGTATAATCAG	31565	GGAAGAAGCGAATACAACCAA
2920	GRSIMSE	17243	GGGAGGAGTATTATGTCTGAG	31566	GGAAGAAGCATCATGAGCGAA
2921	GRSLLRE	17244	GGTAGGAGTCTGTTGCGTGAG	31567	GGAAGAAGCCTCCTCAGAGAA
2922	GRSPIQS	17245	GGTCGGTCTCCTATTCAGAGT	31568	GGAAGAAGCCCAATCCAAAGC
2923	GRSSVAT	17246	GGTCGTTCGTCTGTGGCGACT	31569	GGAAGAAGCAGCGTCGCAACA
2924	GRSVQHL	17247	GGTCGTAGTGTGCAGCATCTG	31570	GGAAGAAGCGTCCAACACCTC
2925	GRTGSPG	17248	GGTCGTACTGGTTCGCCTGGG	31571	GGAAGAACAGGAAGCCCAGGA
2926	GRTSGSS	17249	GGGCGTACTTCTGGTTCGTCG	31572	GGAAGAACAAGCGGAAGCAGC
2927	GRTSMAT	17250	GGTCGGACTAGTATGGCGACT	31573	GGAAGAACAAGCATGGCAACA
2928	GRTSRAE	17251	GGTCGGACGTCTCGTGCTGAG	31574	GGAAGAACAAGCAGAGCAGAA
2929	GRTYQIP	17252	GGTAGGACGTATCAGATTCCT	31575	GGAAGAACATACCAAATCCCA
2930	GRVLLLD	17253	GGTCGGGTTCTGCTGTTGGAT	31576	GGAAGAGTCCTCCTCCTCGAC
2931	GRVQVPP	17254	GGTCGGGTTCAGGTTCCTCCT	31577	GGAAGAGTCCAAGTCCCACCA
2932	GRVVYID	17255	GGTCGTGTTGTTTATATTGAT	31578	GGAAGAGTCGTCTACATCGAC
2933	GRYMAPL	17256	GGGCGTTATATGGCTCCGCTG	31579	GGAAGATACATGGCACCACTC
2934	GRYRAGQ	17257	GGTCGTTATAGGGCGGGTCAG	31580	GGAAGATACAGAGCAGGACAA
2935	GSAISEL	17258	GGTTCGGCGATTAGTGAGCTT	31581	GGAAGCGCAATCAGCGAACTC
2936	GSALPTR	17259	GGGAGTGCTCTGCCTACGCGT	31582	GGAAGCGCACTCCCAACAAGA
2937	GSAPVVL	17260	GGTAGTGCGCCTGTGGTGCTT	31583	GGAAGCGCACCAGTCGTCCTC
2938	GSAQGAR	17261	GGGTCGGCGCAGGGTGCTCGG	31584	GGAAGCGCACAAGGAGCAAGA
2939	GSARTHP	17262	GGGTCTGCGCGGACTCATCCT	31585	GGAAGCGCAAGAACACACCCA
2940	GSASPMM	17263	GGGTCGGCGAGTCCTATGATG	31586	GGAAGCGCAAGCCCAATGATG
2941	GSASSGF	17264	GGTTCGGCTTCTAGTGGGTTT	31587	GGAAGCGCAAGCAGCGGATTC
2942	GSDGFSN	17265	GGGTCTGATGGGTTTTCTAAT	31588	GGAAGCGACGGATTCAGCAAC
2943	GSDGQKG	17266	GGTTCTGATGGGCAGAAGGGT	31589	GGAAGCGACGGACAAAAAGGA
2944	GSDRIVS	17267	GGGTCTGATCGGATTGTTTCG	31590	GGAAGCGACAGAATCGTCAGC
2945	GSDTPSP	17268	GGGTCGGATACTCCTTCGCCT	31591	GGAAGCGACACACCAAGCCCA
2946	GSDTTEI	17269	GGGTCTGATACTACTGAGATT	31592	GGAAGCGACACAACAGAAATC
2947	GSDVIHE	17270	GGTAGTGATGTTATTCATGAG	31593	GGAAGCGACGTCATCCACGAA
2948	GSEVVAC	17271	GGTTCGGAGGTTGTGGCGTGT	31594	GGAAGCGAAGTCGTCGCATGC
2949	GSFTSQI	17272	GGGTCTTTTACTTCTCAGATT	31595	GGAAGCTTCACAAGCCAAATC
2950	GSGLIRG	17273	GGTAGTGGGCTTATTAGGGGG	31596	GGAAGCGGACTCATCAGAGGA
2951	GSGNDVL	17274	GGTTCGGGGAATGATGTGCTG	31597	GGAAGCGGAAACGACGTCCTC
2952	GSGPNKS	17275	GGTTCGGGTCCGAATAAGTCT	31598	GGAAGCGGACCAAACAAAAGC
2953	GSGPTIR	17276	GGGTCTGGTCCGACTATTCGT	31599	GGAAGCGGACCAACAATCAGA
2954	GSGPVEH	17277	GGGTCTGGTCCGGTTGAGCAT	31600	GGAAGCGGACCAGTCGAACAC
2955	GSGSSQT	17278	GGGTCTGGGTCTTCGCAGACT	31601	GGAAGCGGAAGCAGCCAAACA
2956	GSGSTSG	17279	GGTTCTGGTTCGACGTCGGGG	31602	GGAAGCGGAAGCACAAGCGGA
2957	GSGTYTV	17280	GGTAGTGGTACGTATACTGTG	31603	GGAAGCGGAACATACACAGTC
2958	GSHAVTS	17281	GGGAGTCATGCGGTTACTTCT	31604	GGAAGCCACGCAGTCACAAGC
2959	GSHHSPH	17282	GGGTCTCATCATTCTCCTCAT	31605	GGAAGCCACCACAGCCCACAC

2960	GSHITPL	17283	GGTAGTCATATTACGCCGCTG	31606	GGAAGCCACATCACACCACTC
2961	GSHPIVR	17284	GGTTCTCATCCTATTGTGCGT	31607	GGAAGCCACCCAATCGTCAGA
2962	GSHPRGE	17285	GGGTCTCATCCTAGGGGGGAG	31608	GGAAGCCACCCAAGAGGAGAA
2963	GSHQGQS	17286	GGTTCGCATCAGGGTCAGTCT	31609	GGAAGCCACCAAGGACAAAGC
2964	GSHSGGP	17287	GGTTCGCATTCTGGGGGTCCT	31610	GGAAGCCACAGCGGAGGACCA
2965	GSHSPAM	17288	GGTTCGCATTCGCCTGCTATG	31611	GGAAGCCACAGCCCAGCAATG
2966	GSHTWIE	17289	GGTTCTCATACGTGGACGGAG	31612	GGAAGCCACACATGGACAGAA
2967	GSIGEQV	17290	GGGTCGATTGGGGAGCAGGTT	31613	GGAAGCATCGGAGAACAAGTC
2968	GSIQVTA	17291	GGGAGTATTCAGGTTACGGCT	31614	GGAAGCATCCAAGTCACAGCA
2969	GSIVLHE	17292	GGTTCGATTGTTCTTCATGAG	31615	GGAAGCATCGTCCTCCACGAA
2970	GSKNQEK	17293	GGGTCTAAGAATCAGGAGAAG	31616	GGAAGCAAAAACCAAGAAAAA
2971	GSKPFLS	17294	GGGTCGAAGCCTTTTTTGTCG	31617	GGAAGCAAACCATTCCTCAGC
2972	GSKRQDQ	17295	GGGTCGAAGCGTCAGGATCAG	31618	GGAAGCAAAAGACAAGACCAA
2973	GSKSFGS	17296	GGTTCTAAGTCTTTTGGGTCG	31619	GGAAGCAAAAGCTTCGGAAGC
2974	GSKTFLS	17297	GGTTCGAAGACGTTTTTGTCT	31620	GGAAGCAAAACATTCCTCAGC
2975	GSKVAGL	17298	GGTTCGAAGGTGGCTGGTCTG	31621	GGAAGCAAAGTCGCAGGACTC
2976	GSKVGPL	17299	GGTTCTAAGGTTGGGCCTTTG	31622	GGAAGCAAAGTCGGACCACTC
2977	GSLEQRY	17300	GGTAGTTTGGAGCAGCGTTAT	31623	GGAAGCCTCGAACAAAGATAC
2978	GSLGHMR	17301	GGTAGTTTGGGTCATATGAGG	31624	GGAAGCCTCGGACACATGAGA
2979	GSLGTHS	17302	GGTTCGCTTGGTACTCATTCT	31625	GGAAGCCTCGGAACACACAGC
2980	GSLIAAQ	17303	GGGTCGTTGATTGCTGCGCAG	31626	GGAAGCCTCATCGCAGCACAA
2981	GSLNPVP	17304	GGGTCGCTGAATCCTGTTCCG	31627	GGAAGCCTCAACCCAGTCCCA
2982	GSLPYSS	17305	GGGTCTTTGCCTTATTCGTCT	31628	GGAAGCCTCCCATACAGCAGC
2983	GSLYRTE	17306	GGGTCGTTGTATAGGACGGAG	31629	GGAAGCCTCTACAGAACAGAA
2984	GSMAYLG	17307	GGTTCGATGGCTTATCTTGGT	31630	GGAAGCATGGCATACCTCGGA
2985	GSMLAHP	17308	GGGTCGATGCTTGCTCATCCT	31631	GGAAGCATGCTCGCACACCCA
2986	GSMNPPS	17309	GGGTCGATGAATCCTCCTTCT	31632	GGAAGCATGAACCCACCAAGC
2987	GSMPVIV	17310	GGGAGTATGCCGGTTATTGTT	31633	GGAAGCATGCCAGTCATCGTC
2988	GSMRPGE	17311	GGTAGTATGCGGCCTGGTGAG	31634	GGAAGCATGAGACCAGGAGAA
2989	GSMSSAN	17312	GGTTCGATGTCTAGTGCTAAT	31635	GGAAGCATGAGCAGCGCAAAC
2990	GSMTSLI	17313	GGTTCTATGACTTCTTTGATT	31636	GGAAGCATGACAAGCCTCATC
2991	GSMYAVP	17314	GGGAGTATGTATGCTGTTCCG	31637	GGAAGCATGTACGCAGTCCCA
2992	GSNGGIS	17315	GGTTCTAATGGTGGTATTAGT	31638	GGAAGCAACGGAGGAATCAGC
2993	GSNPMSL	17316	GGGTCGAATCCTATGTCGTTG	31639	GGAAGCAACCCAATGAGCCTC
2994	GSPAMAH	17317	GGTAGTCCTGCGATGGCTCAT	31640	GGAAGCCCAGCAATGGCACAC
2995	GSPGRVA	17318	GGTAGTCCTGGGAGGGTGGCG	31641	GGAAGCCCAGGAAGAGTCGCA
2996	GSPIGGM	17319	GGTTCTCCGATTGGGGGGATG	31642	GGAAGCCCAATCGGAGGAATG
2997	GSPKPHV	17320	GGGTCTCCTAAGCCGCATGTT	31643	GGAAGCCCAAAACCACACGTC
2998	GSPMGYT	17321	GGGAGTCCGATGGGTTATACG	31644	GGAAGCCCAATGGGATACACA
2999	GSPMPII	17322	GGGAGTCCGATGCCTATTATT	31645	GGAAGCCCAATGCCAATCATC
3000	GSPNSCM	17323	GGTTCTCCTAATTCTTGTATG	31646	GGAAGCCCAAACAGCTGCATG
3001	GSPPTLR	17324	GGTTCTCCGCCTACGCTGAGG	31647	GGAAGCCCACCAACACTCAGA
3002	GSPRSLS	17325	GGGTCGCCGCGGTCGCTTTCT	31648	GGAAGCCCAAGAAGCCTCAGC
3003	GSPRVGT	17326	GGGTCTCCGCGGGTGGGGACT	31649	GGAAGCCCAAGAGTCGGAACA
3004	GSPSPMR	17327	GGTTCGCCTTCGCCGATGCGG	31650	GGAAGCCCAAGCCCAATGAGA

3005	GSPTTGS	17328	GGTTCTCCTACTACGGGTAGT	31651	GGAAGCCCAACAACAGGAAGC
3006	GSPYSQA	17329	GGTTCGCCGTATTCTCAGGCT	31652	GGAAGCCCATACAGCCAAGCA
3007	GSQLHPV	17330	GGGTCTCAGCTTCATCCGGTT	31653	GGAAGCCAACTCCACCCAGTC
3008	GSQPIRT	17331	GGGTCTCAGCCTATTCGGACG	31654	GGAAGCCAACCAATCAGAACA
3009	GSQQLAA	17332	GGTAGTCAGCAGTTGGCGGCG	31655	GGAAGCCAACAACTCGCAGCA
3010	GSRASDP	17333	GGGTCTCGGGCGTCTGATCCT	31656	GGAAGCAGAGCAAGCGACCCA
3011	GSRLQHD	17334	GGTAGTCGTCTGCAGCATGAT	31657	GGAAGCAGACTCCAACACGAC
3012	GSRNFPT	17335	GGGAGTAGGAATTTTCCTACT	31658	GGAAGCAGAAACTTCCCAACA
3013	GSRNYIA	17336	GGGAGTCGTAATTATATTGCT	31659	GGAAGCAGAAACTACATCGCA
3014	GSRPGSL	17337	GGTTCGCGTCCTGGGAGTTTG	31660	GGAAGCAGACCAGGAAGCCTC
3015	GSRQPAD	17338	GGTTCGAGGCAGCCTGCTGAT	31661	GGAAGCAGACAACCAGCAGAC
3016	GSRTFTG	17339	GGGAGTCGTACGTTTACTGGG	31662	GGAAGCAGAACATTCACAGGA
3017	GSRTGPT	17340	GGTTCTCGGACTGGGCCGACT	31663	GGAAGCAGAACAGGACCAACA
3018	GSRVSGE	17341	GGGTCGCGTGTTAGTGGGGAG	31664	GGAAGCAGAGTCAGCGGAGAA
3019	GSSATVF	17342	GGGTCGTCGGCGACGGTGTTT	31665	GGAAGCAGCGCAACAGTCTTC
3020	GSSDTCV	17343	GGTAGTTCGGATACTTGTGTT	31666	GGAAGCAGCGACACATGCGTC
3021	GSSGIAR	17344	GGGAGTTCGGGTATTGCGCGG	31667	GGAAGCAGCGGAATCGCAAGA
3022	GSSHGIL	17345	GGGTCTTCTCATGGGATTCTT	31668	GGAAGCAGCCACGGAATCCTC
3023	GSSMPPP	17346	GGGTCTTCTATGCCTCCGCCG	31669	GGAAGCAGCATGCCACCACCA
3024	GSSPART	17347	GGGAGTAGTCCTGCTCGGACG	31670	GGAAGCAGCCCAGCAAGAACA
3025	GSSPLHK	17348	GGTTCGTCGCCTCTGCATAAG	31671	GGAAGCAGCCCACTCCACAAA
3026	GSSPVGA	17349	GGTTCTAGTCCTGTGGGTGCT	31672	GGAAGCAGCCCAGTCGGAGCA
3027	GSSQLFL	17350	GGGAGTTCTCAGTTGTTTCTT	31673	GGAAGCAGCCAACTCTTCCTC
3028	GSSRADA	17351	GGTTCTAGTAGGGCTGATGCG	31674	GGAAGCAGCAGAGCAGACGCA
3029	GSSSHVS	17352	GGGTCTTCTTCTCATGTGTCG	31675	GGAAGCAGCAGCCACGTCAGC
3030	GSSSIAS	17353	GGTAGTTCGTCTATTGCGTCT	31676	GGAAGCAGCAGCATCGCAAGC
3031	GSSSLHS	17354	GGGTCGTCGTCTTTGCATTCG	31677	GGAAGCAGCAGCCTCCACAGC
3032	GSSSNAR	17355	GGTTCTAGTTCGAATGCTCGG	31678	GGAAGCAGCAGCAACGCAAGA
3033	GSSYHSP	17356	GGTAGTTCTTATCATTCGCCT	31679	GGAAGCAGCTACCACAGCCCA
3034	GSTGDRQ	17357	GGGAGTACGGGTGATAGGCAG	31680	GGAAGCACAGGAGACAGACAA
3035	GSTGNTV	17358	GGGTCTACGGGTAATACTGTG	31681	GGAAGCACAGGAAACACAGTC
3036	GSTGSAA	17359	GGTAGTACTGGTAGTGCTGCT	31682	GGAAGCACAGGAAGCGCAGCA
3037	GSTGSGH	17360	GGTTCGACGGGTTCTGGGCAT	31683	GGAAGCACAGGAAGCGGACAC
3038	GSTMTIA	17361	GGTAGTACGATGACGATTGCG	31684	GGAAGCACAATGACAATCGCA
3039	GSTNELV	17362	GGTTCGACGAATGAGTTGGTG	31685	GGAAGCACAAACGAACTCGTC
3040	GSTNPLA	17363	GGTTCGACTAATCCTCTGGCT	31686	GGAAGCACAAACCCACTCGCA
3041	GSTNRLA	17364	GGTAGTACTAATCGGCTGGCG	31687	GGAAGCACAAACAGACTCGCA
3042	GSTNSPA	17365	GGGTCTACTAATTCGCCTGCG	31688	GGAAGCACAAACAGCCCAGCA
3043	GSTPLPL	17366	GGGTCGACTCCGCTTCCGCTG	31689	GGAAGCACACCACTCCCACTC
3044	GSTQGSG	17367	GGTAGTACTCAGGGGTCTGGT	31690	GGAAGCACACAAGGAAGCGGA
3045	GSTSKDR	17368	GGTTCGACGTCTAAGGATAGG	31691	GGAAGCACAAGCAAAGACAGA
3046	GSTSSRT	17369	GGTTCTACTTCTTCTCGTACG	31692	GGAAGCACAAGCAGCAGAACA
3047	GSTTRPQ	17370	GGTTCGACTACGCGGCCGCAG	31693	GGAAGCACAACAAGACCACAA
3048	GSTWSSP	17371	GGTTCGACGTGGTCGAGTCCG	31694	GGAAGCACATGGAGCAGCCCA
3049	GSTYASM	17372	GGTTCTACGTATGCTTCTATG	31695	GGAAGCACATACGCAAGCATG

3050	GSVADRV	17373	GGGTCTGTGGCGGATCGGGTG	31696	GGAAGCGTCGCAGACAGAGTC
3051	GSVATNP	17374	GGTTCTGTTGCGACTAATCCG	31697	GGAAGCGTCGCAACAAACCCA
3052	GSVEESR	17375	GGGAGTGTTGAGGAGTCTCGG	31698	GGAAGCGTCGAAGAAAGCAGA
3053	GSVNPRS	17376	GGGTCTGTGAATCCGAGGTCG	31699	GGAAGCGTCAACCCAAGAAGC
3054	GSVPDSR	17377	GGGAGTGTTCCGGATAGTCGG	31700	GGAAGCGTCCCAGACAGCAGA
3055	GSVPNVI	17378	GGGAGTGTGCCGAATGTGATT	31701	GGAAGCGTCCCAAACGTCATC
3056	GSVQIRP	17379	GGTTCTGTGCAGATTCGGCCT	31702	GGAAGCGTCCAAATCAGACCA
3057	GSYANAA	17380	GGTTCTTATGCTAATGCTGCG	31703	GGAAGCTACGCAAACGCAGCA
3058	GTADLVP	17381	GGTACTGCTGATCTGGTTCCG	31704	GGAACAGCAGACCTCGTCCCA
3059	GTAHLKP	17382	GGTACGGCTCATCTGAAGCCT	31705	GGAACAGCACACCTCAAACCA
3060	GTANRNA	17383	GGGACGGCGAATCGTAATGCT	31706	GGAACAGCAAACAGAAACGCA
3061	GTAPSVM	17384	GGTACTGCTCCTTCTGTTATG	31707	GGAACAGCACCAAGCGTCATG
3062	GTAVQRL	17385	GGTACTGCGGTTCAGCGTCTT	31708	GGAACAGCAGTCCAAAGACTC
3063	GTDFVPS	17386	GGGACTGATTTTGTGCCGAGT	31709	GGAACAGACTTCGTCCCAAGC
3064	GTDIRMP	17387	GGGACGGATATTCGGATGCCT	31710	GGAACAGACATCAGAATGCCA
3065	GTEEFGY	17388	GGTACTGAGGAGTTTGGGTAT	31711	GGAACAGAAGAATTCGGATAC
3066	GTEHTTA	17389	GGTACTGAGCATACTACGGCG	31712	GGAACAGAACACACAACAGCA
3067	GTESNGR	17390	GGGACGGAGTCGAATGGGCGG	31713	GGAACAGAAAGCAACGGAAGA
3068	GTEYNTC	17391	GGGACGGAGTATAATACTTGT	31714	GGAACAGAATACAACACATGC
3069	GTFGTTA	17392	GGTACGTTTGGTACGACGGCG	31715	GGAACATTCGGAACAACAGCA
3070	GTFKASH	17393	GGTACTTTTAAGGCTAGTCAT	31716	GGAACATTCAAAGCAAGCCAC
3071	GTGGVKI	17394	GGTACTGGGGGGGTGAAGATT	31717	GGAACAGGAGGAGTCAAAATC
3072	GTGINHL	17395	GGGACGGGTATTAATCATTTG	31718	GGAACAGGAATCAACCACCTC
3073	GTGKPMG	17396	GGTACTGGTAAGCCTATGGGT	31719	GGAACAGGAAAACCAATGGGA
3074	GTGNVGA	17397	GGTACGGGGAATGTTGGTGCT	31720	GGAACAGGAAACGTCGGAGCA
3075	GTGPSVP	17398	GGGACTGGTCCGTCTGTTCCT	31721	GGAACAGGACCAAGCGTCCCA
3076	GTGRDGS	17399	GGTACGGGTCGGGATGGTAGT	31722	GGAACAGGAAGAGACGGAAGC
3077	GTGSRVV	17400	GGTACGGGTTCGAGGGTGGTG	31723	GGAACAGGAAGCAGAGTCGTC
3078	GTIYGPV	17401	GGTACGATTTATGGGCCGGTG	31724	GGAACAATCTACGGACCAGTC
3079	GTKLYTT	17402	GGGACTAAGCTTTATACTACT	31725	GGAACAAAACTCTACACAACA
3080	GTKYAAS	17403	GGTACTAAGTATGCTGCTTCT	31726	GGAACAAAATACGCAGCAAGC
3081	GTLDTVI	17404	GGGACGCTGGATACTGTGATT	31727	GGAACACTCGACACAGTCATC
3082	GTLEYSM	17405	GGGACTCTTGAGTATTCTATG	31728	GGAACACTCGAATACAGCATG
3083	GTLGCRE	17406	GGTACGCTTGGTTGTCGGGAG	31729	GGAACACTCGGATGCAGAGAA
3084	GTLGLRQ	17407	GGGACGCTGGGTCTTCGTCAG	31730	GGAACACTCGGACTCAGACAA
3085	GTLHGSE	17408	GGTACGTTGCATGGGAGTGAG	31731	GGAACACTCCACGGAAGCGAA
3086	GTLNYAS	17409	GGTACTCTTAATTATGCTTCG	31732	GGAACACTCAACTACGCAAGC
3087	GTLSGLE	17410	GGTACTTTGTCTGGTCTTGAG	31733	GGAACACTCAGCGGACTCGAA
3088	GTLTPTM	17411	GGGACGCTTACTCCTACTATG	31734	GGAACACTCACACCAACAATG
3089	GTMNVVI	17412	GGGACGATGAATGTGGTTATT	31735	GGAACAATGAACGTCGTCATC
3090	GTMSLGP	17413	GGGACTATGAGTCTTGGTCCG	31736	GGAACAATGAGCCTCGGACCA
3091	GTMTNSA	17414	GGGACGATGACTAATTCTGCG	31737	GGAACAATGACAAACAGCGCA
3092	GTNGLML	17415	GGTACGAATGGTCTGATGCTG	31738	GGAACAAACGGACTCATGCTC
3093	GTNGLPA	17416	GGTACGAATGGGCTGCCGGCG	31739	GGAACAAACGGACTCCCAGCA
3094	GTNHAQK	17417	GGTACGAATCATGCGCAGAAG	31740	GGAACAAACCACGCACAAAAA

3095	GTNPVLT	17418	GGGACGAATCCGGTTCTTACT	31741	GGAACAAACCCAGTCCTCACA
3096	GTPAHAA	17419	GGTACTCCGGCTCATGCTGCG	31742	GGAACACCAGCACACGCAGCA
3097	GTPERLP	17420	GGGACTCCGGAGAGGCTTCCG	31743	GGAACACCAGAAAGACTCCCA
3098	GTPMTQG	17421	GGGACGCCTATGACTCAGGGG	31744	GGAACACCAATGACACAAGGA
3099	GTPNNRN	17422	GGTACTCCGAATAATCGTAAT	31745	GGAACACCAAACAACAGAAAC
3100	GTPNVHG	17423	GGTACGCCGAATGTTCATGGG	31746	GGAACACCAAACGTCCACGGA
3101	GTPPGPS	17424	GGTACTCCGCCGGGTCCTTCT	31747	GGAACACCACCAGGACCAAGC
3102	GTPPTRL	17425	GGTACGCCGCCTACGCGTTTG	31748	GGAACACCACCAACAAGACTC
3103	GTPVVDC	17426	GGGACTCCTGTTGTTGATTGT	31749	GGAACACCAGTCGTCGACTGC
3104	GTQAERQ	17427	GGGACTCAGGCGGAGAGGCAG	31750	GGAACACAAGCAGAAAGACAA
3105	GTQARIC	17428	GGGACTCAGGCTCGTATTTGT	31751	GGAACACAAGCAAGAATCTGC
3106	GTQMARA	17429	GGTACGCAGATGGCGAGGGCT	31752	GGAACACAAATGGCAAGAGCA
3107	GTQSTYD	17430	GGTACGCAGAGTACTTATGAT	31753	GGAACACAAAGCACATACGAC
3108	GTRPAHV	17431	GGTACGCGTCCGGCGCATGTG	31754	GGAACAAGACCAGCACACGTC
3109	GTRSTFA	17432	GGGACGAGGAGTACTTTTGCG	31755	GGAACAAGAAGCACATTCGCA
3110	GTRTVVL	17433	GGGACTCGTACTGTTGTTCTG	31756	GGAACAAGAACAGTCGTCCTC
3111	GTRVLSY	17434	GGTACTCGTGTTCTTAGTTAT	31757	GGAACAAGAGTCCTCAGCTAC
3112	GTSGYSP	17435	GGTACTTCTGGGTATTCGCCT	31758	GGAACAAGCGGATACAGCCCA
3113	GTSNLSP	17436	GGGACTTCGAATTTGAGTCCG	31759	GGAACAAGCAACCTCAGCCCA
3114	GTSPDQK	17437	GGTACGTCTCCGGATCAGAAG	31760	GGAACAAGCCCAGACCAAAAA
3115	GTSPVMC	17438	GGTACTAGTCCGGTGATGTGT	31761	GGAACAAGCCCAGTCATGTGC
3116	GTSQKLP	17439	GGTACTAGTCAGAAGCTGCCT	31762	GGAACAAGCCAAAAACTCCCA
3117	GTSQKTS	17440	GGGACGTCTCAGAAGACGAGT	31763	GGAACAAGCCAAAAAACAAGC
3118	GTSSRAP	17441	GGGACTTCGTCGCGTGCTCCT	31764	GGAACAAGCAGCAGAGCACCA
3119	GTSSSGL	17442	GGGACTAGTTCGTCGGGGCTG	31765	GGAACAAGCAGCAGCGGACTC
3120	GTTEIHS	17443	GGGACGACGGAGATTCATTCG	31766	GGAACAACAGAAATCCACAGC
3121	GTTHTNI	17444	GGTACGACTCATACTAATATT	31767	GGAACAACACACACAAACATC
3122	GTTKLGP	17445	GGTACTACTAAGCTGGGGCCT	31768	GGAACAACAAAACTCGGACCA
3123	GTTMVPA	17446	GGGACTACTATGGTGCCTGCT	31769	GGAACAACAATGGTCCCAGCA
3124	GTTNLAG	17447	GGTACGACTAATCTTGCGGGT	31770	GGAACAACAAACCTCGCAGGA
3125	GTTNNMF	17448	GGTACGACGAATAATATGTTT	31771	GGAACAACAAACAACATGTTC
3126	GTTNNNA	17449	GGTACGACTAATAATAATGCT	31772	GGAACAACAAACAACAACGCA
3127	GTTSAES	17450	GGTACGACTTCTGCTGAGAGT	31773	GGAACAACAAGCGCAGAAAGC
3128	GTTSPKS	17451	GGGACTACTAGTCCTAAGTCG	31774	GGAACAACAAGCCCAAAAAGC
3129	GTTSSHE	17452	GGGACTACGTCTTCGCATGAG	31775	GGAACAACAAGCAGCCACGAA
3130	GTTTGHS	17453	GGTACGACTACTGGGCATTCT	31776	GGAACAACAACAGGACACAGC
3131	GTVDRGQ	17454	GGTACTGTTGATCGGGGGCAG	31777	GGAACAGTCGACAGAGGACAA
3132	GTVGLNV	17455	GGTACGGTGGGTCTTAATGTG	31778	GGAACAGTCGGACTCAACGTC
3133	GTVGSDR	17456	GGTACGGTGGGGTCTGATCGT	31779	GGAACAGTCGGAAGCGACAGA
3134	GTVHNNL	17457	GGGACTGTTCATAATAATTTG	31780	GGAACAGTCCACAACAACCTC
3135	GTVHTNA	17458	GGTACTGTGCATACGAATGCT	31781	GGAACAGTCCACACAAACGCA
3136	GTVPEGP	17459	GGTACTGTTCCGGAGGGTCCG	31782	GGAACAGTCCCAGAAGGACCA
3137	GTVQKSD	17460	GGGACGGTTCAGAAGTCGGAT	31783	GGAACAGTCCAAAAAAGCGAC
3138	GTVRSAV	17461	GGGACTGTTAGGAGTGCTGTG	31784	GGAACAGTCAGAAGCGCAGTC
3139	GTYANAV	17462	GGGACTTATGCGAATGCTGTT	31785	GGAACATACGCAAACGCAGTC

3140	GTYVEST	17463	GGTACGTATGTGGAGTCTACT	31786	GGAACATACGTCGAAAGCACA
3141	GVAHEKN	17464	GGGGTGGCTCATGAGAAGAAT	31787	GGAGTCGCACACGAAAAAAAC
3142	GVAKLLA	17465	GGGGTTGCGAAGTTGCTGGCG	31788	GGAGTCGCAAAACTCCTCGCA
3143	GVASSPG	17466	GGTGTGGCGTCGTCTCCTGGG	31789	GGAGTCGCAAGCAGCCCAGGA
3144	GVASTRA	17467	GGGGTGGCTTCTACTCGTGCT	31790	GGAGTCGCAAGCACAAGAGCA
3145	GVATLTL	17468	GGTGTTGCGACGCTTACGCTG	31791	GGAGTCGCAACACTCACACTC
3146	GVAVTER	17469	GGTGTGGCTGTTACGGAGCGG	31792	GGAGTCGCAGTCACAGAAAGA
3147	GVCAESW	17470	GGTGTTTGTGCTGAGTCTTGG	31793	GGAGTCTGCGCAGAAAGCTGG
3148	GVDVKWS	17471	GGTGTTGATGTGAAGTGGAGT	31794	GGAGTCGACGTCAAATGGAGC
3149	GVEAMRA	17472	GGGGTGGAGGCTATGCGTGCG	31795	GGAGTCGAAGCAATGAGAGCA
3150	GVEHNDS	17473	GGGGTTGAGCATAATGATTCG	31796	GGAGTCGAACACAACGACAGC
3151	GVFKETG	17474	GGGGTTTTTAAGGAGACTGGT	31797	GGAGTCTTCAAAGAAACAGGA
3152	GVGASHI	17475	GGGGTGGGTGCTAGTCATATT	31798	GGAGTCGGAGCAAGCCACATC
3153	GVGASRS	17476	GGTGTGGGGGCTTCGCGTAGT	31799	GGAGTCGGAGCAAGCAGAAGC
3154	GVGNMPD	17477	GGGGTGGGTAATATGCCTGAT	31800	GGAGTCGGAAACATGCCAGAC
3155	GVGQVRS	17478	GGGGTGGGTCAGGTGCGGTCT	31801	GGAGTCGGACAAGTCAGAAGC
3156	GVHLSSP	17479	GGTGTGCATTTGAGTTCTCCT	31802	GGAGTCCACCTCAGCAGCCCA
3157	GVHSMVE	17480	GGTGTGCATTCGATGGTTGAG	31803	GGAGTCCACAGCATGGTCGAA
3158	GVHVKPE	17481	GGGGTGCATGTTAAGCCGGAG	31804	GGAGTCCACGTCAAACCAGAA
3159	GVIAHHS	17482	GGTGTGATTGCTCATCATTCG	31805	GGAGTCATCGCACACCACAGC
3160	GVILARM	17483	GGGGTGATTCTTGCTCGGATG	31806	GGAGTCATCCTCGCAAGAATG
3161	GVINPTL	17484	GGGGTGATTAATCCGACGCTG	31807	GGAGTCATCAACCCAACACTC
3162	GVKASIL	17485	GGTGTTAAGGCTTCGATTCTG	31808	GGAGTCAAAGCAAGCATCCTC
3163	GVKFGGS	17486	GGTGTTAAGTTTGGGGGTTCT	31809	GGAGTCAAATTCGGAGGAAGC
3164	GVKHGHY	17487	GGGGTGAAGCATGGGCATTAT	31810	GGAGTCAAACACGGACACTAC
3165	GVKLSPS	17488	GGGGTTAAGCTGTCGCCGTCT	31811	GGAGTCAAACTCAGCCCAAGC
3166	GVKPDPV	17489	GGTGTTAAGCCTGATCCTGTT	31812	GGAGTCAAACCAGACCCAGTC
3167	GVLGPPL	17490	GGTGTGCTTGGTCCGCCTCTG	31813	GGAGTCCTCGGACCACCACTC
3168	GVLRMSS	17491	GGTGTGCTTCGGATGTCGAGT	31814	GGAGTCCTCAGAATGAGCAGC
3169	GVLTNIL	17492	GGTGTGCTGACTAATATTTTG	31815	GGAGTCCTCACAAACATCCTC
3170	GVNERNV	17493	GGGGTTAATGAGCGGAATGTG	31816	GGAGTCAACGAAAGAAACGTC
3171	GVNITSL	17494	GGTGTGAATATTACGAGTTTG	31817	GGAGTCAACATCACAAGCCTC
3172	GVNPSRL	17495	GGGGTGAATCCTTCTCGTCTT	31818	GGAGTCAACCCAAGCAGACTC
3173	GVPATSY	17496	GGTGTGCCGGCTACTTCGTAT	31819	GGAGTCCCAGCAACAAGCTAC
3174	GVPGISA	17497	GGTGTTCCGGGTATTTCGGCG	31820	GGAGTCCCAGGAATCAGCGCA
3175	GVPIQTP	17498	GGTGTTCCGATTCAGACTCCT	31821	GGAGTCCCAATCCAAACACCA
3176	GVRDMGL	17499	GGGGTGCGTGATATGGGTCTT	31822	GGAGTCAGAGACATGGGACTC
3177	GVRGAPL	17500	GGTGTGAGGGGGGCGCCTCTG	31823	GGAGTCAGAGGAGCACCACTC
3178	GVRLDAT	17501	GGTGTGCGGTTGGATGCTACT	31824	GGAGTCAGACTCGACGCAACA
3179	GVRLNET	17502	GGGGTTAGGCTGAATGAGACT	31825	GGAGTCAGACTCAACGAAACA
3180	GVRLQNA	17503	GGTGTGAGGTTGCAGAATGCG	31826	GGAGTCAGACTCCAAAACGCA
3181	GVRSHTM	17504	GGTGTTCGTAGTCATACTATG	31827	GGAGTCAGAAGCCACACAATG
3182	GVSFQSM	17505	GGGGTTTCGTTTCAGTCTATG	31828	GGAGTCAGCTTCCAAAGCATG
3183	GVSKIDS	17506	GGGGTTTCTAAGATTGATTCG	31829	GGAGTCAGCAAAATCGACAGC
3184	GVSRSAN	17507	GGGGTTAGTAGGTCTGCTAAT	31830	GGAGTCAGCAGAAGCGCAAAC

3185	GVSSSQR	17508	GGTGTTTCGTCTTCTCAGCGG	31831	GGAGTCAGCAGCAGCCAAAGA
3186	GVSSVQS	17509	GGTGTGTCTTCTGTGCAGAGT	31832	GGAGTCAGCAGCGTCCAAAGC
3187	GVSTARI	17510	GGTGTTAGTACTGCGAGGATT	31833	GGAGTCAGCACAGCAAGAATC
3188	GVSVSRP	17511	GGTGTTAGTGTTTCGCGTCCG	31834	GGAGTCAGCGTCAGCAGACCA
3189	GVTKAVS	17512	GGGGTTACTAAGGCTGTGTCG	31835	GGAGTCACAAAAGCAGTCAGC
3190	GVTPSYS	17513	GGTGTGACTCCTTCTTATAGT	31836	GGAGTCACACCAAGCTACAGC
3191	GVTQATA	17514	GGGGTGACTCAGGCTACGGCG	31837	GGAGTCACACAAGCAACAGCA
3192	GVTSGGG	17515	GGGGTGACGAGTGGTGGGGGT	31838	GGAGTCACAAGCGGAGGAGGA
3193	GVTSTSS	17516	GGTGTTACTAGTACGTCTAGT	31839	GGAGTCACAAGCACAAGCAGC
3194	GVTTSIH	17517	GGGGTTACGACGTCTATTCAT	31840	GGAGTCACAACAAGCATCCAC
3195	GVTTYSA	17518	GGTGTGACGACTTATTCTGCG	31841	GGAGTCACAACATACAGCGCA
3196	GVVGSHH	17519	GGGGTTGTGGGTTCTCATCAT	31842	GGAGTCGTCGGAAGCCACCAC
3197	GVVHTRT	17520	GGGGTGGTGCATACTCGTACT	31843	GGAGTCGTCCACACAAGAACA
3198	GWALTNG	17521	GGGTGGGCTTTGACGAATGGG	31844	GGATGGGCACTCACAAACGGA
3199	GWEPTSD	17522	GGTTGGGAGCCGACGAGTGAT	31845	GGATGGGAACCAACAAGCGAC
3200	GWGAETI	17523	GGGTGGGGTGCGGAGACTATT	31846	GGATGGGGAGCAGAAACAATC
3201	GWGLVND	17524	GGTTGGGGTCTTGTGAATGAT	31847	GGATGGGGACTCGTCAACGAC
3202	GWHPALP	17525	GGTTGGCATCCTGCGCTGCCG	31848	GGATGGCACCCAGCACTCCCA
3203	GWKGHAD	17526	GGGTGGAAGGGTCATGCTGAT	31849	GGATGGAAAGGACACGCAGAC
3204	GWNADAS	17527	GGGTGGAATGCTGATGCTTCG	31850	GGATGGAACGCAGACGCAAGC
3205	GWNVDGL	17528	GGGTGGAATGTGGATGGTCTG	31851	GGATGGAACGTCGACGGACTC
3206	GWPPKYE	17529	GGGTGGCCGCCGAAGTATGAG	31852	GGATGGCCACCAAAATACGAA
3207	GWQGHNL	17530	GGGTGGCAGGGTCATAATCTG	31853	GGATGGCAAGGACACAACCTC
3208	GWREVVD	17531	GGTTGGCGTGAGGTTGTGGAT	31854	GGATGGAGAGAAGTCGTCGAC
3209	GWRSELE	17532	GGGTGGCGTTCTGAGCTTGAG	31855	GGATGGAGAAGCGAACTCGAA
3210	GWSSAGH	17533	GGGTGGTCTAGTGCGGGTCAT	31856	GGATGGAGCAGCGCAGGACAC
3211	GYAMPVP	17534	GGGTATGCGATGCCTGTTCCT	31857	GGATACGCAATGCCAGTCCCA
3212	GYAMSSS	17535	GGGTATGCTATGTCTTCTAGT	31858	GGATACGCAATGAGCAGCAGC
3213	GYATTVH	17536	GGGTATGCTACTACTGTTCAT	31859	GGATACGCAACAACAGTCCAC
3214	GYDFNPG	17537	GGTTATGATTTTAATCCGGGG	31860	GGATACGACTTCAACCCAGGA
3215	GYGPMRQ	17538	GGGTATGGTCCTATGCGTCAG	31861	GGATACGGACCAATGAGACAA
3216	GYGQAYT	17539	GGTTATGGGCAGGCGTATACT	31862	GGATACGGACAAGCATACACA
3217	GYIHVSG	17540	GGTTATATTCATGTGTCTGGT	31863	GGATACATCCACGTCAGCGGA
3218	GYKTATQ	17541	GGTTATAAGACGGCGACGCAG	31864	GGATACAAAACAGCAACACAA
3219	GYLPVDH	17542	GGGTATTTGCCTGTGGATCAT	31865	GGATACCTCCCAGTCGACCAC
3220	GYLSETH	17543	GGTTATCTGTCGGAGACTCAT	31866	GGATACCTCAGCGAAACACAC
3221	GYLSKMP	17544	GGGTATCTTTCTAAGATGCCT	31867	GGATACCTCAGCAAAATGCCA
3222	GYLTERL	17545	GGGTATCTGACTGAGAGGCTG	31868	GGATACCTCACAGAAAGACTC
3223	GYMIKMP	17546	GGGTATATGATTAAGATGCCT	31869	GGATACATGATCAAAATGCCA
3224	GYPSHAA	17547	GGGTATCCTTCTCATGCTGCG	31870	GGATACCCAAGCCACGCAGCA
3225	GYPSKGP	17548	GGGTATCCTAGTAAGGGGCCT	31871	GGATACCCAAGCAAAGGACCA
3226	GYPTASA	17549	GGGTATCCGACTGCGTCGGCG	31872	GGATACCCAACAGCAAGCGCA
3227	GYPVGPA	17550	GGTTATCCGGTTGGGCCGGCG	31873	GGATACCCAGTCGGACCAGCA
3228	GYQSRCA	17551	GGGTATCAGTCGCGTTGTGCG	31874	GGATACCAAAGCAGATGCGCA
3229	GYRATET	17552	GGTTATCGGGCTACGGAGACG	31875	GGATACAGAGCAACAGAAACA

3230	GYRLMPE	17553	GGTTATCGTTTGATGCCTGAG	31876	GGATACAGACTCATGCCAGAA
3231	GYRSNET	17554	GGGTATCGTTCGAATGAGACG	31877	GGATACAGAAGCAACGAAACA
3232	GYSLPVT	17555	GGTTATTCTCTGCCGGTTACT	31878	GGATACAGCCTCCCAGTCACA
3233	GYSNNKP	17556	GGTTATTCGAATAATAAGCCT	31879	GGATACAGCAACAACAAACCA
3234	GYTSGQP	17557	GGGTATACTTCGGGGCAGCCG	31880	GGATACACAAGCGGACAACCA
3235	GYVPVSQ	17558	GGTTATGTTCCGGTTTCGCAG	31881	GGATACGTCCCAGTCAGCCAA
3236	GYWASSN	17559	GGGTATTGGGCTTCGTCTAAT	31882	GGATACTGGGCAAGCAGCAAC
3237	HAAAQPS	17560	CATGCTGCGGCTCAGCCGTCG	31883	CACGCAGCAGCACAACCAAGC
3238	HAAHQSL	17561	CATGCGGCTCATCAGAGTCTG	31884	CACGCAGCACACCAAAGCCTC
3239	HAASPMV	17562	CATGCTGCGTCGCCTATGGTT	31885	CACGCAGCAAGCCCAATGGTC
3240	HAASSVP	17563	CATGCGGCGTCTTCTGTGCCG	31886	CACGCAGCAAGCAGCGTCCCA
3241	HAESAHP	17564	CATGCTGAGTCTGCGCATCCG	31887	CACGCAGAAAGCGCACACCCA
3242	HAGTVKM	17565	CATGCTGGGACTGTGAAGATG	31888	CACGCAGGAACAGTCAAAATG
3243	HAHLTPS	17566	CATGCGCATTTGACGCCTTCG	31889	CACGCACACCTCACACCAAGC
3244	HAIPTLL	17567	CATGCGATTCCTACTCTGCTT	31890	CACGCAATCCCAACACTCCTC
3245	HAKSRNE	17568	CATGCGAAGTCGCGGAATGAG	31891	CACGCAAAAAGCAGAAACGAA
3246	HAKSVSA	17569	CATGCGAAGTCTGTTTCTGCT	31892	CACGCAAAAAGCGTCAGCGCA
3247	HAKTALT	17570	CATGCGAAGACTGCTCTGACG	31893	CACGCAAAAACAGCACTCACA
3248	HAKVMRD	17571	CATGCGAAGGTTATGCGTGAT	31894	CACGCAAAAGTCATGAGAGAC
3249	HALEHFP	17572	CATGCTCTTGAGCATTTTCCG	31895	CACGCACTCGAACACTTCCCA
3250	HALRNTM	17573	CATGCTCTGAGGAATACGATG	31896	CACGCACTCAGAAACACAATG
3251	HALSDSP	17574	CATGCGCTGTCTGATTCGCCT	31897	CACGCACTCAGCGACAGCCCA
3252	HAMSSNV	17575	CATGCGATGAGTTCGAATGTG	31898	CACGCAATGAGCAGCAACGTC
3253	HANKHTQ	17576	CATGCGAATAAGCATACGCAG	31899	CACGCAAACAAACACACACAA
3254	HANNDPH	17577	CATGCGAATAATGATCCGCAT	31900	CACGCAAACAACGACCCACAC
3255	HANPLNG	17578	CATGCTAATCCTTTGAATGGT	31901	CACGCAAACCCACTCAACGGA
3256	HANPVVG	17579	CATGCTAATCCTGTGGTTGGG	31902	CACGCAAACCCAGTCGTCGGA
3257	HANSTTR	17580	CATGCTAATAGTACTACTAGG	31903	CACGCAAACAGCACAACAAGA
3258	HANTTNT	17581	CATGCTAATACTACGAATACT	31904	CACGCAAACACAACAAACACA
3259	HAPPNYA	17582	CATGCTCCGCCTAATTATGCG	31905	CACGCACCACCAAACTACGCA
3260	HAQLSGT	17583	CATGCTCAGCTTTCTGGGACG	31906	CACGCACAACTCAGCGGAACA
3261	HAQQGGL	17584	CATGCGCAGCAGGGTGGGTTG	31907	CACGCACAACAAGGAGGACTC
3262	HAQVETL	17585	CATGCTCAGGTGGAGACTCTG	31908	CACGCACAAGTCGAAACACTC
3263	HARDSSP	17586	CATGCGCGTGATAGTTCGCCT	31909	CACGCAAGAGACAGCAGCCCA
3264	HARDTFP	17587	CATGCTCGGGATACTTTTCCT	31910	CACGCAAGAGACACATTCCCA
3265	HARIDSS	17588	CATGCGCGTATTGATTCGTCT	31911	CACGCAAGAATCGACAGCAGC
3266	HARPGGL	17589	CATGCTCGGCCTGGGGGTCTG	31912	CACGCAAGACCAGGAGGACTC
3267	HARVEAT	17590	CATGCTCGGGTGGAGGCTACT	31913	CACGCAAGAGTCGAAGCAACA
3268	HASGPDH	17591	CATGCTTCGGGTCCTGATCAT	31914	CACGCAAGCGGACCAGACCAC
3269	HASLSLS	17592	CATGCTTCGCTTTCGCTTTCT	31915	CACGCAAGCCTCAGCCTCAGC
3270	HASNSQH	17593	CATGCTTCTAATTCGCAGCAT	31916	CACGCAAGCAACAGCCAACAC
3271	HASPGQT	17594	CATGCTTCGCCGGGTCAGACG	31917	CACGCAAGCCCAGGACAAACA
3272	HASRIGV	17595	CATGCTAGTCGTATTGGGGTG	31918	CACGCAAGCAGAATCGGAGTC
3273	HASSKPD	17596	CATGCGTCTAGTAAGCCTGAT	31919	CACGCAAGCAGCAAACCAGAC
3274	HASSTRQ	17597	CATGCTTCTTCGACGCGTCAG	31920	CACGCAAGCAGCACAAGACAA

3275	HASTVRT	17598	CATGCTTCTACGGTGCGGACT	31921	CACGCAAGCACAGTCAGAACA
3276	HATDQPH	17599	CATGCTACTGATCAGCCGCAT	31922	CACGCAACAGACCAACCACAC
3277	HATEMVR	17600	CATGCGACTGAGATGGTTAGG	31923	CACGCAACAGAAATGGTCAGA
3278	HATIRTH	17601	CATGCGACTATTCGGACGCAT	31924	CACGCAACAATCAGAACACAC
3279	HATSKLT	17602	CATGCTACGTCTAAGCTGACG	31925	CACGCAACAAGCAAACTCACA
3280	HAVDHKS	17603	CATGCTGTTGATCATAAGTCG	31926	CACGCAGTCGACCACAAAAGC
3281	HAVELAD	17604	CATGCTGTGGAGCTTGCTGAT	31927	CACGCAGTCGAACTCGCAGAC
3282	HAYTLDG	17605	CATGCTTATACTTTGGATGGT	31928	CACGCATACACACTCGACGGA
3283	HDASVHR	17606	CATGATGCGAGTGTGCATAGG	31929	CACGACGCAAGCGTCCACAGA
3284	HDDAWTA	17607	CATGATGATGCTTGGACGGCT	31930	CACGACGACGCATGGACAGCA
3285	HDGRVNL	17608	CATGATGGTCGTGTGAATCTT	31931	CACGACGGAAGAGTCAACCTC
3286	HDGSRST	17609	CATGATGGGAGTCGTTCTACG	31932	CACGACGGAAGCAGAAGCACA
3287	HDHLGTP	17610	CATGATCATCTGGGGACGCCT	31933	CACGACCACCTCGGAACACCA
3288	HDIAKTN	17611	CATGATATTGCGAAGACTAAT	31934	CACGACATCGCAAAAACAAAC
3289	HDIEFNT	17612	CATGATATTGAGTTTAATACT	31935	CACGACATCGAATTCAACACA
3290	HDLAYRP	17613	CATGATCTGGCTTATAGGCCT	31936	CACGACCTCGCATACAGACCA
3291	HDLNPEN	17614	CATGATCTTAATCCTGAGAAT	31937	CACGACCTCAACCCAGAAAAC
3292	HDNRIND	17615	CATGATAATCGGATTAATGAT	31938	CACGACAACAGAATCAACGAC
3293	HDPHAVT	17616	CATGATCCTCATGCGGTTACT	31939	CACGACCCACACGCAGTCACA
3294	HDPIRLG	17617	CATGATCCGATTCGTCTTGGT	31940	CACGACCCAATCAGACTCGGA
3295	HDPMMLL	17618	CATGATCCGATGATGTTGTTG	31941	CACGACCCAATGATGCTCCTC
3296	HDPSDGA	17619	CATGATCCTTCGGATGGGGCG	31942	CACGACCCAAGCGACGGAGCA
3297	HDRIAGL	17620	CATGATCGTATTGCTGGGCTT	31943	CACGACAGAATCGCAGGACTC
3298	HDRVSSG	17621	CATGATCGGGTTAGTTCTGGT	31944	CACGACAGAGTCAGCAGCGGA
3299	HDSARHP	17622	CATGATTCTGCGAGGCATCCG	31945	CACGACAGCGCAAGACACCCA
3300	HDSLSEK	17623	CATGATTCGTTGTCGGAGAAG	31946	CACGACAGCCTCAGCGAAAAA
3301	HDSRFAN	17624	CATGATTCTCGGTTTGCTAAT	31947	CACGACAGCAGATTCGCAAAC
3302	HDSTLGS	17625	CATGATTCGACTTTGGGTTCG	31948	CACGACAGCACACTCGGAAGC
3303	HDTIHGI	17626	CATGATACTATTCATGGGATT	31949	CACGACACAATCCACGGAATC
3304	HDVPKNP	17627	CATGATGTGCCGAAGAATCCG	31950	CACGACGTCCCAAAAAACCCA
3305	HDYPRQL	17628	CATGATTATCCGCGTCAGCTT	31951	CACGACTACCCAAGACAACTC
3306	HEALLPN	17629	CATGAGGCGCTTCTTCCGAAT	31952	CACGAAGCACTCCTCCCAAAC
3307	HEALTGL	17630	CATGAGGCGCTTACGGGTCTG	31953	CACGAAGCACTCACAGGACTC
3308	HEDGSAM	17631	CATGAGGATGGTAGTGCTATG	31954	CACGAAGACGGAAGCGCAATG
3309	HEFGVAF	17632	CATGAGTTTGGTGTGGCGTTT	31955	CACGAATTCGGAGTCGCATTC
3310	HEGGHPY	17633	CATGAGGGGGGGCATCCGTAT	31956	CACGAAGGAGGACACCCATAC
3311	HEGHRGV	17634	CATGAGGGTCATCGTGGGGTG	31957	CACGAAGGACACAGAGGAGTC
3312	HEKVRVH	17635	CATGAGAAGGTGCGGGTTCAT	31958	CACGAAAAAGTCAGAGTCCAC
3313	HEQARSI	17636	CATGAGCAGGCTCGGTCTATT	31959	CACGAACAAGCAAGAAGCATC
3314	HEQCEAY	17637	CATGAGCAGTGTGAGGCTTAT	31960	CACGAACAATGCGAAGCATAC
3315	HEQVERP	17638	CATGAGCAGGTTGAGAGGCCT	31961	CACGAACAAGTCGAAAGACCA
3316	HESDQFP	17639	CATGAGTCTGATCAGTTTCCG	31962	CACGAAAGCGACCAATTCCCA
3317	HETRVMS	17640	CATGAGACGAGGGTTATGTCG	31963	CACGAAACAAGAGTCATGAGC
3318	HEVGFMG	17641	CATGAGGTTGGGTTTATGGGT	31964	CACGAAGTCGGATTCATGGGA
3319	HEVNHNT	17642	CATGAGGTTAATCATAATACG	31965	CACGAAGTCAACCACAACACA

3320	HEVRFSQ	17643	CATGAGGTGAGGTTTTCGCAG	31966	CACGAAGTCAGATTCAGCCAA
3321	HEVSVKC	17644	CATGAGGTTTCGGTGAAGTGT	31967	CACGAAGTCAGCGTCAAATGC
3322	HEVYRNM	17645	CATGAGGTGTATCGGAATATG	31968	CACGAAGTCTACAGAAACATG
3323	HFAQAPS	17646	CATTTTGCGCAGGCGCCTTCG	31969	CACTTCGCACAAGCACCAAGC
3324	HFGSSIP	17647	CATTTTGGTAGTAGTATTCCG	31970	CACTTCGGAAGCAGCATCCCA
3325	HFGTNGD	17648	CATTTTGGGACTAATGGTGAT	31971	CACTTCGGAACAAACGGAGAC
3326	HFNDATV	17649	CATTTTAATGATGCTACGGTG	31972	CACTTCAACGACGCAACAGTC
3327	HFNSSSR	17650	CATTTTAATAGTTCGTCTCGT	31973	CACTTCAACAGCAGCAGCAGA
3328	HFRGAML	17651	CATTTTAGGGGTGCGATGTTG	31974	CACTTCAGAGGAGCAATGCTC
3329	HFSHERS	17652	CATTTTTCTCATGAGAGGTCT	31975	CACTTCAGCCACGAAAGAAGC
3330	HFSPKGT	17653	CATTTTTCGCCGAAGGGGACT	31976	CACTTCAGCCCAAAAGGAACA
3331	HFSSTTI	17654	CATTTTTCGTCGACTACGATT	31977	CACTTCAGCAGCACAACAATC
3332	HFTSREL	17655	CATTTTACGTCTCGTGAGCTT	31978	CACTTCACAAGCAGAGAACTC
3333	HFTSTPS	17656	CATTTTACGTCTACGCCGTCT	31979	CACTTCACAAGCACACCAAGC
3334	HFVPSSA	17657	CATTTTGTTCCGTCTTCTGCT	31980	CACTTCGTCCCAAGCAGCGCA
3335	HGAAALV	17658	CATGGTGCTGCGGCTCTTGTT	31981	CACGGAGCAGCAGCACTCGTC
3336	HGAKLLS	17659	CATGGTGCTAAGCTGCTTAGT	31982	CACGGAGCAAAACTCCTCAGC
3337	HGALSEA	17660	CATGGTGCTCTGTCGGAGGCT	31983	CACGGAGCACTCAGCGAAGCA
3338	HGANRLT	17661	CATGGTGCTAATCGGCTGACG	31984	CACGGAGCAAACAGACTCACA
3339	HGDGHST	17662	CATGGTGATGGGCATTCGACT	31985	CACGGAGACGGACACAGCACA
3340	HGDRALM	17663	CATGGGGATCGTGCTCTGATG	31986	CACGGAGACAGAGCACTCATG
3341	HGDVNRT	17664	CATGGGGATGTGAATCGGACG	31987	CACGGAGACGTCAACAGAACA
3342	HGEMMES	17665	CATGGTGAGATGATGGAGTCG	31988	CACGGAGAAATGATGGAAAGC
3343	HGFHTGS	17666	CATGGTTTTCATACTGGTAGT	31989	CACGGATTCCACACAGGAAGC
3344	HGFQNVD	17667	CATGGGTTTCAGAATGTGGAT	31990	CACGGATTCCAAAACGTCGAC
3345	HGGEVTF	17668	CATGGTGGGGAGGTGACGTTT	31991	CACGGAGGAGAAGTCACATTC
3346	HGGFRGE	17669	CATGGTGGGTTTCGGGGTGAG	31992	CACGGAGGATTCAGAGGAGAA
3347	HGHFSMA	17670	CATGGTCATTTTTCTATGGCT	31993	CACGGACACTTCAGCATGGCA
3348	HGKHVFV	17671	CATGGGAAGCATGTTTTTGTT	31994	CACGGAAAACACGTCTTCGTC
3349	HGLIAVA	17672	CATGGTCTTATTGCGGTTGCG	31995	CACGGACTCATCGCAGTCGCA
3350	HGLNSMP	17673	CATGGTCTTAATTCGATGCCT	31996	CACGGACTCAACAGCATGCCA
3351	HGLSEDY	17674	CATGGTCTGAGTGAGGATTAT	31997	CACGGACTCAGCGAAGACTAC
3352	HGLSLKD	17675	CATGGGTTGTCGTTGAAGGAT	31998	CACGGACTCAGCCTCAAAGAC
3353	HGMEDGL	17676	CATGGTATGGAGGATGGGCTT	31999	CACGGAATGGAAGACGGACTC
3354	HGNLNYH	17677	CATGGGAATTTGAATTATCAT	32000	CACGGAAACCTCAACTACCAC
3355	HGPNASD	17678	CATGGTCCGAATGCGTCTGAT	32001	CACGGACCAAACGCAAGCGAC
3356	HGREVHQ	17679	CATGGTAGGGAGGTTCATCAG	32002	CACGGAAGAGAAGTCCACCAA
3357	HGSGSCC	17680	CATGGTAGTGGTAGTTGTTGT	32003	CACGGAAGCGGAAGCTGCTGC
3358	HGSIESQ	17681	CATGGTTCGATTGAGTCGCAG	32004	CACGGAAGCATCGAAAGCCAA
3359	HGSKTMS	17682	CATGGGTCGAAGACGATGTCT	32005	CACGGAAGCAAAACAATGAGC
3360	HGSMWPE	17683	CATGGTTCGATGTGGCCTGAG	32006	CACGGAAGCATGTGGCCAGAA
3361	HGSSTRN	17684	CATGGTTCTAGTACTCGTAAT	32007	CACGGAAGCAGCACAAGAAAC
3362	HGSTENS	17685	CATGGTAGTACGGAGAATTCT	32008	CACGGAAGCACAGAAAACAGC
3363	HGSTKLP	17686	CATGGGAGTACTAAGTTGCCG	32009	CACGGAAGCACAAAACTCCCA
3364	HGTGVFG	17687	CATGGTACGGGGGTTTTTGGT	32010	CACGGAACAGGAGTCTTCGGA

3365	HGTNRTH	17688	CATGGTACGAATCGGACGCAT	32011	CACGGAACAAACAGAACACAC
3366	HGTSKHS	17689	CATGGTACGTCGAAGCATAGT	32012	CACGGAACAAGCAAACACAGC
3367	HGTSSRP	17690	CATGGTACTTCGTCGCGGCCT	32013	CACGGAACAAGCAGCAGACCA
3368	HGVHHQV	17691	CATGGTGTGCATCATCAGGTT	32014	CACGGAGTCCACCACCAAGTC
3369	HGVYPHL	17692	CATGGGGTTTATCCTCATCTT	32015	CACGGAGTCTACCCACACCTC
3370	HHAAGAV	17693	CATCATGCGGCTGGTGCTGTT	32016	CACCACGCAGCAGGAGCAGTC
3371	HHAKANL	17694	CATCATGCTAAGGCTAATCTT	32017	CACCACGCAAAAGCAAACCTC
3372	HHALPPD	17695	CATCATGCTCTTCCGCCTGAT	32018	CACCACGCACTCCCACCAGAC
3373	HHAPNTP	17696	CATCATGCGCCTAATACTCCG	32019	CACCACGCACCAAACACACCA
3374	HHAQGEA	17697	CATCATGCTCAGGGGGAGGCT	32020	CACCACGCACAAGGAGAAGCA
3375	HHDDRLQ	17698	CATCATGATGATCGTTTGCAG	32021	CACCACGACGACAGACTCCAA
3376	HHDLSIP	17699	CATCATGATCTGTCTATTCCT	32022	CACCACGACCTCAGCATCCCA
3377	HHDPTTR	17700	CATCATGATCCGACGACTCGT	32023	CACCACGACCCAACAACAAGA
3378	HHGTDRP	17701	CATCATGGTACTGATCGTCCG	32024	CACCACGGAACAGACAGACCA
3379	HHLAFLD	17702	CATCATCTGGCGTTTTTGGAT	32025	CACCACCTCGCATTCCTCGAC
3380	HHMSTAS	17703	CATCATATGTCGACGGCTTCT	32026	CACCACATGAGCACAGCAAGC
3381	HHNVNSL	17704	CATCATAATGTTAATAGTCTT	32027	CACCACAACGTCAACAGCCTC
3382	HHPRLDT	17705	CATCATCCTAGGCTGGATACT	32028	CACCACCCAAGACTCGACACA
3383	HHRVETG	17706	CATCATAGGGTTGAGACTGGT	32029	CACCACAGAGTCGAAACAGGA
3384	HHSPAIT	17707	CATCATAGTCCTGCTATTACG	32030	CACCACAGCCCAGCAATCACA
3385	HHTNPDP	17708	CATCATACGAATCCTGATCCG	32031	CACCACACAAACCCAGACCCA
3386	HIALTSP	17709	CATATTGCGCTTACGAGTCCT	32032	CACATCGCACTCACAAGCCCA
3387	HILTSAP	17710	CATATTCTGACTTCTGCGCCG	32033	CACATCCTCACAAGCGCACCA
3388	HIPLKQA	17711	CATATTCCTTTGAAGCAGGCT	32034	CACATCCCACTCAAACAAGCA
3389	HIPSSSG	17712	CATATTCCGAGTAGTTCTGGG	32035	CACATCCCAAGCAGCAGCGGA
3390	HIPVMTP	17713	CATATTCCTGTGATGACTCCT	32036	CACATCCCAGTCATGACACCA
3391	HIRHDPK	17714	CATATTAGGCATGATCCGAAG	32037	CACATCAGACACGACCCAAAA
3392	HIRTGMP	17715	CATATTCGGACGGGTATGCCT	32038	CACATCAGAACAGGAATGCCA
3393	HISPMPV	17716	CATATTTCTCCGATGCCGGTG	32039	CACATCAGCCCAATGCCAGTC
3394	HISSSTV	17717	CATATTTCGAGTAGTACTGTG	32040	CACATCAGCAGCAGCACAGTC
3395	HITQQLT	17718	CATATTACTCAGCAGCTTACT	32041	CACATCACACAACAACTCACA
3396	HKADSVS	17719	CATAAGGCGGATTCTGTTTCT	32042	CACAAAGCAGACAGCGTCAGC
3397	HKFSSPL	17720	CATAAGTTTTCTAGTCCGCTG	32043	CACAAATTCAGCAGCCCACTC
3398	HKGLSPL	17721	CATAAGGGGCTTTCGCCTCTT	32044	CACAAAGGACTCAGCCCACTC
3399	HKLGGSF	17722	CATAAGCTGGGTGGGTCTTTT	32045	CACAAACTCGGAGGAAGCTTC
3400	HKLPGHH	17723	CATAAGCTGCCTGGTCATCAT	32046	CACAAACTCCCAGGACACCAC
3401	HKLTSNG	17724	CATAAGCTGACTTCGAATGGT	32047	CACAAACTCACAAGCAACGGA
3402	HKNIGVV	17725	CATAAGAATATTGGGGTGGTG	32048	CACAAAAACATCGGAGTCGTC
3403	HKPPIVP	17726	CATAAGCCTCCGATTGTTCCT	32049	CACAAACCACCAATCGTCCCA
3404	HKPQVGV	17727	CATAAGCCGCAGGTTGGTGTG	32050	CACAAACCACAAGTCGGAGTC
3405	HKPRPEV	17728	CATAAGCCGCGTCCGGAGGTG	32051	CACAAACCAAGACCAGAAGTC
3406	HKQSQAG	17729	CATAAGCAGTCTCAGGCTGGG	32052	CACAAACAAAGCCAAGCAGGA
3407	HKQTMER	17730	CATAAGCAGACGATGGAGCGG	32053	CACAAACAAACAATGGAAAGA
3408	HKSSDRL	17731	CATAAGTCTTCGGATAGGCTG	32054	CACAAAAGCAGCGACAGACTC
3409	HKSVLVP	17732	CATAAGAGTGTGCTGGTTCCT	32055	CACAAAAGCGTCCTCGTCCCA

3410	HKTSVPI	17733	CATAAGACTTCGGTGCCGATT	32056	CACAAAACAAGCGTCCCAATC
3411	HKVPAQN	17734	CATAAGGTTCCTGCGCAGAAT	32057	CACAAAGTCCCAGCACAAAAC
3412	HKVPGLG	17735	CATAAGGTGCCTGGTCTGGGT	32058	CACAAAGTCCCAGGACTCGGA
3413	HKYNLGA	17736	CATAAGTATAATCTGGGTGCT	32059	CACAAATACAACCTCGGAGCA
3414	HLAALSH	17737	CATCTTGCGGCGCTTTCTCAT	32060	CACCTCGCAGCACTCAGCCAC
3415	HLAEVRE	17738	CATTTGGCTGAGGTTAGGGAG	32061	CACCTCGCAGAAGTCAGAGAA
3416	HLAGTGA	17739	CATTTGGCTGGTACTGGTGCT	32062	CACCTCGCAGGAACAGGAGCA
3417	HLALAPS	17740	CATTTGGCTCTGGCTCCGTCT	32063	CACCTCGCACTCGCACCAAGC
3418	HLAPAIN	17741	CATCTGGCGCCGGCTATTAAT	32064	CACCTCGCACCAGCAATCAAC
3419	HLELGTR	17742	CATTTGGAGCTTGGTACTCGG	32065	CACCTCGAACTCGGAACAAGA
3420	HLERPLS	17743	CATCTGGAGCGGCCTTTGTCG	32066	CACCTCGAAAGACCACTCAGC
3421	HLGPDAI	17744	CATTTGGGGCCGGATGCTATT	32067	CACCTCGGACCAGACGCAATC
3422	HLGSSNW	17745	CATCTTGGTAGTTCGAATTGG	32068	CACCTCGGAAGCAGCAACTGG
3423	HLHSDSG	17746	CATTTGCATTCGGATTCTGGG	32069	CACCTCCACAGCGACAGCGGA
3424	HLHSHES	17747	CATTTGCATTCGCATGAGAGT	32070	CACCTCCACAGCCACGAAAGC
3425	HLHYPVA	17748	CATCTTCATTATCCGGTGGCG	32071	CACCTCCACTACCCAGTCGCA
3426	HLNAKFA	17749	CATCTGAATGCGAAGTTTGCT	32072	CACCTCAACGCAAAATTCGCA
3427	HLNAPAT	17750	CATCTTAATGCTCCTGCGACG	32073	CACCTCAACGCACCAGCAACA
3428	HLNLEGR	17751	CATCTGAATCTTGAGGGGCGT	32074	CACCTCAACCTCGAAGGAAGA
3429	HLPAHPL	17752	CATTTGCCTGCGCATCCGCTG	32075	CACCTCCCAGCACACCCACTC
3430	HLPKNPS	17753	CATCTGCCGAAGAATCCTTCG	32076	CACCTCCCAAAAAACCCAAGC
3431	HLPSGLT	17754	CATTTGCCTAGTGGTCTTACT	32077	CACCTCCCAAGCGGACTCACA
3432	HLPTSDA	17755	CATTTGCCTACTAGTGATGCG	32078	CACCTCCCAACAAGCGACGCA
3433	HLPYNVP	17756	CATTTGCCGTATAATGTGCCT	32079	CACCTCCCATACAACGTCCCA
3434	HLQILEA	17757	CATCTTCAGATTCTTGAGGCG	32080	CACCTCCAAATCCTCGAAGCA
3435	HLRELIS	17758	CATCTGAGGGAGCTGATTTCG	32081	CACCTCAGAGAACTCATCAGC
3436	HLRSGVG	17759	CATCTTAGGTCTGGTGTTGGT	32082	CACCTCAGAAGCGGAGTCGGA
3437	HLSDWPI	17760	CATTTGTCTGATTGGCCGATT	32083	CACCTCAGCGACTGGCCAATC
3438	HLSGMHA	17761	CATCTGTCTGGTATGCATGCT	32084	CACCTCAGCGGAATGCACGCA
3439	HLSIAAS	17762	CATCTGTCTATTGCTGCTTCT	32085	CACCTCAGCATCGCAGCAAGC
3440	HLSPFTD	17763	CATCTGTCGCCTTTTACTGAT	32086	CACCTCAGCCCATTCACAGAC
3441	HLSPLVR	17764	CATCTGAGTCCTTTGGTTCGT	32087	CACCTCAGCCCACTCGTCAGA
3442	HLSPRPP	17765	CATTTGTCTCCTCGTCCTCCT	32088	CACCTCAGCCCAAGACCACCA
3443	HLSVRLS	17766	CATCTTTCTGTGCGTTTGAGT	32089	CACCTCAGCGTCAGACTCAGC
3444	HLSVSGS	17767	CATCTTTCTGTTTCTGGGTCT	32090	CACCTCAGCGTCAGCGGAAGC
3445	HLTALTG	17768	CATTTGACTGCTTTGACTGGT	32091	CACCTCACAGCACTCACAGGA
3446	HLTDTRR	17769	CATTTGACGGATACGCGTCGG	32092	CACCTCACAGACACAAGAAGA
3447	HLTSGAA	17770	CATCTTACGTCTGGTGCTGCT	32093	CACCTCACAAGCGGAGCAGCA
3448	HLTSNSL	17771	CATTTGACGTCGAATTCGCTT	32094	CACCTCACAAGCAACAGCCTC
3449	HLTSRAG	17772	CATCTGACGTCGCGGGCGGGT	32095	CACCTCACAAGCAGAGCAGGA
3450	HLVRGEP	17773	CATCTTGTTAGGGGTGAGCCG	32096	CACCTCGTCAGAGGAGAACCA
3451	HLVSNRS	17774	CATCTTGTTAGTAATCGGTCG	32097	CACCTCGTCAGCAACAGAAGC
3452	HLVSTTS	17775	CATTTGGTGTCTACGACTTCG	32098	CACCTCGTCAGCACAACAAGC
3453	HLVSTVA	17776	CATCTGGTGTCTACGGTGGCT	32099	CACCTCGTCAGCACAGTCGCA
3454	HMAGGDY	17777	CATATGGCTGGGGGTGATTAT	32100	CACATGGCAGGAGGAGACTAC

3455	HMDSTIS	17778	CATATGGATTCGACGATTTCG	32101	CACATGGACAGCACAATCAGC
3456	HMGDMNR	17779	CATATGGGTGATATGAATCGT	32102	CACATGGGAGACATGAACAGA
3457	HMIIVDS	17780	CATATGATTATTGTGGATAGT	32103	CACATGATCATCGTCGACAGC
3458	HMKPQSD	17781	CATATGAAGCCGCAGTCGGAT	32104	CACATGAAACCACAAAGCGAC
3459	HMLTHTH	17782	CATATGTTGACGCATACTCAT	32105	CACATGCTCACACACACACAC
3460	HMMKLGS	17783	CATATGATGAAGTTGGGGAGT	32106	CACATGATGAAACTCGGAAGC
3461	HMMSHGP	17784	CATATGATGTCGCATGGTCCG	32107	CACATGATGAGCCACGGACCA
3462	HMNADHK	17785	CATATGAATGCTGATCATAAG	32108	CACATGAACGCAGACCACAAA
3463	HMNLKDA	17786	CATATGAATCTTAAGGATGCG	32109	CACATGAACCTCAAAGACGCA
3464	HMPDDPS	17787	CATATGCCTGATGATCCGAGT	32110	CACATGCCAGACGACCCAAGC
3465	HMPNMYS	17788	CATATGCCTAATATGTATTCG	32111	CACATGCCAAACATGTACAGC
3466	HMSNPSF	17789	CATATGTCTAATCCTAGTTTT	32112	CACATGAGCAACCCAAGCTTC
3467	HMSVLQK	17790	CATATGAGTGTGCTGCAGAAG	32113	CACATGAGCGTCCTCCAAAAA
3468	HMSVRDP	17791	CATATGTCTGTTCGTGATCCT	32114	CACATGAGCGTCAGAGACCCA
3469	HMTGTNL	17792	CATATGACTGGTACTAATCTT	32115	CACATGACAGGAACAAACCTC
3470	HMVANPA	17793	CATATGGTTGCTAATCCTGCT	32116	CACATGGTCGCAAACCCAGCA
3471	HNAAQNQ	17794	CATAATGCGGCTCAGAATCAG	32117	CACAACGCAGCACAAAACCAA
3472	HNAGYMP	17795	CATAATGCTGGTTATATGCCG	32118	CACAACGCAGGATACATGCCA
3473	HNASAVN	17796	CATAATGCTTCGGCTGTGAAT	32119	CACAACGCAAGCGCAGTCAAC
3474	HNELPPP	17797	CATAATGAGTTGCCGCCTCCG	32120	CACAACGAACTCCCACCACCA
3475	HNEPDKG	17798	CATAATGAGCCTGATAAGGGT	32121	CACAACGAACCAGACAAAGGA
3476	HNHDTVL	17799	CATAATCATGATACGGTGCTT	32122	CACAACCACGACACAGTCCTC
3477	HNHIVHA	17800	CATAATCATATTGTGCATGCG	32123	CACAACCACATCGTCCACGCA
3478	HNKSSYV	17801	CATAATAAGTCGTCTTATGTT	32124	CACAACAAAAGCAGCTACGTC
3479	HNMRIPS	17802	CATAATATGCGGATTCCTTCT	32125	CACAACATGAGAATCCCAAGC
3480	HNNTVNQ	17803	CATAATAATACTGTGAATCAG	32126	CACAACAACACAGTCAACCAA
3481	HNPPKLT	17804	CATAATCCGCCTAAGCTGACT	32127	CACAACCCACCAAAACTCACA
3482	HNPRELG	17805	CATAATCCTCGGGAGTTGGGG	32128	CACAACCCAAGAGAACTCGGA
3483	HNPSLRT	17806	CATAATCCGTCTCTTCGTACT	32129	CACAACCCAAGCCTCAGAACA
3484	HNQTLGS	17807	CATAATCAGACTCTGGGGTCT	32130	CACAACCAAACACTCGGAAGC
3485	HNRNDGF	17808	CATAATAGGAATGATGGTTTT	32131	CACAACAGAAACGACGGATTC
3486	HNSHHYA	17809	CATAATAGTCATCATTATGCT	32132	CACAACAGCCACCACTACGCA
3487	HNSHSMR	17810	CATAATTCTCATAGTATGAGG	32133	CACAACAGCCACAGCATGAGA
3488	HNSPGVG	17811	CATAATTCGCCTGGTGTTGGG	32134	CACAACAGCCCAGGAGTCGGA
3489	HNSSFDM	17812	CATAATTCGTCTTTTGATATG	32135	CACAACAGCAGCTTCGACATG
3490	HPAILQL	17813	CATCCTGCTATTCTGCAGCTG	32136	CACCCAGCAATCCTCCAACTC
3491	HPATKLG	17814	CATCCTGCGACGAAGCTTGGG	32137	CACCCAGCAACAAAACTCGGA
3492	HPDPHST	17815	CATCCTGATCCGCATTCTACG	32138	CACCCAGACCCACACAGCACA
3493	HPEKRNP	17816	CATCCGGAGAAGCGGAATCCG	32139	CACCCAGAAAAAAGAAACCCA
3494	HPELPLH	17817	CATCCTGAGCTGCCGCTGCAT	32140	CACCCAGAACTCCCACTCCAC
3495	HPEMLVT	17818	CATCCTGAGATGCTTGTTACG	32141	CACCCAGAAATGCTCGTCACA
3496	HPFGTAS	17819	CATCCGTTTGGTACGGCGTCT	32142	CACCCATTCGGAACAGCAAGC
3497	HPGFNHD	17820	CATCCGGGGTTTAATCATGAT	32143	CACCCAGGATTCAACCACGAC
3498	HPGPLVA	17821	CATCCGGGGCCGTTGGTGGCT	32144	CACCCAGGACCACTCGTCGCA
3499	HPGQSPV	17822	CATCCTGGTCAGAGTCCGGTT	32145	CACCCAGGACAAAGCCCAGTC

3500	HPGYSSN	17823	CATCCTGGTTATAGTTCTAAT	32146	CACCCAGGATACAGCAGCAAC
3501	HPIIPIS	17824	CATCCGATTATTCCTATTTCG	32147	CACCCAATCATCCCAATCAGC
3502	HPINTRS	17825	CATCCGATTAATACTAGGTCT	32148	CACCCAATCAACACAAGAAGC
3503	HPIPFPG	17826	CATCCTATTCCGTTTCCTGGT	32149	CACCCAATCCCATTCCCAGGA
3504	HPKGEPP	17827	CATCCTAAGGGGGAGCCGCCG	32150	CACCCAAAAGGAGAACCACCA
3505	HPKLVSV	17828	CATCCTAAGTTGGTTTCGGTT	32151	CACCCAAAACTCGTCAGCGTC
3506	HPLEDQL	17829	CATCCTTTGGAGGATCAGCTT	32152	CACCCACTCGAAGACCAACTC
3507	HPLNARP	17830	CATCCTCTTAATGCGCGGCCG	32153	CACCCACTCAACGCAAGACCA
3508	HPMTSNS	17831	CATCCTATGACGTCGAATTCT	32154	CACCCAATGACAAGCAACAGC
3509	HPPKYVT	17832	CATCCTCCTAAGTATGTGACG	32155	CACCCACCAAAATACGTCACA
3510	HPPPSHM	17833	CATCCTCCTCCGTCTCATATG	32156	CACCCACCACCAAGCCACATG
3511	HPPPTDS	17834	CATCCGCCGCCTACTGATTCT	32157	CACCCACCACCAACAGACAGC
3512	HPPRTPA	17835	CATCCTCCGAGGACTCCTGCG	32158	CACCCACCAAGAACACCAGCA
3513	HPQRQAS	17836	CATCCTCAGCGGCAGGCTTCT	32159	CACCCACAAAGACAAGCAAGC
3514	HPQSSHW	17837	CATCCTCAGTCGAGTCATTGG	32160	CACCCACAAAGCAGCCACTGG
3515	HPSFSPL	17838	CATCCGTCTTTTTCGCCTCTT	32161	CACCCAAGCTTCAGCCCACTC
3516	HPSGYSN	17839	CATCCTAGTGGTTATTCTAAT	32162	CACCCAAGCGGATACAGCAAC
3517	HPSIAGM	17840	CATCCGAGTATTGCTGGGATG	32163	CACCCAAGCATCGCAGGAATG
3518	HPSIVRD	17841	CATCCTTCTATTGTGCGTGAT	32164	CACCCAAGCATCGTCAGAGAC
3519	HPSLAIG	17842	CATCCGAGTCTTGCGATTGGT	32165	CACCCAAGCCTCGCAATCGGA
3520	HPSRVIM	17843	CATCCTTCTCGGGTGATTATG	32166	CACCCAAGCAGAGTCATCATG
3521	HPSSQLH	17844	CATCCTTCTTCTCAGTTGCAT	32167	CACCCAAGCAGCCAACTCCAC
3522	HPSYSSG	17845	CATCCGTCGTATTCGTCGGGG	32168	CACCCAAGCTACAGCAGCGGA
3523	HPTAKLP	17846	CATCCTACGGCTAAGCTGCCG	32169	CACCCAACAGCAAAACTCCCA
3524	HPTETTE	17847	CATCCTACTGAGACTACTGAG	32170	CACCCAACAGAAACAACAGAA
3525	HPTGTKD	17848	CATCCGACGGGTACGAAGGAT	32171	CACCCAACAGGAACAAAAGAC
3526	HPTLSHY	17849	CATCCTACGCTGTCTCATTAT	32172	CACCCAACACTCAGCCACTAC
3527	HPTNNSN	17850	CATCCGACGAATAATAGTAAT	32173	CACCCAACAAACAACAGCAAC
3528	HPTSIIL	17851	CATCCGACGTCGATTATTCTG	32174	CACCCAACAAGCATCATCCTC
3529	HPTTRFG	17852	CATCCTACTACTCGGTTTGGT	32175	CACCCAACAACAAGATTCGGA
3530	HPVSSRQ	17853	CATCCTGTTTCGAGTCGGCAG	32176	CACCCAGTCAGCAGCAGACAA
3531	HPYQNSL	17854	CATCCGTATCAGAATTCGCTG	32177	CACCCATACCAAAACAGCCTC
3532	HQAEAYS	17855	CATCAGGCGGAGGCTTATTCG	32178	CACCAAGCAGAAGCATACAGC
3533	HQAPGLQ	17856	CATCAGGCTCCTGGTCTTCAG	32179	CACCAAGCACCAGGACTCCAA
3534	HQDIAHL	17857	CATCAGGATATTGCTCATTTG	32180	CACCAAGACATCGCACACCTC
3535	HQFNREP	17858	CATCAGTTTAATAGGGAGCCT	32181	CACCAATTCAACAGAGAACCA
3536	HQGDQNI	17859	CATCAGGGTGATCAGAATATT	32182	CACCAAGGAGACCAAAACATC
3537	HQGHPRD	17860	CATCAGGGTCATCCTCGTGAT	32183	CACCAAGGACACCCAAGAGAC
3538	HQGSPTF	17861	CATCAGGGGTCTCCTACGTTT	32184	CACCAAGGAAGCCCAACATTC
3539	HQLGSQM	17862	CATCAGTTGGGTTCGCAGATG	32185	CACCAACTCGGAAGCCAAATG
3540	HQPHIVQ	17863	CATCAGCCGCATATTGTGCAG	32186	CACCAACCACACATCGTCCAA
3541	HQPHSSL	17864	CATCAGCCGCATTCTTCGTTG	32187	CACCAACCACACAGCAGCCTC
3542	HQQSTNN	17865	CATCAGCAGTCGACGAATAAT	32188	CACCAACAAAGCACAAACAAC
3543	HQRTVGV	17866	CATCAGAGGACTGTTGGTGTG	32189	CACCAAAGAACAGTCGGAGTC
3544	HQSPSDR	17867	CATCAGAGTCCTTCGGATAGG	32190	CACCAAAGCCCAAGCGACAGA

3545	HQTASVL	17868	CATCAGACTGCTTCTGTTTTG	32191	CACCAAACAGCAAGCGTCCTC
3546	HQTVGQN	17869	CATCAGACGGTGGGTCAGAAT	32192	CACCAAACAGTCGGACAAAAC
3547	HRASYVD	17870	CATCGGGCTAGTTATGTGGAT	32193	CACAGAGCAAGCTACGTCGAC
3548	HRDALQQ	17871	CATAGGGATGCTTTGCAGCAG	32194	CACAGAGACGCACTCCAACAA
3549	HRDISTG	17872	CATAGGGATATTTCGACGGGT	32195	CACAGAGACATCAGCACAGGA
3550	HREEKAS	17873	CATCGGGAGGAGAAGGCTTCG	32196	CACAGAGAAGAAAAAGCAAGC
3551	HREGLEH	17874	CATCGTGAGGGTTTGGAGCAT	32197	CACAGAGAAGGACTCGAACAC
3552	HREHGYP	17875	CATCGTGAGCATGGTTATCCT	32198	CACAGAGAACACGGATACCCA
3553	HRENKVA	17876	CATCGTGAGAATAAGGTGGCG	32199	CACAGAGAAAACAAAGTCGCA
3554	HRIGDVP	17877	CATCGGATTGGGGATGTGCCG	32200	CACAGAATCGGAGACGTCCCA
3555	HRLPNVA	17878	CATCGGTTGCCGAATGTGGCG	32201	CACAGACTCCCAAACGTCGCA
3556	HRPEMLS	17879	CATCGTCCGGAGATGCTGTCT	32202	CACAGACCAGAAATGCTCAGC
3557	HRPIATY	17880	CATCGGCCTATTGCTACGTAT	32203	CACAGACCAATCGCAACATAC
3558	HRTGLPE	17881	CATCGTACTGGTCTTCCGGAG	32204	CACAGAACAGGACTCCCAGAA
3559	HRTSMPL	17882	CATCGTACGTCTATGCCTCTT	32205	CACAGAACAAGCATGCCACTC
3560	HRTTNNF	17883	CATAGGACTACGAATAATTTT	32206	CACAGAACAACAAACAACTTC
3561	HRVGGLS	17884	CATCGGGTGGGGGGTCTGTCT	32207	CACAGAGTCGGAGGACTCAGC
3562	HRVVAIP	17885	CATCGTGTTGTTGCTATTCCG	32208	CACAGAGTCGTCGCAATCCCA
3563	HSAALCM	17886	CATAGTGCTGCTCTTTGTATG	32209	CACAGCGCAGCACTCTGCATG
3564	HSAAMPS	17887	CATTCGGCTGCGATGCCTTCT	32210	CACAGCGCAGCAATGCCAAGC
3565	HSAGTET	17888	CATTCGGCGGGGACGGAGACT	32211	CACAGCGCAGGAACAGAAACA
3566	HSAKMSG	17889	CATTCGGCTAAGATGTCTGGG	32212	CACAGCGCAAAAATGAGCGGA
3567	HSAKSMH	17890	CATAGTGCTAAGTCTATGCAT	32213	CACAGCGCAAAAAGCATGCAC
3568	HSALLHM	17891	CATTCGGCGTTGTTGCATATG	32214	CACAGCGCACTCCTCCACATG
3569	HSAQITI	17892	CATAGTGCTCAGATTACTATT	32215	CACAGCGCACAAATCACAATC
3570	HSATMCS	17893	CATTCGGCTACTATGTGTAGT	32216	CACAGCGCAACAATGTGCAGC
3571	HSDRSSA	17894	CATAGTGATCGTTCTTCTGCT	32217	CACAGCGACAGAAGCAGCGCA
3572	HSEKSGF	17895	CATAGTGAGAAGTCTGGTTTT	32218	CACAGCGAAAAAAGCGGATTC
3573	HSEYPTK	17896	CATAGTGAGTATCCTACGAAG	32219	CACAGCGAATACCCAACAAAA
3574	HSFLDLE	17897	CATAGTTTTCTTGATTTGGAG	32220	CACAGCTTCCTCGACCTCGAA
3575	HSFSMME	17898	CATTCTTTTTCTATGATGGAG	32221	CACAGCTTCAGCATGATGGAA
3576	HSGHSQG	17899	CATAGTGGTCATAGTCAGGGT	32222	CACAGCGGACACAGCCAAGGA
3577	HSGKILH	17900	CATTCTGGTAAGATTTTGCAT	32223	CACAGCGGAAAAATCCTCCAC
3578	HSGRAYS	17901	CATAGTGGTCGTGCTTATTCT	32224	CACAGCGGAAGAGCATACAGC
3579	HSGSSET	17902	CATAGTGGGTCTTCGGAGACT	32225	CACAGCGGAAGCAGCGAAACA
3580	HSHGVPS	17903	CATTCGCATGGGGTGCCTTCT	32226	CACAGCCACGGAGTCCCAAGC
3581	HSHVNSS	17904	CATAGTCATGTTAATAGTTCG	32227	CACAGCCACGTCAACAGCAGC
3582	HSIHSRE	17905	CATTCTATTCATAGTAGGGAG	32228	CACAGCATCCACAGCAGAGAA
3583	HSIQHIP	17906	CATAGTATTCAGCATATTCCT	32229	CACAGCATCCAACACATCCCA
3584	HSKASVI	17907	CATTCTAAGGCGTCTGTGATT	32230	CACAGCAAAGCAAGCGTCATC
3585	HSKPAQI	17908	CATTCTAAGCCTGCGCAGATT	32231	CACAGCAAACCAGCACAAATC
3586	HSKSVVT	17909	CATTCGAAGAGTGTTGTGACT	32232	CACAGCAAAAGCGTCGTCACA
3587	HSLGAIP	17910	CATTCTCTGGGTGCGATTCCT	32233	CACAGCCTCGGAGCAATCCCA
3588	HSLGTSG	17911	CATTCGTTGGGTACGAGTGGG	32234	CACAGCCTCGGAACAAGCGGA
3589	HSLLNST	17912	CATAGTCTTTTGAATAGTACT	32235	CACAGCCTCCTCAACAGCACA

3590	HSLPGLK	17913	CATTCGCTTCCTGGGCTGAAG	32236	CACAGCCTCCCAGGACTCAAA
3591	HSLRTPQ	17914	CATTCTCTTCGTACGCCTCAG	32237	CACAGCCTCAGAACACCACAA
3592	HSMEEAL	17915	CATAGTATGGAGGAGGCGCTG	32238	CACAGCATGGAAGAAGCACTC
3593	HSMPDQI	17916	CATTCGATGCCGGATCAGATT	32239	CACAGCATGCCAGACCAAATC
3594	HSMSEAK	17917	CATTCTATGTCGGAGGCTAAG	32240	CACAGCATGAGCGAAGCAAAA
3595	HSNKQPN	17918	CATTCTAATAAGCAGCCGAAT	32241	CACAGCAACAAACAACCAAAC
3596	HSNKTSL	17919	CATTCGAATAAGACGTCGCTG	32242	CACAGCAACAAAACAAGCCTC
3597	HSNLRAM	17920	CATAGTAATCTTAGGGCGATG	32243	CACAGCAACCTCAGAGCAATG
3598	HSNTISS	17921	CATTCTAATACGATTTCTTCT	32244	CACAGCAACACAATCAGCAGC
3599	HSPARTA	17922	CATTCTCCGGCTCGGACTGCT	32245	CACAGCCCAGCAAGAACAGCA
3600	HSPASPP	17923	CATTCGCCTGCTAGTCCTCCG	32246	CACAGCCCAGCAAGCCCACCA
3601	HSPGQIS	17924	CATTCTCCGGGTCAGATTTCG	32247	CACAGCCCAGGACAAATCAGC
3602	HSPMAVP	17925	CATAGTCCGATGGCGGTTCCT	32248	CACAGCCCAATGGCAGTCCCA
3603	HSPNGYA	17926	CATTCTCCTAATGGTTATGCT	32249	CACAGCCCAAACGGATACGCA
3604	HSQAQMS	17927	CATTCGCAGGCGCAGATGTCG	32250	CACAGCCAAGCACAAATGAGC
3605	HSQNQYS	17928	CATTCGCAGAATCAGTATAGT	32251	CACAGCCAAAACCAATACAGC
3606	HSQRAVP	17929	CATAGTCAGAGGGCTGTTCCT	32252	CACAGCCAAAGAGCAGTCCCA
3607	HSRASPE	17930	CATAGTAGGGCGAGTCCGGAG	32253	CACAGCAGAGCAAGCCCAGAA
3608	HSRDNRN	17931	CATTCTAGGGATAATCGGAAT	32254	CACAGCAGAGACAACAGAAAC
3609	HSRELSP	17932	CATTCTAGGGAGCTTAGTCCG	32255	CACAGCAGAGAACTCAGCCCA
3610	HSRGTML	17933	CATTCGCGGGGTACTATGCTT	32256	CACAGCAGAGGAACAATGCTC
3611	HSRHDML	17934	CATTCGAGGCATGATATGTTG	32257	CACAGCAGACACGACATGCTC
3612	HSRPQPQ	17935	CATAGTAGGCCTCAGCCTCAG	32258	CACAGCAGACCACAACCACAA
3613	HSRPSGC	17936	CATTCTCGGCCGAGTGGTTGT	32259	CACAGCAGACCAAGCGGATGC
3614	HSRSTFA	17937	CATTCTCGGTCTACGTTTGCT	32260	CACAGCAGAAGCACATTCGCA
3615	HSSIPGP	17938	CATAGTTCTATTCCTGGTCCT	32261	CACAGCAGCATCCCAGGACCA
3616	HSSMATM	17939	CATTCTTCTATGGCTACGATG	32262	CACAGCAGCATGGCAACAATG
3617	HSSNLGV	17940	CATTCTTCGAATCTTGGTGTT	32263	CACAGCAGCAACCTCGGAGTC
3618	HSSSVNP	17941	CATTCTTCGTCGGTGAATCCT	32264	CACAGCAGCAGCGTCAACCCA
3619	HSSTGAN	17942	CATTCGAGTACGGGTGCGAAT	32265	CACAGCAGCACAGGAGCAAAC
3620	HSSVPGA	17943	CATTCTTCGGTTCCTGGTGCG	32266	CACAGCAGCGTCCCAGGAGCA
3621	HSTDSLP	17944	CATTCTACGGATTCGTTGCCG	32267	CACAGCACAGACAGCCTCCCA
3622	HSTHREL	17945	CATTCTACTCATAGGGAGCTG	32268	CACAGCACACACAGAGAACTC
3623	HSTLISH	17946	CATTCTACTCTGATTTCGCAT	32269	CACAGCACACTCATCAGCCAC
3624	HSTPLNS	17947	CATAGTACGCCGTTGAATTCT	32270	CACAGCACACCACTCAACAGC
3625	HSTREGF	17948	CATTCTACTCGTGAGGGTTTT	32271	CACAGCACAAGAGAAGGATTC
3626	HSTTDPL	17949	CATTCTACTACGGATCCTCTG	32272	CACAGCACAACAGACCCACTC
3627	HSVASVT	17950	CATAGTGTTGCGTCTGTGACT	32273	CACAGCGTCGCAAGCGTCACA
3628	HSVDSRG	17951	CATAGTGTGGATTCGCGGGGG	32274	CACAGCGTCGACAGCAGAGGA
3629	HSVERDH	17952	CATTCGGTGGAGCGGGATCAT	32275	CACAGCGTCGAAAGAGACCAC
3630	HSYVDSF	17953	CATTCTTATGTGGATAGTTTT	32276	CACAGCTACGTCGACAGCTTC
3631	HTAGDAE	17954	CATACGGCGGGTGATGCGGAG	32277	CACACAGCAGGAGACGCAGAA
3632	HTALLSN	17955	CATACGGCGCTTTTGTCTAAT	32278	CACACAGCACTCCTCAGCAAC
3633	HTARTTP	17956	CATACGGCTCGGACTACTCCG	32279	CACACAGCAAGAACAACACCA
3634	HTASLPA	17957	CATACTGCTTCGTTGCCGGCG	32280	CACACAGCAAGCCTCCCAGCA

3635	HTDRYAV	17958	CATACGGATCGGTATGCGGTT	32281	CACACAGACAGATACGCAGTC
3636	HTEAGRV	17959	CATACTGAGGCTGGGAGGGTG	32282	CACACAGAAGCAGGAAGAGTC
3637	HTETFGE	17960	CATACGGAGACGTTTGGGGAG	32283	CACACAGAAACATTCGGAGAA
3638	HTGLVRG	17961	CATACGGGTCTTGTTCGGGGG	32284	CACACAGGACTCGTCAGAGGA
3639	HTGSLSS	17962	CATACGGGGTCTCTGTCTTCT	32285	CACACAGGAAGCCTCAGCAGC
3640	HTHLASL	17963	CATACGCATCTGGCTAGTCTT	32286	CACACACACCTCGCAAGCCTC
3641	HTIKDAY	17964	CATACTATTAAGGATGCTTAT	32287	CACACAATCAAAGACGCATAC
3642	HTKSPHP	17965	CATACTAAGTCTCCTCATCCG	32288	CACACAAAAAGCCCACACCCA
3643	HTLKPDV	17966	CATACTCTTAAGCCGGATGTG	32289	CACACACTCAAACCAGACGTC
3644	HTLPSTS	17967	CATACTTTGCCGAGTACGTCG	32290	CACACACTCCCAAGCACAAGC
3645	HTLPTTA	17968	CATACGTTGCCTACTACGGCT	32291	CACACACTCCCAACAACAGCA
3646	HTMASGS	17969	CATACGATGGCTTCGGGGTCG	32292	CACACAATGGCAAGCGGAAGC
3647	HTNSNTG	17970	CATACGAATTCTAATACGGGG	32293	CACACAAACAGCAACACAGGA
3648	HTPAVNF	17971	CATACTCCTGCTGTGAATTTT	32294	CACACACCAGCAGTCAACTTC
3649	HTPGLHT	17972	CATACGCCTGGGTTGCATACT	32295	CACACACCAGGACTCCACACA
3650	HTPLTSH	17973	CATACTCCTTTGACGTCGCAT	32296	CACACACCACTCACAAGCCAC
3651	HTPNILY	17974	CATACGCCGAATATTCTTTAT	32297	CACACACCAAACATCCTCTAC
3652	HTPQPNA	17975	CATACGCCGCAGCCTAATGCT	32298	CACACACCACAACCAAACGCA
3653	HTQLRTP	17976	CATACGCAGTTGAGGACTCCG	32299	CACACACAACTCAGAACACCA
3654	HTQRLSS	17977	CATACTCAGCGGCTGAGTTCG	32300	CACACACAAAGACTCAGCAGC
3655	HTQVTRC	17978	CATACGCAGGTGACGCGTTGT	32301	CACACACAAGTCACAAGATGC
3656	HTRDSDP	17979	CATACTAGGGATTCTGATCCT	32302	CACACAAGAGACAGCGACCCA
3657	HTRGKAE	17980	CATACGCGTGGGAAGGCGGAG	32303	CACACAAGAGGAAAAGCAGAA
3658	HTSGESY	17981	CATACGAGTGGTGAGTCGTAT	32304	CACACAAGCGGAGAAAGCTAC
3659	HTSHQLP	17982	CATACTAGTCATCAGTTGCCG	32305	CACACAAGCCACCAACTCCCA
3660	HTSIDYV	17983	CATACTTCTATTGATTATGTT	32306	CACACAAGCATCGACTACGTC
3661	HTSKSAL	17984	CATACGTCTAAGTCTGCTCTG	32307	CACACAAGCAAAAGCGCACTC
3662	HTSPPIS	17985	CATACTTCGCCTCCGATTTCG	32308	CACACAAGCCCACCAATCAGC
3663	HTSPVYD	17986	CATACGAGTCCTGTTTATGAT	32309	CACACAAGCCCAGTCTACGAC
3664	HTSQQRQ	17987	CATACGTCTCAGCAGAGGCAG	32310	CACACAAGCCAACAAAGACAA
3665	HTSTTKW	17988	CATACGTCGACTACGAAGTGG	32311	CACACAAGCACAACAAAATGG
3666	HTSWDGL	17989	CATACGTCTTGGGATGGTCTG	32312	CACACAAGCTGGGACGGACTC
3667	HTTAAPP	17990	CATACTACTGCGGCGCCTCCT	32313	CACACAACAGCAGCACCACCA
3668	HTTKVDP	17991	CATACGACGAAGGTGGATCCG	32314	CACACAACAAAAGTCGACCCA
3669	HTTPTHT	17992	CATACGACTCCGACTCATACG	32315	CACACAACACCAACACACACA
3670	HTTQCTM	17993	CATACGACGCAGTGTACGATG	32316	CACACAACACAATGCACAATG
3671	HTTTIHG	17994	CATACTACGACTATTCATGGG	32317	CACACAACAACAATCCACGGA
3672	HTVRSGL	17995	CATACGGTGAGGTCTGGGCTT	32318	CACACAGTCAGAAGCGGACTC
3673	HTVTSAG	17996	CATACTGTTACGTCGGCGGGG	32319	CACACAGTCACAAGCGCAGGA
3674	HTVVQSS	17997	CATACGGTGGTTCAGAGTTCT	32320	CACACAGTCGTCCAAAGCAGC
3675	HTYSSED	17998	CATACTTATTCTTCTGAGGAT	32321	CACACATACAGCAGCGAAGAC
3676	HVDRSGA	17999	CATGTGGATCGGAGTGGGGCG	32322	CACGTCGACAGAAGCGGAGCA
3677	HVDRTQF	18000	CATGTTGATAGGACGCAGTTT	32323	CACGTCGACAGAACACAATTC
3678	HVGITSA	18001	CATGTGGGGATTACTTCGGCG	32324	CACGTCGGAATCACAAGCGCA
3679	HVGYGPS	18002	CATGTGGGGTATGGTCCTTCG	32325	CACGTCGGATACGGACCAAGC

3680	HVGYKAD	18003	CATGTTGGGTATAAGGCGGAT	32326	CACGTCGGATACAAAGCAGAC
3681	HVHTNSS	18004	CATGTGCATACTAATTCTTCG	32327	CACGTCCACACAAACAGCAGC
3682	HVIDSAG	18005	CATGTGATTGATTCTGCGGGG	32328	CACGTCATCGACAGCGCAGGA
3683	HVKALGS	18006	CATGTGAAGGCGCTTGGGTCT	32329	CACGTCAAAGCACTCGGAAGC
3684	HVKLSSN	18007	CATGTGAAGCTGAGTAGTAAT	32330	CACGTCAAACTCAGCAGCAAC
3685	HVLKNPT	18008	CATGTTCTTAAGAATCCTACG	32331	CACGTCCTCAAAAACCCAACA
3686	HVLPTRP	18009	CATGTGCTTCCTACTCGTCCT	32332	CACGTCCTCCCAACAAGACCA
3687	HVLSPTR	18010	CATGTTTTGTCGCCGACTCGG	32333	CACGTCCTCAGCCCAACAAGA
3688	HVMEASS	18011	CATGTTATGGAGGCGTCGTCT	32334	CACGTCATGGAAGCAAGCAGC
3689	HVPMSMP	18012	CATGTGCCGATGTCGATGCCT	32335	CACGTCCCAATGAGCATGCCA
3690	HVQNSQT	18013	CATGTTCAGAATTCGCAGACG	32336	CACGTCCAAAACAGCCAAACA
3691	HVRGTGS	18014	CATGTGCGTGGGACGGGTTCT	32337	CACGTCAGAGGAACAGGAAGC
3692	HVRPGFT	18015	CATGTTCGTCCTGGGTTTACG	32338	CACGTCAGACCAGGATTCACA
3693	HVSEHTY	18016	CATGTTAGTGAGCATACGTAT	32339	CACGTCAGCGAACACACATAC
3694	HVSGPRA	18017	CATGTTTCGGGGCCGCGTGCG	32340	CACGTCAGCGGACCAAGAGCA
3695	HVSHAMQ	18018	CATGTGAGTCATGCTATGCAG	32341	CACGTCAGCCACGCAATGCAA
3696	HVSHSVI	18019	CATGTTTCTCATTCGGTGATT	32342	CACGTCAGCCACAGCGTCATC
3697	HVSKLDT	18020	CATGTGAGTAAGCTGGATACT	32343	CACGTCAGCAAACTCGACACA
3698	HVSMSVP	18021	CATGTGAGTATGTCTGTTCCT	32344	CACGTCAGCATGAGCGTCCCA
3699	HVSNIIS	18022	CATGTTTCGAATATTATTTCT	32345	CACGTCAGCAACATCATCAGC
3700	HVSNQLN	18023	CATGTGTCGAATCAGCTTAAT	32346	CACGTCAGCAACCAACTCAAC
3701	HVSPPAN	18024	CATGTGTCTCCTCCTGCGAAT	32347	CACGTCAGCCCACCAGCAAAC
3702	HVSSASL	18025	CATGTGTCGTCTGCTTCTTTG	32348	CACGTCAGCAGCGCAAGCCTC
3703	HVSSDSR	18026	CATGTGAGTTCTGATTCTCGT	32349	CACGTCAGCAGCGACAGCAGA
3704	HVSSPSL	18027	CATGTTTCTTCTCCGTCGCTG	32350	CACGTCAGCAGCCCAAGCCTC
3705	HVSTEPS	18028	CATGTGAGTACTGAGCCGAGT	32351	CACGTCAGCACAGAACCAAGC
3706	HVSYDLT	18029	CATGTTTCTTATGATCTTACT	32352	CACGTCAGCTACGACCTCACA
3707	HVTPGFE	18030	CATGTTACGCCTGGTTTTGAG	32353	CACGTCACACCAGGATTCGAA
3708	HVTSPYL	18031	CATGTTACTTCGCCTTATCTG	32354	CACGTCACAAGCCCATACCTC
3709	HVVGGSS	18032	CATGTTGTTGGTGGGTCTTCT	32355	CACGTCGTCGGAGGAAGCAGC
3710	HVVSRFV	18033	CATGTTGTGTCGCGTTTTGTG	32356	CACGTCGTCAGCAGATTCGTC
3711	HYAPICE	18034	CATTATGCTCCTATTTGTGAG	32357	CACTACGCACCAATCTGCGAA
3712	HYDSNAP	18035	CATTATGATAGTAATGCGCCG	32358	CACTACGACAGCAACGCACCA
3713	HYEFVDK	18036	CATTATGAGTTTGTGGATAAG	32359	CACTACGAATTCGTCGACAAA
3714	HYESCNP	18037	CATTATGAGAGTTGTAATCCG	32360	CACTACGAAAGCTGCAACCCA
3715	HYESNDV	18038	CATTATGAGTCGAATGATGTG	32361	CACTACGAAAGCAACGACGTC
3716	HYFDMGP	18039	CATTATTTTGATATGGGTCCT	32362	CACTACTTCGACATGGGACCA
3717	HYGMVSA	18040	CATTATGGTATGGTGTCGGCT	32363	CACTACGGAATGGTCAGCGCA
3718	HYGSTRE	18041	CATTATGGTAGTACGAGGGAG	32364	CACTACGGAAGCACAAGAGAA
3719	HYINPTN	18042	CATTATATTAATCCTACTAAT	32365	CACTACATCAACCCAACAAAC
3720	HYPPTYD	18043	CATTATCCGCCGACTTATGAT	32366	CACTACCCACCAACATACGAC
3721	HYPSTSS	18044	CATTATCCTTCTACTTCTAGT	32367	CACTACCCAAGCACAAGCAGC
3722	HYQISTT	18045	CATTATCAGATTTCGACGACT	32368	CACTACCAAATCAGCACAACA
3723	HYSISGA	18046	CATTATAGTATTTCGGGGGCT	32369	CACTACAGCATCAGCGGAGCA
3724	HYSPKPS	18047	CATTATAGTCCTAAGCCGAGT	32370	CACTACAGCCCAAAACCAAGC

3725	HYVEHRQ	18048	CATTATGTTGAGCATCGTCAG	32371	CACTACGTCGAACACAGACAA
3726	IAAAAMT	18049	ATTGCGGCGGCTGCTATGACG	32372	ATCGCAGCAGCAGCAATGACA
3727	IAANMHN	18050	ATTGCGGCGAATATGCATAAT	32373	ATCGCAGCAAACATGCACAAC
3728	IAATPEQ	18051	ATTGCGGCTACTCCTGAGCAG	32374	ATCGCAGCAACACCAGAACAA
3729	IACSSEL	18052	ATTGCTTGTTCGAGTGAGCTG	32375	ATCGCATGCAGCAGCGAACTC
3730	IADVLGY	18053	ATTGCTGATGTTTTGGGGTAT	32376	ATCGCAGACGTCCTCGGATAC
3731	IAGISDI	18054	ATTGCTGGGATTTCGGATATT	32377	ATCGCAGGAATCAGCGACATC
3732	IAHERSD	18055	ATTGCTCATGAGAGGAGTGAT	32378	ATCGCACACGAAAGAAGCGAC
3733	IAHRASA	18056	ATTGCTCATAGGGCTAGTGCG	32379	ATCGCACACAGAGCAAGCGCA
3734	IALPKVA	18057	ATTGCTTTGCCTAAGGTTGCG	32380	ATCGCACTCCCAAAAGTCGCA
3735	IANLTQS	18058	ATTGCTAATTTGACGCAGTCG	32381	ATCGCAAACCTCACACAAAGC
3736	IAPGVSS	18059	ATTGCGCCTGGTGTGTCTAGT	32382	ATCGCACCAGGAGTCAGCAGC
3737	IAPLTVS	18060	ATTGCGCCTCTGACTGTGTCT	32383	ATCGCACCACTCACAGTCAGC
3738	IAPNKLT	18061	ATTGCGCCTAATAAGCTTACG	32384	ATCGCACCAAACAAACTCACA
3739	IAQQHQI	18062	ATTGCGCAGCAGCATCAGATT	32385	ATCGCACAACAACACCAAATC
3740	IARAANF	18063	ATTGCTCGTGCGGCTAATTTT	32386	ATCGCAAGAGCAGCAAACTTC
3741	IARGQPF	18064	ATTGCGCGTGGGCAGCCTTTT	32387	ATCGCAAGAGGACAACCATTC
3742	IARGYDN	18065	ATTGCTCGGGGTTATGATAAT	32388	ATCGCAAGAGGATACGACAAC
3743	IARHPTQ	18066	ATTGCGCGTCATCCGACGCAG	32389	ATCGCAAGACACCCAACACAA
3744	IASEYRQ	18067	ATTGCGTCGGAGTATCGTCAG	32390	ATCGCAAGCGAATACAGACAA
3745	IASSQLR	18068	ATTGCTAGTTCTCAGCTGCGT	32391	ATCGCAAGCAGCCAACTCAGA
3746	IATPESL	18069	ATTGCTACTCCTGAGTCGCTG	32392	ATCGCAACACCAGAAAGCCTC
3747	IAVHGRG	18070	ATTGCGGTTCATGGGCGTGGT	32393	ATCGCAGTCCACGGAAGAGGA
3748	IDASKRF	18071	ATTGATGCGAGTAAGCGTTTT	32394	ATCGACGCAAGCAAAAGATTC
3749	IDGGSSD	18072	ATTGATGGTGGGAGTTCTGAT	32395	ATCGACGGAGGAAGCAGCGAC
3750	IDGRVIG	18073	ATTGATGGTCGTGTGATTGGT	32396	ATCGACGGAAGAGTCATCGGA
3751	IDKLLTF	18074	ATTGATAAGCTTCTGACGTTT	32397	ATCGACAAACTCCTCACATTC
3752	IDLLVRS	18075	ATTGATCTGTTGGTTCGGTCG	32398	ATCGACCTCCTCGTCAGAAGC
3753	IDNLHAG	18076	ATTGATAATCTTCATGCGGGT	32399	ATCGACAACCTCCACGCAGGA
3754	IDNPVRP	18077	ATTGATAATCCGGTGCGTCCT	32400	ATCGACAACCCAGTCAGACCA
3755	IDNVKPV	18078	ATTGATAATGTTAAGCCTGTG	32401	ATCGACAACGTCAAACCAGTC
3756	IDSATTD	18079	ATTGATAGTGCGACTACGGAT	32402	ATCGACAGCGCAACAACAGAC
3757	IDSHPSS	18080	ATTGATAGTCATCCGTCTTCT	32403	ATCGACAGCCACCCAAGCAGC
3758	IDSSTNC	18081	ATTGATAGTTCGACGAATTGT	32404	ATCGACAGCAGCACAAACTGC
3759	IDSYTPP	18082	ATTGATTCTTATACGCCTCCG	32405	ATCGACAGCTACACACCACCA
3760	IDTISTS	18083	ATTGATACGATTTCGACTAGT	32406	ATCGACACAATCAGCACAAGC
3761	IDTPRGT	18084	ATTGATACTCCTCGTGGGACT	32407	ATCGACACACCAAGAGGAACA
3762	IDTVPSR	18085	ATTGATACTGTTCCTAGTCGT	32408	ATCGACACAGTCCCAAGCAGA
3763	IDVFTNA	18086	ATTGATGTTTTTACTAATGCG	32409	ATCGACGTCTTCACAAACGCA
3764	IDYKSSS	18087	ATTGATTATAAGTCTAGTTCG	32410	ATCGACTACAAAAGCAGCAGC
3765	IDYRAAA	18088	ATTGATTATCGGGCTGCTGCG	32411	ATCGACTACAGAGCAGCAGCA
3766	IEASRVQ	18089	ATTGAGGCGAGTCGGGTGCAG	32412	ATCGAAGCAAGCAGAGTCCAA
3767	IEKNLTL	18090	ATTGAGAAGAATCTGACGCTG	32413	ATCGAAAAAAACCTCACACTC
3768	IEKVNRV	18091	ATTGAGAAGGTGAATAGGGTT	32414	ATCGAAAAAGTCAACAGAGTC
3769	IELASSC	18092	ATTGAGCTGGCTTCTTCGTGT	32415	ATCGAACTCGCAAGCAGCTGC

3770	IELKMTS	18093	ATTGAGCTTAAGATGACGTCT	32416	ATCGAACTCAAAATGACAAGC
3771	IEMLKTA	18094	ATTGAGATGCTTAAGACTGCG	32417	ATCGAAATGCTCAAAACAGCA
3772	IEPKTHL	18095	ATTGAGCCGAAGACGCATCTT	32418	ATCGAACCAAAAACACACCTC
3773	IEPSHYP	18096	ATTGAGCCGTCTCATTATCCT	32419	ATCGAACCAAGCCACTACCCA
3774	IERPTSP	18097	ATTGAGAGGCCGACGTCGCCT	32420	ATCGAAAGACCAACAAGCCCA
3775	IERTSSM	18098	ATTGAGCGTACGTCGAGTATG	32421	ATCGAAAGAACAAGCAGCATG
3776	IESANLN	18099	ATTGAGTCTGCTAATCTGAAT	32422	ATCGAAAGCGCAAACCTCAAC
3777	IESHLPR	18100	ATTGAGTCTCATTTGCCTAGG	32423	ATCGAAAGCCACCTCCCAAGA
3778	IETAPDH	18101	ATTGAGACGGCGCCGGATCAT	32424	ATCGAAACAGCACCAGACCAC
3779	IETVNKT	18102	ATTGAGACGGTGAATAAGACT	32425	ATCGAAACAGTCAACAAAACA
3780	IEVRTSI	18103	ATTGAGGTGCGGACGTCGATT	32426	ATCGAAGTCAGAACAAGCATC
3781	IEWGWED	18104	ATTGAGTGGGGTTGGGAGGAT	32427	ATCGAATGGGGATGGGAAGAC
3782	IFAGTGE	18105	ATTTTTGCGGGGACTGGTGAG	32428	ATCTTCGCAGGAACAGGAGAA
3783	IFAGVLH	18106	ATTTTTGCTGGGGTTCTTCAT	32429	ATCTTCGCAGGAGTCCTCCAC
3784	IFAVAAE	18107	ATTTTTGCTGTTGCGGCTGAG	32430	ATCTTCGCAGTCGCAGCAGAA
3785	IFKPAMT	18108	ATTTTTAAGCCTGCGATGACT	32431	ATCTTCAAACCAGCAATGACA
3786	IFNNAAP	18109	ATTTTTAATAATGCTGCTCCT	32432	ATCTTCAACAACGCAGCACCA
3787	IFPLTGS	18110	ATTTTTCCGCTGACGGGGTCG	32433	ATCTTCCCACTCACAGGAAGC
3788	IFRDGVS	18111	ATTTTTCGTGATGGTGTTTCT	32434	ATCTTCAGAGACGGAGTCAGC
3789	IFSAGPL	18112	ATTTTTTCTGCTGGGCCGTTG	32435	ATCTTCAGCGCAGGACCACTC
3790	IFSHVGS	18113	ATTTTTTCTCATGTTGGGTCG	32436	ATCTTCAGCCACGTCGGAAGC
3791	IFVPEPG	18114	ATTTTTGTTCCTGAGCCTGGT	32437	ATCTTCGTCCCAGAACCAGGA
3792	IGAGASM	18115	ATTGGGGCTGGGGCGTCTATG	32438	ATCGGAGCAGGAGCAAGCATG
3793	IGAIADV	18116	ATTGGTGCTATTGCGGATGTG	32439	ATCGGAGCAATCGCAGACGTC
3794	IGALVSP	18117	ATTGGGGCGTTGGTGTCTCCT	32440	ATCGGAGCACTCGTCAGCCCA
3795	IGAMSSA	18118	ATTGGTGCGATGTCTTCTGCT	32441	ATCGGAGCAATGAGCAGCGCA
3796	IGAPYNS	18119	ATTGGTGCTCCTTATAATAGT	32442	ATCGGAGCACCATACAACAGC
3797	IGASLLG	18120	ATTGGGGCGAGTTTGCTGGGT	32443	ATCGGAGCAAGCCTCCTCGGA
3798	IGERRPV	18121	ATTGGTGAGCGTAGGCCGGTG	32444	ATCGGAGAAAGAAGACCAGTC
3799	IGGFVKA	18122	ATTGGTGGGTTTGTGAAGGCG	32445	ATCGGAGGATTCGTCAAAGCA
3800	IGGTMTH	18123	ATTGGGGGTACTATGACTCAT	32446	ATCGGAGGAACAATGACACAC
3801	IGHGHPN	18124	ATTGGGCATGGGCATCCTAAT	32447	ATCGGACACGGACACCCAAAC
3802	IGHSDNT	18125	ATTGGTCATTCTGATAATACG	32448	ATCGGACACAGCGACAACACA
3803	IGKLLNT	18126	ATTGGGAAGCTGCTTAATACT	32449	ATCGGAAAACTCCTCAACACA
3804	IGKNHSS	18127	ATTGGTAAGAATCATTCGTCG	32450	ATCGGAAAAAACCACAGCAGC
3805	IGKPGYL	18128	ATTGGTAAGCCGGGTTATTTG	32451	ATCGGAAAACCAGGATACCTC
3806	IGLAKTL	18129	ATTGGTCTTGCGAAGACTTTG	32452	ATCGGACTCGCAAAAACACTC
3807	IGLTSQV	18130	ATTGGTCTTACTAGTCAGGTT	32453	ATCGGACTCACAAGCCAAGTC
3808	IGMHSQS	18131	ATTGGTATGCATTCTCAGTCT	32454	ATCGGAATGCACAGCCAAAGC
3809	IGNSRLG	18132	ATTGGTAATTCGCGGCTTGGG	32455	ATCGGAAACAGCAGACTCGGA
3810	IGQFSRV	18133	ATTGGGCAGTTTTCGCGTGTT	32456	ATCGGACAATTCAGCAGAGTC
3811	IGRDMHA	18134	ATTGGGAGGGATATGCATGCT	32457	ATCGGAAGAGACATGCACGCA
3812	IGRPSYE	18135	ATTGGGCGGCCTAGTTATGAG	32458	ATCGGAAGACCAAGCTACGAA
3813	IGRQTGI	18136	ATTGGTCGTCAGACTGGGATT	32459	ATCGGAAGACAAACAGGAATC
3814	IGRSEGT	18137	ATTGGTCGGTCTGAGGGTACT	32460	ATCGGAAGAAGCGAAGGAACA

3815	IGRSPSP	18138	ATTGGGAGGTCGCCTAGTCCG	32461	ATCGGAAGAAGCCCAAGCCCA
3816	IGSHHSN	18139	ATTGGGTCTCATCATTCGAAT	32462	ATCGGAAGCCACCACAGCAAC
3817	IGSNALS	18140	ATTGGTTCGAATGCTTTGTCG	32463	ATCGGAAGCAACGCACTCAGC
3818	IGSTMYQ	18141	ATTGGGTCGACGATGTATCAG	32464	ATCGGAAGCACAATGTACCAA
3819	IGTSTYV	18142	ATTGGGACGAGTACTTATGTT	32465	ATCGGAACAAGCACATACGTC
3820	IGTTMKG	18143	ATTGGGACGACTATGAAGGGT	32466	ATCGGAACAACAATGAAAGGA
3821	IGVKTLP	18144	ATTGGTGTGAAGACTCTGCCG	32467	ATCGGAGTCAAAACACTCCCA
3822	IGVLHLP	18145	ATTGGTGTGCTGCATCTGCCG	32468	ATCGGAGTCCTCCACCTCCCA
3823	IHAASTD	18146	ATTCATGCTGCTAGTACTGAT	32469	ATCCACGCAGCAAGCACAGAC
3824	IHANWID	18147	ATTCATGCGAATTGGATTGAT	32470	ATCCACGCAAACTGGATCGAC
3825	IHDFTSV	18148	ATTCATGATTTTACTTCTGTG	32471	ATCCACGACTTCACAAGCGTC
3826	IHELSGL	18149	ATTCATGAGCTGTCGGGGCTG	32472	ATCCACGAACTCAGCGGACTC
3827	IHFQSSQ	18150	ATTCATTTTCAGTCTTCTCAG	32473	ATCCACTTCCAAAGCAGCCAA
3828	IHGGSYT	18151	ATTCATGGTGGTTCGTATACT	32474	ATCCACGGAGGAAGCTACACA
3829	IHGSTDR	18152	ATTCATGGGAGTACGGATAGG	32475	ATCCACGGAAGCACAGACAGA
3830	IHHDPAS	18153	ATTCATCATGATCCGGCGTCT	32476	ATCCACCACGACCCAGCAAGC
3831	IHLPTSL	18154	ATTCATCTTCCGACTTCGTTG	32477	ATCCACCTCCCAACAAGCCTC
3832	IHNRPLM	18155	ATTCATAATAGGCCGTTGATG	32478	ATCCACAACAGACCACTCATG
3833	IHNTLAA	18156	ATTCATAATACTTTGGCGGCT	32479	ATCCACAACACACTCGCAGCA
3834	IHNVVVQ	18157	ATTCATAATGTTGTTGTTCAG	32480	ATCCACAACGTCGTCGTCCAA
3835	IHPGRVA	18158	ATTCATCCGGGTCGTGTTGCT	32481	ATCCACCCAGGAAGAGTCGCA
3836	IHPTRQG	18159	ATTCATCCTACGAGGCAGGGG	32482	ATCCACCCAACAAGACAAGGA
3837	IHQAGQP	18160	ATTCATCAGGCTGGGCAGCCG	32483	ATCCACCAAGCAGGACAACCA
3838	IHQSSES	18161	ATTCATCAGTCGTCGGAGTCT	32484	ATCCACCAAAGCAGCGAAAGC
3839	IHRVITS	18162	ATTCATCGGGTGATTACTTCT	32485	ATCCACAGAGTCATCACAAGC
3840	IHSEGSL	18163	ATTCATTCGGAGGGTTCTCTT	32486	ATCCACAGCGAAGGAAGCCTC
3841	IHSLQQE	18164	ATTCATTCTCTGCAGCAGGAG	32487	ATCCACAGCCTCCAACAAGAA
3842	IHSSIDF	18165	ATTCATAGTTCGATTGATTTT	32488	ATCCACAGCAGCATCGACTTC
3843	IHSSPAA	18166	ATTCATAGTTCGCCTGCTGCG	32489	ATCCACAGCAGCCCAGCAGCA
3844	IHSYDRS	18167	ATTCATAGTTATGATCGGAGT	32490	ATCCACAGCTACGACAGAAGC
3845	IHTAVEL	18168	ATTCATACTGCGGTTGAGTTG	32491	ATCCACACAGCAGTCGAACTC
3846	IHTGNYM	18169	ATTCATACTGGGAATTATATG	32492	ATCCACACAGGAAACTACATG
3847	IHTNAPP	18170	ATTCATACGAATGCGCCGCCT	32493	ATCCACACAAACGCACCACCA
3848	IHTTQRT	18171	ATTCATACTACGCAGCGGACT	32494	ATCCACACAACACAAAGAACA
3849	IIAEHPA	18172	ATTATTGCGGAGCATCCGGCG	32495	ATCATCGCAGAACACCCAGCA
3850	IIARLPP	18173	ATTATTGCTAGGCTTCCTCCG	32496	ATCATCGCAAGACTCCCACCA
3851	IIDNHIR	18174	ATTATTGATAATCATATTCGT	32497	ATCATCGACAACCACATCAGA
3852	IIFQDMP	18175	ATTATTTTTCAGGATATGCCT	32498	ATCATCTTCCAAGACATGCCA
3853	IIGANEP	18176	ATTATTGGTGCTAATGAGCCT	32499	ATCATCGGAGCAAACGAACCA
3854	IIGKGTG	18177	ATTATTGGGAAGGGGACTGGG	32500	ATCATCGGAAAAGGAACAGGA
3855	IIHDTHN	18178	ATTATTCATGATACTCATAAT	32501	ATCATCCACGACACACACAAC
3856	IIHEARP	18179	ATTATTCATGAGGCGCGTCCT	32502	ATCATCCACGAAGCAAGACCA
3857	IIRDSQL	18180	ATTATTCGTGATAGTCAGCTG	32503	ATCATCAGAGACAGCCAACTC
3858	IISLTTS	18181	ATTATTTCTCTTACGACTTCT	32504	ATCATCAGCCTCACAACAAGC
3859	IKDAGSP	18182	ATTAAGGATGCGGGTTCTCCT	32505	ATCAAAGACGCAGGAAGCCCA

3860	IKDAQPW	18183	ATTAAGGATGCGCAGCCTTGG	32506	ATCAAAGACGCACAACCATGG
3861	IKDQWNM	18184	ATTAAGGATCAGTGGAATATG	32507	ATCAAAGACCAATGGAACATG
3862	IKFPTAD	18185	ATTAAGTTTCCTACTGCGGAT	32508	ATCAAATTCCCAACAGCAGAC
3863	IKIEDPR	18186	ATTAAGATTGAGGATCCTCGG	32509	ATCAAAATCGAAGACCCAAGA
3864	IKMAQGF	18187	ATTAAGATGGCGCAGGGTTTT	32510	ATCAAAATGGCACAAGGATTC
3865	IKNLASH	18188	ATTAAGAATCTGGCGTCTCAT	32511	ATCAAAAACCTCGCAAGCCAC
3866	IKPIGGV	18189	ATTAAGCCTATTGGTGGGGTG	32512	ATCAAACCAATCGGAGGAGTC
3867	IKPMSGT	18190	ATTAAGCCTATGTCTGGGACG	32513	ATCAAACCAATGAGCGGAACA
3868	IKQPLHN	18191	ATTAAGCAGCCGCTTCATAAT	32514	ATCAAACAACCACTCCACAAC
3869	IKRTLSD	18192	ATTAAGCGTACTCTGAGTGAT	32515	ATCAAAAGAACACTCAGCGAC
3870	IKSDDGS	18193	ATTAAGTCTGATGATGGTTCT	32516	ATCAAAAGCGACGACGGAAGC
3871	IKSEGSL	18194	ATTAAGAGTGAGGGTAGTCTG	32517	ATCAAAAGCGAAGGAAGCCTC
3872	IKTEWSH	18195	ATTAAGACGGAGTGGTCGCAT	32518	ATCAAAACAGAATGGAGCCAC
3873	IKTFTSS	18196	ATTAAGACGTTTACGTCGTCG	32519	ATCAAAACATTCACAAGCAGC
3874	ILDFLPD	18197	ATTCTGGATTTTCTGCCTGAT	32520	ATCCTCGACTTCCTCCCAGAC
3875	ILGGLDR	18198	ATTCTGGGGGGTCTTGATCGG	32521	ATCCTCGGAGGACTCGACAGA
3876	ILGNTRE	18199	ATTCTGGGGAATACGCGGGAG	32522	ATCCTCGGAAACACAAGAGAA
3877	ILGRSAA	18200	ATTTTGGGTCGTTCGGCGGCG	32523	ATCCTCGGAAGAAGCGCAGCA
3878	ILGTRPL	18201	ATTCTGGGTACGCGTCCGTTG	32524	ATCCTCGGAACAAGACCACTC
3879	ILGTSVQ	18202	ATTCTGGGGACGTCTGTGCAG	32525	ATCCTCGGAACAAGCGTCCAA
3880	ILHGRGA	18203	ATTTTGCATGGTCGGGGGGCG	32526	ATCCTCCACGGAAGAGGAGCA
3881	ILHLVRL	18204	ATTCTTCATCTGGTGCGTCTT	32527	ATCCTCCACCTCGTCAGACTC
3882	ILHSPTV	18205	ATTCTTCATTCTCCTACGGTT	32528	ATCCTCCACAGCCCAACAGTC
3883	ILHVEMR	18206	ATTTTGCATGTTGAGATGAGG	32529	ATCCTCCACGTCGAAATGAGA
3884	ILKHIGL	18207	ATTCTTAAGCATATTGGGCTT	32530	ATCCTCAAACACATCGGACTC
3885	ILKQQAN	18208	ATTTTGAAGCAGCAGGCTAAT	32531	ATCCTCAAACAACAAGCAAAC
3886	ILLDDES	18209	ATTCTGTTGGATGATGAGAGT	32532	ATCCTCCTCGACGACGAAAGC
3887	ILLHPRG	18210	ATTTTGCTGCATCCGCGTGGG	32533	ATCCTCCTCCACCCAAGAGGA
3888	ILLMGTS	18211	ATTTTGCTGATGGGTACTTCT	32534	ATCCTCCTCATGGGAACAAGC
3889	ILLRKDP	18212	ATTCTTCTTCGGAAGGATCCT	32535	ATCCTCCTCAGAAAAGACCCA
3890	ILLSEGH	18213	ATTCTTCTGTCGGAGGGGCAT	32536	ATCCTCCTCAGCGAAGGACAC
3891	ILLSIRD	18214	ATTTTGCTTAGTATTCGGGAT	32537	ATCCTCCTCAGCATCAGAGAC
3892	ILMSAQS	18215	ATTCTTATGTCTGCGCAGTCT	32538	ATCCTCATGAGCGCACAAAGC
3893	ILMVDDT	18216	ATTCTTATGGTGGATGATACT	32539	ATCCTCATGGTCGACGACACA
3894	ILNDRSA	18217	ATTCTGAATGATCGTAGTGCT	32540	ATCCTCAACGACAGAAGCGCA
3895	ILNHGKG	18218	ATTCTTAATCATGGTAAGGGG	32541	ATCCTCAACCACGGAAAAGGA
3896	ILNKPLS	18219	ATTCTTAATAAGCCGTTGTCG	32542	ATCCTCAACAAACCACTCAGC
3897	ILPHTTT	18220	ATTCTGCCGCATACGACTACT	32543	ATCCTCCCACACACAACAACA
3898	ILPNSMP	18221	ATTCTTCCTAATTCTATGCCT	32544	ATCCTCCCAAACAGCATGCCA
3899	ILPNTGP	18222	ATTCTGCCTAATACGGGGCCG	32545	ATCCTCCCAAACACAGGACCA
3900	ILPPITD	18223	ATTTTGCCGCCGATTACGGAT	32546	ATCCTCCCACCAATCACAGAC
3901	ILPSLTA	18224	ATTCTGCCTTCGCTTACTGCT	32547	ATCCTCCCAAGCCTCACAGCA
3902	ILPSSFS	18225	ATTCTTCCGTCTTCGTTTTCG	32548	ATCCTCCCAAGCAGCTTCAGC
3903	ILPYSSP	18226	ATTCTTCCTTATTCTTCTCCG	32549	ATCCTCCCATACAGCAGCCCA
3904	ILQAHQT	18227	ATTTTGCAGGCGCATCAGACT	32550	ATCCTCCAAGCACACCAAACA

3905	ILQSEFT	18228	ATTCTTCAGTCGGAGTTTACG	32551	ATCCTCCAAAGCGAATTCACA
3906	ILRGDGP	18229	ATTCTGAGGGGGGATGGTCCG	32552	ATCCTCAGAGGAGACGGACCA
3907	ILRGNGS	18230	ATTCTGAGGGGTAATGGGAGT	32553	ATCCTCAGAGGAAACGGAAGC
3908	ILRTEYK	18231	ATTCTTCGTACTGAGTATAAG	32554	ATCCTCAGAACAGAATACAAA
3909	ILRVHTP	18232	ATTCTGCGGGTGCATACTCCT	32555	ATCCTCAGAGTCCACACACCA
3910	ILSERTP	18233	ATTTTGAGTGAGAGGACTCCT	32556	ATCCTCAGCGAAAGAACACCA
3911	ILSMDTA	18234	ATTCTTTCTATGGATACGGCT	32557	ATCCTCAGCATGGACACAGCA
3912	ILTGSHA	18235	ATTCTGACTGGTTCTCATGCT	32558	ATCCTCACAGGAAGCCACGCA
3913	ILTKDVS	18236	ATTCTGACTAAGGATGTGAGT	32559	ATCCTCACAAAAGACGTCAGC
3914	ILTKSPT	18237	ATTCTTACGAAGTCGCCGACG	32560	ATCCTCACAAAAAGCCCAACA
3915	ILTRVSP	18238	ATTTTGACTCGTGTTAGTCCT	32561	ATCCTCACAAGAGTCAGCCCA
3916	ILTSVTK	18239	ATTCTGACGTCTGTGACGAAG	32562	ATCCTCACAAGCGTCACAAAA
3917	ILVSELR	18240	ATTTTGGTTTCGGAGCTGCGG	32563	ATCCTCGTCAGCGAACTCAGA
3918	IMAPTTQ	18241	ATTATGGCGCCGACTACGCAG	32564	ATCATGGCACCAACAACACAA
3919	IMDAHIA	18242	ATTATGGATGCGCATATTGCG	32565	ATCATGGACGCACACATCGCA
3920	IMDVKFH	18243	ATTATGGATGTTAAGTTTCAT	32566	ATCATGGACGTCAAATTCCAC
3921	IMEVRGP	18244	ATTATGGAGGTGCGGGGGCCG	32567	ATCATGGAAGTCAGAGGACCA
3922	IMGEPRK	18245	ATTATGGGTGAGCCTCGTAAG	32568	ATCATGGGAGAACCAAGAAAA
3923	IMGSAPS	18246	ATTATGGGGTCTGCTCCTTCT	32569	ATCATGGGAAGCGCACCAAGC
3924	IMGSAPY	18247	ATTATGGGTAGTGCGCCTTAT	32570	ATCATGGGAAGCGCACCATAC
3925	IMLPDAD	18248	ATTATGTTGCCTGATGCTGAT	32571	ATCATGCTCCCAGACGCAGAC
3926	IMNANRA	18249	ATTATGAATGCTAATCGTGCT	32572	ATCATGAACGCAAACAGAGCA
3927	IMNRISA	18250	ATTATGAATCGGATTTCTGCG	32573	ATCATGAACAGAATCAGCGCA
3928	IMPNSSD	18251	ATTATGCCTAATAGTTCGGAT	32574	ATCATGCCAAACAGCAGCGAC
3929	IMPSSTN	18252	ATTATGCCTAGTTCGACTAAT	32575	ATCATGCCAAGCAGCACAAAC
3930	IMRPSDP	18253	ATTATGCGGCCTTCTGATCCT	32576	ATCATGAGACCAAGCGACCCA
3931	IMSTTTL	18254	ATTATGTCTACTACTACTCTG	32577	ATCATGAGCACAACAACACTC
3932	IMTMTPS	18255	ATTATGACTATGACTCCGAGT	32578	ATCATGACAATGACACCAAGC
3933	INAQTHL	18256	ATTAATGCGCAGACTCATCTT	32579	ATCAACGCACAAACACACCTC
3934	INAYHVP	18257	ATTAATGCGTATCATGTTCCG	32580	ATCAACGCATACCACGTCCCA
3935	INEHVRL	18258	ATTAATGAGCATGTGCGTTTG	32581	ATCAACGAACACGTCAGACTC
3936	INESNRG	18259	ATTAATGAGTCTAATCGGGGT	32582	ATCAACGAAAGCAACAGAGGA
3937	INGSDRQ	18260	ATTAATGGTTCGGATCGGCAG	32583	ATCAACGGAAGCGACAGACAA
3938	INGTAKH	18261	ATTAATGGGACGGCTAAGCAT	32584	ATCAACGGAACAGCAAAACAC
3939	INHSSMG	18262	ATTAATCATAGTTCTATGGGT	32585	ATCAACCACAGCAGCATGGGA
3940	INIASAG	18263	ATTAATATTGCGAGTGCGGGT	32586	ATCAACATCGCAAGCGCAGGA
3941	INKPSNG	18264	ATTAATAAGCCGTCGAATGGG	32587	ATCAACAAACCAAGCAACGGA
3942	INLHVKS	18265	ATTAATCTGCATGTTAAGAGT	32588	ATCAACCTCCACGTCAAAAGC
3943	INLRPAA	18266	ATTAATTTGCGTCCGGCTGCG	32589	ATCAACCTCAGACCAGCAGCA
3944	INLTPRF	18267	ATTAATCTGACGCCTCGTTTT	32590	ATCAACCTCACACCAAGATTC
3945	INMAGVH	18268	ATTAATATGGCTGGGGTGCAT	32591	ATCAACATGGCAGGAGTCCAC
3946	INMSTGS	18269	ATTAATATGAGTACTGGGTCT	32592	ATCAACATGAGCACAGGAAGC
3947	INPQNRT	18270	ATTAATCCTCAGAATCGTACG	32593	ATCAACCCACAAAACAGAACA
3948	INRGVNS	18271	ATTAATAGGGGGGTGAATAGT	32594	ATCAACAGAGGAGTCAACAGC
3949	INRTTME	18272	ATTAATCGTACTACGATGGAG	32595	ATCAACAGAACAACAATGGAA

3950	INRVTAE	18273	ATTAATCGTGTGACTGCGGAG	32596	ATCAACAGAGTCACAGCAGAA
3951	INSAAVL	18274	ATTAATTCGGCGGCTGTTCTT	32597	ATCAACAGCGCAGCAGTCCTC
3952	INSGRSN	18275	ATTAATAGTGGGAGGTCTAAT	32598	ATCAACAGCGGAAGAAGCAAC
3953	INSHTLQ	18276	ATTAATTCGCATACTCTTCAG	32599	ATCAACAGCCACACACTCCAA
3954	INSQKPP	18277	ATTAATTCGCAGAAGCCTCCG	32600	ATCAACAGCCAAAAACCACCA
3955	INSRNGV	18278	ATTAATTCTCGGAATGGTGTT	32601	ATCAACAGCAGAAACGGAGTC
3956	INTLGNS	18279	ATTAATACTCTTGGTAATTCG	32602	ATCAACACACTCGGAAACAGC
3957	INTPGYT	18280	ATTAATACGCCGGGGTATACG	32603	ATCAACACACCAGGATACACA
3958	INVLRSA	18281	ATTAATGTTCTTCGTTCGGCG	32604	ATCAACGTCCTCAGAAGCGCA
3959	IPANSQV	18282	ATTCCGGCTAATTCTCAGGTT	32605	ATCCCAGCAAACAGCCAAGTC
3960	IPASSSW	18283	ATTCCTGCTTCGTCTAGTTGG	32606	ATCCCAGCAAGCAGCAGCTGG
3961	IPDLKRT	18284	ATTCCGGATTTGAAGCGTACG	32607	ATCCCAGACCTCAAAAGAACA
3962	IPEGLPL	18285	ATTCCTGAGGGGCTGCCGCTG	32608	ATCCCAGAAGGACTCCCACTC
3963	IPGFPKS	18286	ATTCCGGGGTTTCCGAAGAGT	32609	ATCCCAGGATTCCCAAAAAGC
3964	IPGTELQ	18287	ATTCCTGGGACGGAGCTGCAG	32610	ATCCCAGGAACAGAACTCCAA
3965	IPHNQAY	18288	ATTCCTCATAATCAGGCTTAT	32611	ATCCCACACAACCAAGCATAC
3966	IPHPANS	18289	ATTCCGCATCCGGCTAATTCT	32612	ATCCCACACCCAGCAAACAGC
3967	IPHTQTQ	18290	ATTCCTCATACTCAGACTCAG	32613	ATCCCACACACACAAACACAA
3968	IPIGYKT	18291	ATTCCTATTGGTTATAAGACG	32614	ATCCCAATCGGATACAAAACA
3969	IPIKNGM	18292	ATTCCGATTAAGAATGGGATG	32615	ATCCCAATCAAAAACGGAATG
3970	IPIPVAM	18293	ATTCCTATTCCTGTTGCGATG	32616	ATCCCAATCCCAGTCGCAATG
3971	IPKTRPE	18294	ATTCCTAAGACGCGGCCGGAG	32617	ATCCCAAAAACAAGACCAGAA
3972	IPLKAYG	18295	ATTCCGCTTAAGGCTTATGGT	32618	ATCCCACTCAAAGCATACGGA
3973	IPLPNDG	18296	ATTCCTCTTCCTAATGATGGT	32619	ATCCCACTCCCAAACGACGGA
3974	IPLTSHT	18297	ATTCCTCTGACGAGTCATACT	32620	ATCCCACTCACAAGCCACACA
3975	IPMSAAK	18298	ATTCCGATGAGTGCTGCTAAG	32621	ATCCCAATGAGCGCAGCAAAA
3976	IPNFVHS	18299	ATTCCTAATTTTGTGCATTCT	32622	ATCCCAAACTTCGTCCACAGC
3977	IPNHKSI	18300	ATTCCTAATCATAAGAGTATT	32623	ATCCCAAACCACAAAAGCATC
3978	IPNKTPF	18301	ATTCCGAATAAGACGCCGTTT	32624	ATCCCAAACAAAACACCATTC
3979	IPNLKIS	18302	ATTCCTAATCTGAAGATTTCG	32625	ATCCCAAACCTCAAAATCAGC
3980	IPNPPMA	18303	ATTCCTAATCCTCCTATGGCT	32626	ATCCCAAACCCACCAATGGCA
3981	IPNRHLS	18304	ATTCCGAATCGGCATCTGTCG	32627	ATCCCAAACAGACACCTCAGC
3982	IPNVSHQ	18305	ATTCCTAATGTTTCGCATCAG	32628	ATCCCAAACGTCAGCCACCAA
3983	IPNYAVS	18306	ATTCCTAATTATGCGGTTAGT	32629	ATCCCAAACTACGCAGTCAGC
3984	IPPRSNS	18307	ATTCCTCCGAGGTCGAATTCT	32630	ATCCCACCAAGAAGCAACAGC
3985	IPQASLM	18308	ATTCCGCAGGCGAGTCTTATG	32631	ATCCCACAAGCAAGCCTCATG
3986	IPQNRIL	18309	ATTCCGCAGAATCGTATTTTG	32632	ATCCCACAAAACAGAATCCTC
3987	IPQPVHL	18310	ATTCCGCAGCCGGTTCATTTG	32633	ATCCCACAACCAGTCCACCTC
3988	IPRADAR	18311	ATTCCGCGTGCGGATGCTCGG	32634	ATCCCAAGAGCAGACGCAAGA
3989	IPRFSTM	18312	ATTCCTCGGTTTTCGACGATG	32635	ATCCCAAGATTCAGCACAATG
3990	IPRPSVH	18313	ATTCCGCGGCCGTCTGTGCAT	32636	ATCCCAAGACCAAGCGTCCAC
3991	IPRSNIS	18314	ATTCCTAGGTCGAATATTTCT	32637	ATCCCAAGAAGCAACATCAGC
3992	IPRTALQ	18315	ATTCCTCGGACTGCTTTGCAG	32638	ATCCCAAGAACAGCACTCCAA
3993	IPSFKRE	18316	ATTCCGAGTTTTAAGCGTGAG	32639	ATCCCAAGCTTCAAAAGAGAA
3994	IPSFSKP	18317	ATTCCTTCGTTTTCTAAGCCT	32640	ATCCCAAGCTTCAGCAAACCA

3995	IPSNCKP	18318	ATTCCTTCTAATTGTAAGCCT	32641	ATCCCAAGCAACTGCAAACCA
3996	IPSPSHE	18319	ATTCCGAGTCCTTCTCATGAG	32642	ATCCCAAGCCCAAGCCACGAA
3997	IPSRYAM	18320	ATTCCGTCTCGTTATGCTATG	32643	ATCCCAAGCAGATACGCAATG
3998	IPSVPVS	18321	ATTCCGTCTGTGCCGGTGTCT	32644	ATCCCAAGCGTCCCAGTCAGC
3999	IPTISHG	18322	ATTCCGACTATTTCGCATGGG	32645	ATCCCAACAATCAGCCACGGA
4000	IPTLPAM	18323	ATTCCTACTCTGCCTGCTATG	32646	ATCCCAACACTCCCAGCAATG
4001	IPTPNNV	18324	ATTCCGACGCCTAATAATGTT	32647	ATCCCAACACCAAACAACGTC
4002	IPTTALG	18325	ATTCCTACTACTGCTTTGGGG	32648	ATCCCAACAACAGCACTCGGA
4003	IPVFRSE	18326	ATTCCGGTTTTTCGTTCTGAG	32649	ATCCCAGTCTTCAGAAGCGAA
4004	IPVGQYN	18327	ATTCCGGTTGGTCAGTATAAT	32650	ATCCCAGTCGGACAATACAAC
4005	IPVRLTQ	18328	ATTCCTGTTAGGCTGACGCAG	32651	ATCCCAGTCAGACTCACACAA
4006	IPYMLDP	18329	ATTCCTTATATGCTTGATCCT	32652	ATCCCATACATGCTCGACCCA
4007	IQAVSSL	18330	ATTCAGGCTGTGTCGAGTTTG	32653	ATCCAAGCAGTCAGCAGCCTC
4008	IQDETVS	18331	ATTCAGGATGAGACGGTGTCT	32654	ATCCAAGACGAAACAGTCAGC
4009	IQESARM	18332	ATTCAGGAGTCGGCTAGGATG	32655	ATCCAAGAAAGCGCAAGAATG
4010	IQFRSAT	18333	ATTCAGTTTAGGTCGGCTACG	32656	ATCCAATTCAGAAGCGCAACA
4011	IQFVPVD	18334	ATTCAGTTTGTGCCTGTTGAT	32657	ATCCAATTCGTCCCAGTCGAC
4012	IQGLSAL	18335	ATTCAGGGTTTGAGTGCGCTG	32658	ATCCAAGGACTCAGCGCACTC
4013	IQGRLTT	18336	ATTCAGGGGCGTCTTACGACT	32659	ATCCAAGGAAGACTCACAACA
4014	IQHQPLT	18337	ATTCAGCATCAGCCGCTGACT	32660	ATCCAACACCAACCACTCACA
4015	IQIKSLN	18338	ATTCAGATTAAGTCTCTTAAT	32661	ATCCAAATCAAAAGCCTCAAC
4016	IQIQERR	18339	ATTCAGATTCAGGAGAGGCGT	32662	ATCCAAATCCAAGAAAGAAGA
4017	IQLKSTV	18340	ATTCAGTTGAAGAGTACTGTT	32663	ATCCAACTCAAAAGCACAGTC
4018	IQLRINA	18341	ATTCAGCTTAGGATTAATGCT	32664	ATCCAACTCAGAATCAACGCA
4019	IQLSAAS	18342	ATTCAGCTTTCGGCTGCTTCG	32665	ATCCAACTCAGCGCAGCAAGC
4020	IQNGYQF	18343	ATTCAGAATGGTTATCAGTTT	32666	ATCCAAAACGGATACCAATTC
4021	IQNHHQL	18344	ATTCAGAATCATCATCAGTTG	32667	ATCCAAAACCACCACCAACTC
4022	IQNTPPT	18345	ATTCAGAATACTCCTCCGACT	32668	ATCCAAAACACACCACCAACA
4023	IQNVPLH	18346	ATTCAGAATGTGCCTTTGCAT	32669	ATCCAAAACGTCCCACTCCAC
4024	IQRPSDI	18347	ATTCAGCGGCCGAGTGATATT	32670	ATCCAAAGACCAAGCGACATC
4025	IQRSVEA	18348	ATTCAGCGTTCGGTTGAGGCG	32671	ATCCAAAGAAGCGTCGAAGCA
4026	IQRVAQG	18349	ATTCAGCGGGTGGCTCAGGGG	32672	ATCCAAAGAGTCGCACAAGGA
4027	IQSINLP	18350	ATTCAGAGTATTAATCTTCCG	32673	ATCCAAAGCATCAACCTCCCA
4028	IQSPLLA	18351	ATTCAGAGTCCGCTGTTGGCG	32674	ATCCAAAGCCCACTCCTCGCA
4029	IQSTRLV	18352	ATTCAGTCTACTAGGCTGGTG	32675	ATCCAAAGCACAAGACTCGTC
4030	IQSYNTL	18353	ATTCAGTCGTATAATACTTTG	32676	ATCCAAAGCTACAACACACTC
4031	IQTRSDM	18354	ATTCAGACTCGTAGTGATATG	32677	ATCCAAACAAGAAGCGACATG
4032	IQTVSAV	18355	ATTCAGACGGTTTCGGCTGTG	32678	ATCCAAACAGTCAGCGCAGTC
4033	IRALAGH	18356	ATTCGTGCTCTGGCTGGGCAT	32679	ATCAGAGCACTCGCAGGACAC
4034	IRASQTI	18357	ATTAGGGCTTCTCAGACTATT	32680	ATCAGAGCAAGCCAAACAATC
4035	IRATSSE	18358	ATTCGGGCGACGTCTTCGGAG	32681	ATCAGAGCAACAAGCAGCGAA
4036	IRDVHVV	18359	ATTCGGGATGTGCATGTGGTT	32682	ATCAGAGACGTCCACGTCGTC
4037	IREPTAM	18360	ATTAGGGAGCCGACGGCTATG	32683	ATCAGAGAACCAACAGCAATG
4038	IRGALGI	18361	ATTAGGGGGGCGTTGGGTATT	32684	ATCAGAGGAGCACTCGGAATC
4039	IRGNFLS	18362	ATTCGGGGTAATTTTCTGTCT	32685	ATCAGAGGAAACTTCCTCAGC

4040	IRGTPAF	18363	ATTCGTGGTACTCCTGCGTTT	32686	ATCAGAGGAACACCAGCATTC
4041	IRHGIAA	18364	ATTAGGCATGGGATTGCTGCT	32687	ATCAGACACGGAATCGCAGCA
4042	IRIPELP	18365	ATTAGGATTCCTGAGCTGCCG	32688	ATCAGAATCCCAGAACTCCCA
4043	IRIPMTP	18366	ATTCGTATTCCGATGACTCCT	32689	ATCAGAATCCCAATGACACCA
4044	IRKSPNE	18367	ATTAGGAAGTCGCCGAATGAG	32690	ATCAGAAAAAGCCCAAACGAA
4045	IRLEYSA	18368	ATTCGTCTGGAGTATTCGGCG	32691	ATCAGACTCGAATACAGCGCA
4046	IRLGSFA	18369	ATTCGTTTGGGGTCTTTTGCT	32692	ATCAGACTCGGAAGCTTCGCA
4047	IRLQNSI	18370	ATTCGGCTTCAGAATTCTATT	32693	ATCAGACTCCAAAACAGCATC
4048	IRLSDKA	18371	ATTCGTCTTTCTGATAAGGCT	32694	ATCAGACTCAGCGACAAAGCA
4049	IRMSTQL	18372	ATTCGGATGAGTACGCAGCTT	32695	ATCAGAATGAGCACACAACTC
4050	IRNGSDD	18373	ATTCGGAATGGTAGTGATGAT	32696	ATCAGAAACGGAAGCGACGAC
4051	IRNIIDF	18374	ATTCGTAATATTATTGATTTT	32697	ATCAGAAACATCATCGACTTC
4052	IRPLNMP	18375	ATTAGGCCTCTGAATATGCCT	32698	ATCAGACCACTCAACATGCCA
4053	IRPTEGM	18376	ATTCGTCCTACTGAGGGGATG	32699	ATCAGACCAACAGAAGGAATG
4054	IRQECRI	18377	ATTAGGCAGGAGTGTCGTATT	32700	ATCAGACAAGAATGCAGAATC
4055	IRQIPYA	18378	ATTAGGCAGATTCCGTATGCT	32701	ATCAGACAAATCCCATACGCA
4056	IRQSSVN	18379	ATTCGTCAGAGTTCGGTTAAT	32702	ATCAGACAAAGCAGCGTCAAC
4057	IRSGQPL	18380	ATTCGGAGTGGTCAGCCGCTG	32703	ATCAGAAGCGGACAACCACTC
4058	IRSITDT	18381	ATTCGTTCTATTACTGATACG	32704	ATCAGAAGCATCACAGACACA
4059	IRSLATA	18382	ATTCGGAGTCTTGCGACTGCG	32705	ATCAGAAGCCTCGCAACAGCA
4060	IRSPLPS	18383	ATTCGGAGTCCTCTTCCTAGT	32706	ATCAGAAGCCCACTCCCAAGC
4061	IRSSGMM	18384	ATTCGTAGTAGTGGTATGATG	32707	ATCAGAAGCAGCGGAATGATG
4062	IRSSPPT	18385	ATTAGGTCTTCTCCTCCGACG	32708	ATCAGAAGCAGCCCACCAACA
4063	IRSVSEV	18386	ATTAGGTCGGTTAGTGAGGTT	32709	ATCAGAAGCGTCAGCGAAGTC
4064	IRTLGST	18387	ATTAGGACGCTTGGTAGTACT	32710	ATCAGAACACTCGGAAGCACA
4065	IRTTAAF	18388	ATTCGTACGACGGCGGCTTTT	32711	ATCAGAACAACAGCAGCATTC
4066	IRVENEL	18389	ATTAGGGTGGAGAATGAGCTG	32712	ATCAGAGTCGAAAACGAACTC
4067	IRVNDTG	18390	ATTCGGGTTAATGATACTGGG	32713	ATCAGAGTCAACGACACAGGA
4068	IRVPTSS	18391	ATTCGGGTGCCGACGAGTTCG	32714	ATCAGAGTCCCAACAAGCAGC
4069	IRVSAIH	18392	ATTCGGGTTTCTGCGATTCAT	32715	ATCAGAGTCAGCGCAATCCAC
4070	ISAASRA	18393	ATTTCTGCTGCTAGTCGTGCG	32716	ATCAGCGCAGCAAGCAGAGCA
4071	ISAAVMA	18394	ATTAGTGCTGCGGTTATGGCT	32717	ATCAGCGCAGCAGTCATGGCA
4072	ISAGPMP	18395	ATTAGTGCTGGGCCGATGCCG	32718	ATCAGCGCAGGACCAATGCCA
4073	ISAISAQ	18396	ATTTCTGCGATTTCTGCTCAG	32719	ATCAGCGCAATCAGCGCACAA
4074	ISANMFS	18397	ATTTCTGCTAATATGTTTAGT	32720	ATCAGCGCAAACATGTTCAGC
4075	ISARPTI	18398	ATTTCTGCTCGTCCTACGATT	32721	ATCAGCGCAAGACCAACAATC
4076	ISASHSS	18399	ATTAGTGCGTCGCATAGTAGT	32722	ATCAGCGCAAGCCACAGCAGC
4077	ISATTSS	18400	ATTTCTGCTACTACGTCGTCT	32723	ATCAGCGCAACAACAAGCAGC
4078	ISDQQYT	18401	ATTTCGGATCAGCAGTATACG	32724	ATCAGCGACCAACAATACACA
4079	ISECVGG	18402	ATTTCGGAGTGTGTTGGGGGT	32725	ATCAGCGAATGCGTCGGAGGA
4080	ISEHIMS	18403	ATTTCTGAGCATATTATGAGT	32726	ATCAGCGAACACATCATGAGC
4081	ISEPTSV	18404	ATTAGTGAGCCTACTAGTGTG	32727	ATCAGCGAACCAACAAGCGTC
4082	ISESSRY	18405	ATTAGTGAGAGTTCTCGTTAT	32728	ATCAGCGAAAGCAGCAGATAC
4083	ISFRIEN	18406	ATTTCTTTTCGGATTGAGAAT	32729	ATCAGCTTCAGAATCGAAAAC
4084	ISGAVDR	18407	ATTTCTGGTGCGGTTGATCGT	32730	ATCAGCGGAGCAGTCGACAGA

4085	ISGKLAT	18408	ATTAGTGGTAAGTTGGCGACT	32731	ATCAGCGGAAAACTCGCAACA
4086	ISGNPNA	18409	ATTAGTGGTAATCCGAATGCT	32732	ATCAGCGGAAACCCAAACGCA
4087	ISGPPTP	18410	ATTTCTGGGCCGCCTACTCCG	32733	ATCAGCGGACCACCAACACCA
4088	ISGRNAT	18411	ATTTCGGGTCGGAATGCGACT	32734	ATCAGCGGAAGAAACGCAACA
4089	ISHSDNA	18412	ATTTCGCATTCGGATAATGCG	32735	ATCAGCCACAGCGACAACGCA
4090	ISIQLRD	18413	ATTTCTATTCAGCTGCGTGAT	32736	ATCAGCATCCAACTCAGAGAC
4091	ISIRTGP	18414	ATTAGTATTAGGACGGGGCCT	32737	ATCAGCATCAGAACAGGACCA
4092	ISKAEAI	18415	ATTAGTAAGGCGGAGGCGATT	32738	ATCAGCAAAGCAGAAGCAATC
4093	ISKAYPN	18416	ATTTCGAAGGCGTATCCTAAT	32739	ATCAGCAAAGCATACCCAAAC
4094	ISKDGAV	18417	ATTAGTAAGGATGGTGCTGTG	32740	ATCAGCAAAGACGGAGCAGTC
4095	ISKDNAL	18418	ATTTCGAAGGATAATGCTCTG	32741	ATCAGCAAAGACAACGCACTC
4096	ISKLNGP	18419	ATTTCTAAGCTTAATGGTCCG	32742	ATCAGCAAACTCAACGGACCA
4097	ISKSYNG	18420	ATTTCGAAGTCTTATAATGGG	32743	ATCAGCAAAAGCTACAACGGA
4098	ISLDRHS	18421	ATTTCGTTGGATCGGCATTCT	32744	ATCAGCCTCGACAGACACAGC
4099	ISLLRNT	18422	ATTAGTCTTTTGCGTAATACT	32745	ATCAGCCTCCTCAGAAACACA
4100	ISLQTSL	18423	ATTTCTTTGCAGACTTCGCTG	32746	ATCAGCCTCCAAACAAGCCTC
4101	ISLRFND	18424	ATTAGTCTTCGGTTTAATGAT	32747	ATCAGCCTCAGATTCAACGAC
4102	ISLSALA	18425	ATTAGTCTGTCTGCTCTGGCT	32748	ATCAGCCTCAGCGCACTCGCA
4103	ISMKPIS	18426	ATTTCGATGAAGCCGATTTCT	32749	ATCAGCATGAAACCAATCAGC
4104	ISMLRPT	18427	ATTTCTATGCTTCGTCCGACT	32750	ATCAGCATGCTCAGACCAACA
4105	ISMTVHS	18428	ATTAGTATGACTGTTCATTCT	32751	ATCAGCATGACAGTCCACAGC
4106	ISMVRQG	18429	ATTTCGATGGTTCGGCAGGGG	32752	ATCAGCATGGTCAGACAAGGA
4107	ISNAMTQ	18430	ATTTCTAATGCGATGACTCAG	32753	ATCAGCAACGCAATGACACAA
4108	ISNGRAV	18431	ATTTCGAATGGGCGTGCTGTT	32754	ATCAGCAACGGAAGAGCAGTC
4109	ISNSRST	18432	ATTAGTAATAGTCGGTCGACG	32755	ATCAGCAACAGCAGAAGCACA
4110	ISNSSPS	18433	ATTTCGAATTCGAGTCCGTCT	32756	ATCAGCAACAGCAGCCCAAGC
4111	ISNVQLA	18434	ATTAGTAATGTGCAGCTTGCG	32757	ATCAGCAACGTCCAACTCGCA
4112	ISPAPFP	18435	ATTTCTCCGGCGCCTTTTCCG	32758	ATCAGCCCAGCACCATTCCCA
4113	ISPDPML	18436	ATTAGTCCGGATCCGATGTTG	32759	ATCAGCCCAGACCCAATGCTC
4114	ISPFTVE	18437	ATTTCGCCGTTTACGGTTGAG	32760	ATCAGCCCATTCACAGTCGAA
4115	ISPRDVS	18438	ATTTCTCCGCGTGATGTTAGT	32761	ATCAGCCCAAGAGACGTCAGC
4116	ISPRKAT	18439	ATTTCTCCTAGGAAGGCTACG	32762	ATCAGCCCAAGAAAAGCAACA
4117	ISPRNNS	18440	ATTAGTCCGAGGAATAATTCT	32763	ATCAGCCCAAGAAACAACAGC
4118	ISPRYPH	18441	ATTAGTCCTCGGTATCCTCAT	32764	ATCAGCCCAAGATACCCACAC
4119	ISPSGPA	18442	ATTTCGCCGTCTGGTCCGGCT	32765	ATCAGCCCAAGCGGACCAGCA
4120	ISPVRNV	18443	ATTTCGCCGGTGCGGAATGTG	32766	ATCAGCCCAGTCAGAAACGTC
4121	ISPYENA	18444	ATTAGTCCTTATGAGAATGCG	32767	ATCAGCCCATACGAAAACGCA
4122	ISPYRVS	18445	ATTTCGCCTTATCGGGTTAGT	32768	ATCAGCCCATACAGAGTCAGC
4123	ISQQRLK	18446	ATTTCTCAGCAGCGGCTTAAG	32769	ATCAGCCAACAAAGACTCAAA
4124	ISQRWPD	18447	ATTTCGCAGCGTTGGCCTGAT	32770	ATCAGCCAAAGATGGCCAGAC
4125	ISQTRYD	18448	ATTAGTCAGACGAGGTATGAT	32771	ATCAGCCAAACAAGATACGAC
4126	ISRDTVM	18449	ATTTCTCGTGATACTGTTATG	32772	ATCAGCAGAGACACAGTCATG
4127	ISRLVSS	18450	ATTAGTAGGCTGGTTTCTTCG	32773	ATCAGCAGACTCGTCAGCAGC
4128	ISRSNII	18451	ATTAGTCGTAGTAATATTATT	32774	ATCAGCAGAAGCAACATCATC
4129	ISRVVTM	18452	ATTTCGCGGGTGGTTACGATG	32775	ATCAGCAGAGTCGTCACAATG

4130	ISSAFAP	18453	ATTTCGTCGGCTTTTGCTCCG	32776	ATCAGCAGCGCATTCGCACCA
4131	ISSHCMA	18454	ATTTCTAGTCATTGTATGGCT	32777	ATCAGCAGCCACTGCATGGCA
4132	ISSKLVS	18455	ATTTCTAGTAAGCTTGTTAGT	32778	ATCAGCAGCAAACTCGTCAGC
4133	ISSNPTV	18456	ATTTCGTCGAATCCGACTGTT	32779	ATCAGCAGCAACCCAACAGTC
4134	ISSSATL	18457	ATTTCGTCTTCGGCTACTTTG	32780	ATCAGCAGCAGCGCAACACTC
4135	ISSTNTA	18458	ATTAGTTCTACTAATACGGCT	32781	ATCAGCAGCACAAACACAGCA
4136	ISSTVEI	18459	ATTAGTAGTACGGTTGAGATT	32782	ATCAGCAGCACAGTCGAAATC
4137	ISSVQNP	18460	ATTTCGTCGGTGCAGAATCCT	32783	ATCAGCAGCGTCCAAAACCCA
4138	ISTHLKS	18461	ATTTCGACGCATCTGAAGAGT	32784	ATCAGCACACACCTCAAAAGC
4139	ISTHTKS	18462	ATTTCTACTCATACGAAGAGT	32785	ATCAGCACACACACAAAAAGC
4140	ISTNVRS	18463	ATTTCTACTAATGTGAGGTCT	32786	ATCAGCACAAACGTCAGAAGC
4141	ISTRNPE	18464	ATTTCGACGCGTAATCCTGAG	32787	ATCAGCACAAGAAACCCAGAA
4142	ISTSQQH	18465	ATTTCTACGAGTCAGCAGCAT	32788	ATCAGCACAAGCCAACAACAC
4143	ISTTTVP	18466	ATTTCTACGACGACGGTGCCG	32789	ATCAGCACAACAACAGTCCCA
4144	ISTVLVD	18467	ATTTCTACGGTTTTGGTGGAT	32790	ATCAGCACAGTCCTCGTCGAC
4145	ISTWEYE	18468	ATTAGTACGTGGGAGTATGAG	32791	ATCAGCACATGGGAATACGAA
4146	ISTWRPT	18469	ATTTCTACGTGGCGTCCTACT	32792	ATCAGCACATGGAGACCAACA
4147	ISVKGQP	18470	ATTTCGGTTAAGGGTCAGCCT	32793	ATCAGCGTCAAAGGACAACCA
4148	ISVSQTD	18471	ATTTCGGTGTCGCAGACGGAT	32794	ATCAGCGTCAGCCAAACAGAC
4149	ISVTSSS	18472	ATTTCGGTTACTTCTTCTAGT	32795	ATCAGCGTCACAAGCAGCAGC
4150	ISYGTRS	18473	ATTTCGTATGGTACGAGGAGT	32796	ATCAGCTACGGAACAAGAAGC
4151	ISYNAKV	18474	ATTTCTTATAATGCTAAGGTT	32797	ATCAGCTACAACGCAAAAGTC
4152	ISYPKPV	18475	ATTAGTTATCCGAAGCCGGTT	32798	ATCAGCTACCCAAAACCAGTC
4153	ITAPHSM	18476	ATTACTGCTCCTCATTCGATG	32799	ATCACAGCACCACACAGCATG
4154	ITARVNA	18477	ATTACTGCTCGTGTGAATGCT	32800	ATCACAGCAAGAGTCAACGCA
4155	ITARYPT	18478	ATTACGGCTCGTTATCCGACG	32801	ATCACAGCAAGATACCCAACA
4156	ITASGLV	18479	ATTACGGCGTCGGGTTTGGTT	32802	ATCACAGCAAGCGGACTCGTC
4157	ITATQRM	18480	ATTACTGCTACTCAGCGTATG	32803	ATCACAGCAACACAAAGAATG
4158	ITDAANP	18481	ATTACGGATGCTGCGAATCCT	32804	ATCACAGACGCAGCAAACCCA
4159	ITDRVAI	18482	ATTACTGATAGGGTTGCGATT	32805	ATCACAGACAGAGTCGCAATC
4160	ITERSCT	18483	ATTACTGAGAGGTCTTGTACT	32806	ATCACAGAAAGAAGCTGCACA
4161	ITEVKRG	18484	ATTACGGAGGTTAAGCGTGGG	32807	ATCACAGAAGTCAAAAGAGGA
4162	ITFDHVT	18485	ATTACGTTTGATCATGTTACT	32808	ATCACATTCGACCACGTCACA
4163	ITFSGSS	18486	ATTACTTTTTCTGGTTCTTCG	32809	ATCACATTCAGCGGAAGCAGC
4164	ITGDLNG	18487	ATTACTGGTGATCTTAATGGG	32810	ATCACAGGAGACCTCAACGGA
4165	ITGGRPG	18488	ATTACGGGTGGGCGGCCGGGT	32811	ATCACAGGAGGAAGACCAGGA
4166	ITGNRTP	18489	ATTACTGGTAATCGGACTCCT	32812	ATCACAGGAAACAGAACACCA
4167	ITGSNRD	18490	ATTACTGGGTCTAATCGTGAT	32813	ATCACAGGAAGCAACAGAGAC
4168	ITHASSD	18491	ATTACGCATGCGTCGTCGGAT	32814	ATCACACACGCAAGCAGCGAC
4169	ITHIRLD	18492	ATTACTCATATTCGTCTTGAT	32815	ATCACACACATCAGACTCGAC
4170	ITHSIQR	18493	ATTACGCATAGTATTCAGCGG	32816	ATCACACACAGCATCCAAAGA
4171	ITLGSTG	18494	ATTACTCTTGGGTCTACTGGG	32817	ATCACACTCGGAAGCACAGGA
4172	ITLSSQG	18495	ATTACTCTTAGTAGTCAGGGG	32818	ATCACACTCAGCAGCCAAGGA
4173	ITLYPNS	18496	ATTACTCTGTATCCTAATAGT	32819	ATCACACTCTACCCAAACAGC
4174	ITMLAGD	18497	ATTACTATGTTGGCTGGTGAT	32820	ATCACAATGCTCGCAGGAGAC

4175	ITNDRTV	18498	ATTACTAATGATCGTACGGTG	32821	ATCACAAACGACAGAACAGTC
4176	ITNEPPR	18499	ATTACGAATGAGCCTCCTCGT	32822	ATCACAAACGAACCACCAAGA
4177	ITPLTAG	18500	ATTACTCCTCTTACGGCGGGT	32823	ATCACACCACTCACAGCAGGA
4178	ITPMSIV	18501	ATTACTCCTATGTCTATTGTG	32824	ATCACACCAATGAGCATCGTC
4179	ITPSHGS	18502	ATTACGCCGTCGCATGGGTCT	32825	ATCACACCAAGCCACGGAAGC
4180	ITPVHAE	18503	ATTACTCCTGTTCATGCGGAG	32826	ATCACACCAGTCCACGCAGAA
4181	ITPYVRG	18504	ATTACGCCGTATGTGAGGGGG	32827	ATCACACCATACGTCAGAGGA
4182	ITQPHAK	18505	ATTACTCAGCCTCATGCGAAG	32828	ATCACACAACCACACGCAAAA
4183	ITRLKLD	18506	ATTACTAGGCTGAAGCTTGAT	32829	ATCACAAGACTCAAACTCGAC
4184	ITRSVAP	18507	ATTACGCGGTCGGTGGCTCCT	32830	ATCACAAGAAGCGTCGCACCA
4185	ITSADPQ	18508	ATTACGAGTGCGGATCCTCAG	32831	ATCACAAGCGCAGACCCACAA
4186	ITSKTQA	18509	ATTACTTCTAAGACTCAGGCT	32832	ATCACAAGCAAAACACAAGCA
4187	ITSPRLQ	18510	ATTACGTCTCCTAGGTTGCAG	32833	ATCACAAGCCCAAGACTCCAA
4188	ITSTLPP	18511	ATTACTTCGACGCTGCCGCCG	32834	ATCACAAGCACACTCCCACCA
4189	ITSTRAS	18512	ATTACTTCTACGCGTGCGTCG	32835	ATCACAAGCACAAGAGCAAGC
4190	ITSVDRL	18513	ATTACTAGTGTGGATAGGCTT	32836	ATCACAAGCGTCGACAGACTC
4191	ITSVPVS	18514	ATTACGAGTGTTCCTGTTTCT	32837	ATCACAAGCGTCCCAGTCAGC
4192	ITTKYSQ	18515	ATTACGACTAAGTATTCTCAG	32838	ATCACAACAAAATACAGCCAA
4193	ITTLGPT	18516	ATTACGACTCTGGGGCCTACT	32839	ATCACAACACTCGGACCAACA
4194	ITTNSGR	18517	ATTACGACGAATTCTGGGAGG	32840	ATCACAACAAACAGCGGAAGA
4195	ITTPAEQ	18518	ATTACTACTCCTGCGGAGCAG	32841	ATCACAACACCAGCAGAACAA
4196	ITTRETT	18519	ATTACGACTCGTGAGACTACG	32842	ATCACAACAAGAGAAACAACA
4197	ITTSDRA	18520	ATTACTACTTCTGATAGGGCG	32843	ATCACAACAAGCGACAGAGCA
4198	ITTYNEN	18521	ATTACGACTTATAATGAGAAT	32844	ATCACAACATACAACGAAAAC
4199	ITVPHHY	18522	ATTACTGTGCCGCATCATTAT	32845	ATCACAGTCCCACACCACTAC
4200	ITVSRAD	18523	ATTACTGTTTCTCGGGCGGAT	32846	ATCACAGTCAGCAGAGCAGAC
4201	ITYQNAE	18524	ATTACGTATCAGAATGCGGAG	32847	ATCACATACCAAAACGCAGAA
4202	IVATCTA	18525	ATTGTTGCTACTTGTACTGCG	32848	ATCGTCGCAACATGCACAGCA
4203	IVEASII	18526	ATTGTTGAGGCTAGTATTATT	32849	ATCGTCGAAGCAAGCATCATC
4204	IVEGLGD	18527	ATTGTTGAGGGGCTTGGGGAT	32850	ATCGTCGAAGGACTCGGAGAC
4205	IVETYLT	18528	ATTGTTGAGACTTATCTTACG	32851	ATCGTCGAAACATACCTCACA
4206	IVGSKLD	18529	ATTGTTGGTTCGAAGTTGGAT	32852	ATCGTCGGAAGCAAACTCGAC
4207	IVKGIPM	18530	ATTGTTAAGGGGATTCCTATG	32853	ATCGTCAAAGGAATCCCAATG
4208	IVLESMS	18531	ATTGTTTTGGAGTCTATGTCT	32854	ATCGTCCTCGAAAGCATGAGC
4209	IVLHLDG	18532	ATTGTGTTGCATTTGGATGGG	32855	ATCGTCCTCCACCTCGACGGA
4210	IVNLSTY	18533	ATTGTGAATCTTTCTACGTAT	32856	ATCGTCAACCTCAGCACATAC
4211	IVQVATS	18534	ATTGTTCAGGTGGCGACGTCT	32857	ATCGTCCAAGTCGCAACAAGC
4212	IVRQTIS	18535	ATTGTGAGGCAGACGATTAGT	32858	ATCGTCAGACAAACAATCAGC
4213	IVRSRPE	18536	ATTGTTCGGTCTCGGCCTGAG	32859	ATCGTCAGAAGCAGACCAGAA
4214	IVSHDFE	18537	ATTGTTTCGCATGATTTTGAG	32860	ATCGTCAGCCACGACTTCGAA
4215	IVSRINS	18538	ATTGTGTCTCGGATTAATTCG	32861	ATCGTCAGCAGAATCAACAGC
4216	IVSSYTD	18539	ATTGTGTCGTCGTATACTGAT	32862	ATCGTCAGCAGCTACACAGAC
4217	IVTGSGG	18540	ATTGTTACTGGGTCGGGTGGG	32863	ATCGTCACAGGAAGCGGAGGA
4218	IVTGSRE	18541	ATTGTGACTGGTAGTCGTGAG	32864	ATCGTCACAGGAAGCAGAGAA
4219	IVTKCPG	18542	ATTGTGACTAAGTGTCCGGGG	32865	ATCGTCACAAAATGCCCAGGA

4220	IVTSNVT	18543	ATTGTGACTTCGAATGTTACT	32866	ATCGTCACAAGCAACGTCACA
4221	IVTSTQP	18544	ATTGTTACGTCTACGCAGCCT	32867	ATCGTCACAAGCACACAACCA
4222	IWDSCRD	18545	ATTTGGGATTCTTGTAGGGAT	32868	ATCTGGGACAGCTGCAGAGAC
4223	IYKVDSS	18546	ATTTATAAGGTTGATTCGTCT	32869	ATCTACAAAGTCGACAGCAGC
4224	IYLRNDQ	18547	ATTTATCTTCGGAATGATCAG	32870	ATCTACCTCAGAAACGACCAA
4225	IYQSESH	18548	ATTTATCAGTCTGAGAGTCAT	32871	ATCTACCAAAGCGAAAGCCAC
4226	IYQSQHH	18549	ATTTATCAGTCGCAGCATCAT	32872	ATCTACCAAAGCCAACACCAC
4227	IYSAKQP	18550	ATTTATAGTGCTAAGCAGCCT	32873	ATCTACAGCGCAAAACAACCA
4228	IYSVGAT	18551	ATTTATAGTGTGGGGGCTACT	32874	ATCTACAGCGTCGGAGCAACA
4229	IYTGQVH	18552	ATTTATACTGGGCAGGTTCAT	32875	ATCTACACAGGACAAGTCCAC
4230	KAAKLLD	18553	AAGGCGGCTAAGCTGTTGGAT	32876	AAAGCAGCAAAACTCCTCGAC
4231	KAANQSS	18554	AAGGCGGCTAATCAGAGTTCT	32877	AAAGCAGCAAACCAAAGCAGC
4232	KADHSKE	18555	AAGGCTGATCATTCTAAGGAG	32878	AAAGCAGACCACAGCAAAGAA
4233	KADIQVR	18556	AAGGCTGATATTCAGGTGCGT	32879	AAAGCAGACATCCAAGTCAGA
4234	KAETVAP	18557	AAGGCGGAGACTGTGGCGCCT	32880	AAAGCAGAAACAGTCGCACCA
4235	KAFIGID	18558	AAGGCTTTTATTGGGATTGAT	32881	AAAGCATTCATCGGAATCGAC
4236	KAFSPAL	18559	AAGGCTTTTAGTCCGGCGCTT	32882	AAAGCATTCAGCCCAGCACTC
4237	KAGCSIS	18560	AAGGCGGGTTGTTCGATTAGT	32883	AAAGCAGGATGCAGCATCAGC
4238	KAGVPVP	18561	AAGGCTGGTGTTCCTGTTCCG	32884	AAAGCAGGAGTCCCAGTCCCA
4239	KAHSTQT	18562	AAGGCTCATTCTACTCAGACT	32885	AAAGCACACAGCACACAAACA
4240	KAISQPF	18563	AAGGCGATTTCTCAGCCTTTT	32886	AAAGCAATCAGCCAACCATTC
4241	KALPNYS	18564	AAGGCTCTTCCTAATTATAGT	32887	AAAGCACTCCCAAACTACAGC
4242	KALQRYD	18565	AAGGCTTTGCAGAGGTATGAT	32888	AAAGCACTCCAAAGATACGAC
4243	KAMSMDS	18566	AAGGCGATGTCGATGGATTCG	32889	AAAGCAATGAGCATGGACAGC
4244	KANQLDT	18567	AAGGCGAATCAGCTTGATACT	32890	AAAGCAAACCAACTCGACACA
4245	KAPLPDF	18568	AAGGCGCCGCTTCCGGATTTT	32891	AAAGCACCACTCCCAGACTTC
4246	KAPTPSV	18569	AAGGCTCCTACGCCGTCTGTG	32892	AAAGCACCAACACCAAGCGTC
4247	KAQERAT	18570	AAGGCTCAGGAGCGGGCGACT	32893	AAAGCACAAGAAAGAGCAACA
4248	KAQSANF	18571	AAGGCTCAGTCGGCTAATTTT	32894	AAAGCACAAAGCGCAAACTTC
4249	KASASIA	18572	AAGGCGAGTGCGAGTATTGCG	32895	AAAGCAAGCGCAAGCATCGCA
4250	KASFSPD	18573	AAGGCGAGTTTTTCGCCTGAT	32896	AAAGCAAGCTTCAGCCCAGAC
4251	KASQACM	18574	AAGGCGTCTCAGGCTTGTATG	32897	AAAGCAAGCCAAGCATGCATG
4252	KASQFSP	18575	AAGGCGTCGCAGTTTTCTCCG	32898	AAAGCAAGCCAATTCAGCCCA
4253	KASQSGT	18576	AAGGCGTCGCAGTCTGGTACG	32899	AAAGCAAGCCAAAGCGGAACA
4254	KATPGVH	18577	AAGGCTACTCCTGGGGTTCAT	32900	AAAGCAACACCAGGAGTCCAC
4255	KATPNVG	18578	AAGGCTACTCCGAATGTTGGT	32901	AAAGCAACACCAAACGTCGGA
4256	KAVASTF	18579	AAGGCTGTGGCGTCTACTTTT	32902	AAAGCAGTCGCAAGCACATTC
4257	KAVISPT	18580	AAGGCGGTTATTTCTCCTACT	32903	AAAGCAGTCATCAGCCCAACA
4258	KAVNGLS	18581	AAGGCTGTGAATGGTCTGTCG	32904	AAAGCAGTCAACGGACTCAGC
4259	KAVSWGP	18582	AAGGCTGTGTCTTGGGGGCCT	32905	AAAGCAGTCAGCTGGGGACCA
4260	KCRTCSV	18583	AAGTGTCGGACGTGTAGTGTT	32906	AAATGCAGAACATGCAGCGTC
4261	KDEPNYG	18584	AAGGATGAGCCTAATTATGGG	32907	AAAGACGAACCAAACTACGGA
4262	KDFSNTL	18585	AAGGATTTTTCGAATACTTTG	32908	AAAGACTTCAGCAACACACTC
4263	KDGPFPM	18586	AAGGATGGGCCTTTTCCTATG	32909	AAAGACGGACCATTCCCAATG
4264	KDKNPSD	18587	AAGGATAAGAATCCTTCGGAT	32910	AAAGACAAAAACCCAAGCGAC

4265	KDKVEMN	18588	AAGGATAAGGTTGAGATGAAT	32911	AAAGACAAAGTCGAAATGAAC
4266	KDLTRHA	18589	AAGGATTTGACGCGTCATGCG	32912	AAAGACCTCACAAGACACGCA
4267	KDMRSKD	18590	AAGGATATGCGGTCTAAGGAT	32913	AAAGACATGAGAAGCAAAGAC
4268	KDNKIQS	18591	AAGGATAATAAGATTCAGAGT	32914	AAAGACAACAAAATCCAAAGC
4269	KDPGRIS	18592	AAGGATCCTGGTCGTATTTCG	32915	AAAGACCCAGGAAGAATCAGC
4270	KDPISSV	18593	AAGGATCCTATTTCTTCGGTT	32916	AAAGACCCAATCAGCAGCGTC
4271	KDPLNCA	18594	AAGGATCCTCTTAATTGTGCG	32917	AAAGACCCACTCAACTGCGCA
4272	KDPPQLH	18595	AAGGATCCTCCGCAGCTGCAT	32918	AAAGACCCACCACAACTCCAC
4273	KDPQTTD	18596	AAGGATCCTCAGACTACTGAT	32919	AAAGACCCACAAACAACAGAC
4274	KDRSAPP	18597	AAGGATAGGTCGGCTCCTCCT	32920	AAAGACAGAAGCGCACCACCA
4275	KDRSLDP	18598	AAGGATCGGTCGCTGGATCCG	32921	AAAGACAGAAGCCTCGACCCA
4276	KDSAANF	18599	AAGGATTCTGCTGCGAATTTT	32922	AAAGACAGCGCAGCAAACTTC
4277	KDSTLLS	18600	AAGGATTCGACGTTGCTGAGT	32923	AAAGACAGCACACTCCTCAGC
4278	KDTDPLS	18601	AAGGATACGGATCCTTTGTCG	32924	AAAGACACAGACCCACTCAGC
4279	KDTIHVS	18602	AAGGATACGATTCATGTTAGT	32925	AAAGACACAATCCACGTCAGC
4280	KDTLTFR	18603	AAGGATACGCTTACTTTTAGG	32926	AAAGACACACTCACATTCAGA
4281	KDTPNTV	18604	AAGGATACTCCGAATACGGTT	32927	AAAGACACACCAAACACAGTC
4282	KDTVFYP	18605	AAGGATACTGTGTTTTATCCT	32928	AAAGACACAGTCTTCTACCCA
4283	KEDSYHP	18606	AAGGAGGATTCGTATCATCCG	32929	AAAGAAGACAGCTACCACCCA
4284	KEDTNRT	18607	AAGGAGGATACTAATCGGACG	32930	AAAGAAGACACAAACAGAACA
4285	KEGGEPR	18608	AAGGAGGGTGGGGAGCCTCGG	32931	AAAGAAGGAGGAGAACCAAGA
4286	KEGSNRG	18609	AAGGAGGGTTCTAATCGGGGT	32932	AAAGAAGGAAGCAACAGAGGA
4287	KEHGVIF	18610	AAGGAGCATGGTGTTATTTTT	32933	AAAGAACACGGAGTCATCTTC
4288	KEIGFAT	18611	AAGGAGATTGGTTTTGCGACT	32934	AAAGAAATCGGATTCGCAACA
4289	KEKPLNS	18612	AAGGAGAAGCCGTTGAATTCT	32935	AAAGAAAAACCACTCAACAGC
4290	KELAVGL	18613	AAGGAGTTGGCGGTTGGGTTG	32936	AAAGAACTCGCAGTCGGACTC
4291	KELELHP	18614	AAGGAGCTTGAGTTGCATCCT	32937	AAAGAACTCGAACTCCACCCA
4292	KEMDIHW	18615	AAGGAGATGGATATTCATTGG	32938	AAAGAAATGGACATCCACTGG
4293	KEMSPTR	18616	AAGGAGATGTCTCCGACTCGG	32939	AAAGAAATGAGCCCAACAAGA
4294	KENPAIV	18617	AAGGAGAATCCTGCTATTGTT	32940	AAAGAAAACCCAGCAATCGTC
4295	KEPKVWL	18618	AAGGAGCCGAAGGTTTGGCTG	32941	AAAGAACCAAAAGTCTGGCTC
4296	KEPSTTS	18619	AAGGAGCCGTCGACGACGAGT	32942	AAAGAACCAAGCACAACAAGC
4297	KESIRQS	18620	AAGGAGTCTATTCGGCAGAGT	32943	AAAGAAAGCATCAGACAAAGC
4298	KESSSYL	18621	AAGGAGTCTTCTTCTTATCTG	32944	AAAGAAAGCAGCAGCTACCTC
4299	KETQNMP	18622	AAGGAGACGCAGAATATGCCG	32945	AAAGAAACACAAAACATGCCA
4300	KEVKTSG	18623	AAGGAGGTTAAGACTTCTGGT	32946	AAAGAAGTCAAAACAAGCGGA
4301	KEWTNSG	18624	AAGGAGTGGACTAATTCGGGT	32947	AAAGAATGGACAAACAGCGGA
4302	KFAAMLN	18625	AAGTTTGCGGCGATGCTTAAT	32948	AAATTCGCAGCAATGCTCAAC
4303	KFDLASD	18626	AAGTTTGATTTGGCGTCGGAT	32949	AAATTCGACCTCGCAAGCGAC
4304	KFDSELS	18627	AAGTTTGATAGTGAGTTGTCT	32950	AAATTCGACAGCGAACTCAGC
4305	KFGDNVL	18628	AAGTTTGGGGATAATGTGCTT	32951	AAATTCGGAGACAACGTCCTC
4306	KFNSASD	18629	AAGTTTAATTCTGCGTCTGAT	32952	AAATTCAACAGCGCAAGCGAC
4307	KFPEAQG	18630	AAGTTTCCGGAGGCTCAGGGT	32953	AAATTCCCAGAAGCACAAGGA
4308	KFPHPPA	18631	AAGTTTCCTCATCCGCCTGCG	32954	AAATTCCCACACCCACCAGCA
4309	KFQRDQV	18632	AAGTTTCAGCGTGATCAGGTT	32955	AAATTCCAAAGAGACCAAGTC

4310	KFQSVGI	18633	AAGTTTCAGTCGGTGGGGATT	32956	AAATTCCAAAGCGTCGGAATC
4311	KFSQTVP	18634	AAGTTTTCTCAGACGGTGCCG	32957	AAATTCAGCCAAACAGTCCCA
4312	KFSSNID	18635	AAGTTTTCGTCTAATATTGAT	32958	AAATTCAGCAGCAACATCGAC
4313	KGALGVP	18636	AAGGGTGCTTTGGGTGTTCCT	32959	AAAGGAGCACTCGGAGTCCCA
4314	KGDHVTD	18637	AAGGGGGATCATGTTACGGAT	32960	AAAGGAGACCACGTCACAGAC
4315	KGDIISE	18638	AAGGGTGATATTATTTCGGAG	32961	AAAGGAGACATCATCAGCGAA
4316	KGDIQVS	18639	AAGGGTGATATTCAGGTGTCG	32962	AAAGGAGACATCCAAGTCAGC
4317	KGEIPIE	18640	AAGGGGGAGATTCCTATTGAG	32963	AAAGGAGAAATCCCAATCGAA
4318	KGEVQSM	18641	AAGGGTGAGGTGCAGAGTATG	32964	AAAGGAGAAGTCCAAAGCATG
4319	KGEWPRE	18642	AAGGGGGAGTGGCCTCGGGAG	32965	AAAGGAGAATGGCCAAGAGAA
4320	KGFDERS	18643	AAGGGTTTTGATGAGAGGAGT	32966	AAAGGATTCGACGAAAGAAGC
4321	KGGVAQY	18644	AAGGGGGGTGTTGCGCAGTAT	32967	AAAGGAGGAGTCGCACAATAC
4322	KGLGVVP	18645	AAGGGTTTGGGTGTGGTGCCG	32968	AAAGGACTCGGAGTCGTCCCA
4323	KGPSIAW	18646	AAGGGGCCTAGTATTGCTTGG	32969	AAAGGACCAAGCATCGCATGG
4324	KGPSPGL	18647	AAGGGTCCTTCTCCGGGGTTG	32970	AAAGGACCAAGCCCAGGACTC
4325	KGQGQLN	18648	AAGGGTCAGGGGCAGTTGAAT	32971	AAAGGACAAGGACAACTCAAC
4326	KGQSSNS	18649	AAGGGGCAGTCGTCGAATTCG	32972	AAAGGACAAAGCAGCAACAGC
4327	KGRDATS	18650	AAGGGTCGTGATGCGACGTCG	32973	AAAGGAAGAGACGCAACAAGC
4328	KGSGVIV	18651	AAGGGTTCGGGGGTGATTGTG	32974	AAAGGAAGCGGAGTCATCGTC
4329	KGSSSMH	18652	AAGGGTTCGTCTTCTATGCAT	32975	AAAGGAAGCAGCAGCATGCAC
4330	KGTDLLA	18653	AAGGGGACTGATTTGCTTGCT	32976	AAAGGAACAGACCTCCTCGCA
4331	KGTTVSN	18654	AAGGGGACTACTGTGTCGAAT	32977	AAAGGAACAACAGTCAGCAAC
4332	KGTTVVV	18655	AAGGGGACGACGGTTGTTGTT	32978	AAAGGAACAACAGTCGTCGTC
4333	KGTYANT	18656	AAGGGTACTTATGCTAATACG	32979	AAAGGAACATACGCAAACACA
4334	KGTYNAH	18657	AAGGGTACTTATAATGCTCAT	32980	AAAGGAACATACAACGCACAC
4335	KGVIPEK	18658	AAGGGTGTGATTCCTGAGAAG	32981	AAAGGAGTCATCCCAGAAAAA
4336	KGVLTAV	18659	AAGGGGGTTCTGACGGCTGTT	32982	AAAGGAGTCCTCACAGCAGTC
4337	KGVNFLD	18660	AAGGGGGTTAATTTTCTGGAT	32983	AAAGGAGTCAACTTCCTCGAC
4338	KHAQTIP	18661	AAGCATGCTCAGACTATTCCT	32984	AAACACGCACAAACAATCCCA
4339	KHDDSGM	18662	AAGCATGATGATTCTGGGATG	32985	AAACACGACGACAGCGGAATG
4340	KHENWMT	18663	AAGCATGAGAATTGGATGACT	32986	AAACACGAAAACTGGATGACA
4341	KHEPHGS	18664	AAGCATGAGCCTCATGGGTCG	32987	AAACACGAACCACACGGAAGC
4342	KHGVEIL	18665	AAGCATGGGGTTGAGATTCTT	32988	AAACACGGAGTCGAAATCCTC
4343	KHHTVEM	18666	AAGCATCATACTGTGGAGATG	32989	AAACACCACACAGTCGAAATG
4344	KHIPGPD	18667	AAGCATATTCCGGGGCCTGAT	32990	AAACACATCCCAGGACCAGAC
4345	KHIPSDR	18668	AAGCATATTCCTTCGGATAGG	32991	AAACACATCCCAAGCGACAGA
4346	KHPNVPT	18669	AAGCATCCTAATGTTCCGACG	32992	AAACACCCAAACGTCCCAACA
4347	KHPPALT	18670	AAGCATCCTCCTGCGTTGACT	32993	AAACACCCACCAGCACTCACA
4348	KHPPAVL	18671	AAGCATCCTCCTGCTGTTCTT	32994	AAACACCCACCAGCAGTCCTC
4349	KHQSTII	18672	AAGCATCAGAGTACGATTATT	32995	AAACACCAAAGCACAATCATC
4350	KHSAELG	18673	AAGCATTCTGCTGAGCTGGGG	32996	AAACACAGCGCAGAACTCGGA
4351	KHSMATN	18674	AAGCATTCTATGGCGACTAAT	32997	AAACACAGCATGGCAACAAAC
4352	KHSNTPN	18675	AAGCATTCGAATACTCCGAAT	32998	AAACACAGCAACACACCAAAC
4353	KHSYMET	18676	AAGCATTCTTATATGGAGACT	32999	AAACACAGCTACATGGAAACA
4354	KHTALVP	18677	AAGCATACGGCGTTGGTGCCT	33000	AAACACACAGCACTCGTCCCA

4355	KHTASMA	18678	AAGCATACTGCTTCGATGGCG	33001	AAACACACAGCAAGCATGGCA
4356	KHTQNDG	18679	AAGCATACTCAGAATGATGGG	33002	AAACACACACAAAACGACGGA
4357	KHTSFAQ	18680	AAGCATACTAGTTTTGCTCAG	33003	AAACACACAAGCTTCGCACAA
4358	KHTTTMF	18681	AAGCATACGACGACGATGTTT	33004	AAACACACAACAACAATGTTC
4359	KIAPMPH	18682	AAGATTGCTCCTATGCCTCAT	33005	AAAATCGCACCAATGCCACAC
4360	KIARSEG	18683	AAGATTGCTCGTTCTGAGGGG	33006	AAAATCGCAAGAAGCGAAGGA
4361	KIASSLG	18684	AAGATTGCTTCTTCGCTTGGT	33007	AAAATCGCAAGCAGCCTCGGA
4362	KIATTPL	18685	AAGATTGCGACGACGCCGCTG	33008	AAAATCGCAACAACACCACTC
4363	KIHNLNS	18686	AAGATTCATAATTTGAATTCG	33009	AAAATCCACAACCTCAACAGC
4364	KINTALT	18687	AAGATTAATACTGCTCTTACT	33010	AAAATCAACACAGCACTCACA
4365	KIPMQSA	18688	AAGATTCCGATGCAGTCGGCG	33011	AAAATCCCAATGCAAAGCGCA
4366	KITATVT	18689	AAGATTACGGCGACTGTTACG	33012	AAAATCACAGCAACAGTCACA
4367	KKDLSMY	18690	AAGAAGGATCTTTCTATGTAT	33013	AAAAAAGACCTCAGCATGTAC
4368	KKDTGIN	18691	AAGAAGGATACGGGTATTAAT	33014	AAAAAAGACACAGGAATCAAC
4369	KKPEDWR	18692	AAGAAGCCTGAGGATTGGAGG	33015	AAAAAACCAGAAGACTGGAGA
4370	KKQSVEP	18693	AAGAAGCAGAGTGTTGAGCCG	33016	AAAAAACAAAGCGTCGAACCA
4371	KKVSDAL	18694	AAGAAGGTGTCGGATGCTTTG	33017	AAAAAAGTCAGCGACGCACTC
4372	KLAGKSD	18695	AAGCTGGCGGGTAAGAGTGAT	33018	AAACTCGCAGGAAAAAGCGAC
4373	KLAPSVT	18696	AAGTTGGCGCCTAGTGTTACG	33019	AAACTCGCACCAAGCGTCACA
4374	KLASGLP	18697	AAGTTGGCGTCTGGGTTGCCT	33020	AAACTCGCAAGCGGACTCCCA
4375	KLASPSP	18698	AAGCTTGCTAGTCCTTCTCCG	33021	AAACTCGCAAGCCCAAGCCCA
4376	KLASVSV	18699	AAGCTGGCGTCTGTGAGTGTT	33022	AAACTCGCAAGCGTCAGCGTC
4377	KLATTRD	18700	AAGTTGGCGACTACGCGGGAT	33023	AAACTCGCAACAACAAGAGAC
4378	KLDINYP	18701	AAGCTTGATATTAATTATCCG	33024	AAACTCGACATCAACTACCCA
4379	KLENGSW	18702	AAGCTGGAGAATGGTTCGTGG	33025	AAACTCGAAAACGGAAGCTGG
4380	KLGAVSL	18703	AAGTTGGGTGCTGTTTCGCTT	33026	AAACTCGGAGCAGTCAGCCTC
4381	KLGENTD	18704	AAGCTGGGTGAGAATACGGAT	33027	AAACTCGGAGAAAACACAGAC
4382	KLGHLHS	18705	AAGTTGGGGCATCTTCATTCT	33028	AAACTCGGACACCTCCACAGC
4383	KLGTTSS	18706	AAGTTGGGGACTACGTCGTCG	33029	AAACTCGGAACAACAAGCAGC
4384	KLHVNTP	18707	AAGCTTCATGTGAATACGCCG	33030	AAACTCCACGTCAACACACCA
4385	KLLGAVG	18708	AAGTTGCTGGGTGCTGTGGGG	33031	AAACTCCTCGGAGCAGTCGGA
4386	KLLKAPL	18709	AAGCTTCTGAAGGCGCCTCTG	33032	AAACTCCTCAAAGCACCACTC
4387	KLLPEPG	18710	AAGTTGCTTCCGGAGCCGGGG	33033	AAACTCCTCCCAGAACCAGGA
4388	KLLPGQP	18711	AAGCTTCTTCCGGGGCAGCCT	33034	AAACTCCTCCCAGGACAACCA
4389	KLLPNPP	18712	AAGCTGCTGCCGAATCCTCCT	33035	AAACTCCTCCCAAACCCACCA
4390	KLLSIMG	18713	AAGCTTCTTTCGATTATGGGG	33036	AAACTCCTCAGCATCATGGGA
4391	KLLSTGT	18714	AAGCTGTTGTCTACTGGTACG	33037	AAACTCCTCAGCACAGGAACA
4392	KLNSPDD	18715	AAGCTGAATAGTCCGGATGAT	33038	AAACTCAACAGCCCAGACGAC
4393	KLPNVTP	18716	AAGCTTCCTAATGTTACTCCT	33039	AAACTCCCAAACGTCACACCA
4394	KLPSELI	18717	AAGCTTCCTTCGGAGTTGATT	33040	AAACTCCCAAGCGAACTCATC
4395	KLQVPFS	18718	AAGCTTCAGGTTCCTTTTTCT	33041	AAACTCCAAGTCCCATTCAGC
4396	KLRDIYP	18719	AAGTTGCGGGATATTTATCCT	33042	AAACTCAGAGACATCTACCCA
4397	KLSGEIV	18720	AAGCTGTCTGGTGAGATTGTG	33043	AAACTCAGCGGAGAAATCGTC
4398	KLSHQQF	18721	AAGCTTAGTCATCAGCAGTTT	33044	AAACTCAGCCACCAACAATTC
4399	KLSPTLS	18722	AAGCTTAGTCCGACTCTGTCT	33045	AAACTCAGCCCAACACTCAGC

4400	KLSSPAL	18723	AAGCTTAGTTCTCCTGCGCTG	33046	AAACTCAGCAGCCCAGCACTC
4401	KLSSSSW	18724	AAGTTGTCTTCTTCGTCTTGG	33047	AAACTCAGCAGCAGCAGCTGG
4402	KLSTESW	18725	AAGCTTTCGACTGAGTCTTGG	33048	AAACTCAGCACAGAAAGCTGG
4403	KLSYSTL	18726	AAGCTTAGTTATTCGACGCTG	33049	AAACTCAGCTACAGCACACTC
4404	KLTEIVA	18727	AAGCTTACTGAGATTGTTGCG	33050	AAACTCACAGAAATCGTCGCA
4405	KLTGCND	18728	AAGTTGACGGGTTGTAATGAT	33051	AAACTCACAGGATGCAACGAC
4406	KLTMTAP	18729	AAGCTGACGATGACGGCTCCT	33052	AAACTCACAATGACAGCACCA
4407	KLTSPYA	18730	AAGCTTACTTCGCCTTATGCG	33053	AAACTCACAAGCCCATACGCA
4408	KLTSSPT	18731	AAGCTGACGTCTTCTCCTACT	33054	AAACTCACAAGCAGCCCAACA
4409	KLTSSTV	18732	AAGCTTACTTCGAGTACGGTT	33055	AAACTCACAAGCAGCACAGTC
4410	KMAEDKV	18733	AAGATGGCTGAGGATAAGGTT	33056	AAAATGGCAGAAGACAAAGTC
4411	KMDSVLP	18734	AAGATGGATAGTGTGCTTCCG	33057	AAAATGGACAGCGTCCTCCCA
4412	KMEHRML	18735	AAGATGGAGCATCGGATGCTG	33058	AAAATGGAACACAGAATGCTC
4413	KMGTTLG	18736	AAGATGGGGACTACTCTTGGG	33059	AAAATGGGAACAACACTCGGA
4414	KMLSPQV	18737	AAGATGCTTTCTCCGCAGGTG	33060	AAAATGCTCAGCCCACAAGTC
4415	KMNSAAG	18738	AAGATGAATAGTGCTGCGGGT	33061	AAAATGAACAGCGCAGCAGGA
4416	KMPEALR	18739	AAGATGCCTGAGGCGTTGCGG	33062	AAAATGCCAGAAGCACTCAGA
4417	KMPIPVP	18740	AAGATGCCTATTCCGGTGCCG	33063	AAAATGCCAATCCCAGTCCCA
4418	KMSHSLD	18741	AAGATGTCTCATTCTTTGGAT	33064	AAAATGAGCCACAGCCTCGAC
4419	KNAINMI	18742	AAGAATGCGATTAATATGATT	33065	AAAAACGCAATCAACATGATC
4420	KNAKTIP	18743	AAGAATGCGAAGACTATTCCT	33066	AAAAACGCAAAAACAATCCCA
4421	KNALPTS	18744	AAGAATGCTCTGCCGACGAGT	33067	AAAAACGCACTCCCAACAAGC
4422	KNAVSGS	18745	AAGAATGCGGTGTCTGGTTCT	33068	AAAAACGCAGTCAGCGGAAGC
4423	KNAVTSV	18746	AAGAATGCTGTGACTAGTGTT	33069	AAAAACGCAGTCACAAGCGTC
4424	KNERLPM	18747	AAGAATGAGCGTCTGCCGATG	33070	AAAAACGAAAGACTCCCAATG
4425	KNETSSP	18748	AAGAATGAGACTTCGTCTCCT	33071	AAAAACGAAACAAGCAGCCCA
4426	KNGDIHC	18749	AAGAATGGGGATATTCATTGT	33072	AAAAACGGAGACATCCACTGC
4427	KNGITPN	18750	AAGAATGGTATTACTCCTAAT	33073	AAAAACGGAATCACACCAAAC
4428	KNGLSPA	18751	AAGAATGGTCTGAGTCCTGCG	33074	AAAAACGGACTCAGCCCAGCA
4429	KNGTAQS	18752	AAGAATGGTACGGCTCAGTCT	33075	AAAAACGGAACAGCACAAAGC
4430	KNHQYAA	18753	AAGAATCATCAGTATGCGGCG	33076	AAAAACCACCAATACGCAGCA
4431	KNLPLVS	18754	AAGAATCTGCCGTTGGTTTCG	33077	AAAAACCTCCCACTCGTCAGC
4432	KNLSLGG	18755	AAGAATCTGTCTTTGGGTGGT	33078	AAAAACCTCAGCCTCGGAGGA
4433	KNPLLSP	18756	AAGAATCCTCTGTTGTCGCCG	33079	AAAAACCCACTCCTCAGCCCA
4434	KNPMTAP	18757	AAGAATCCTATGACTGCGCCG	33080	AAAAACCCAATGACAGCACCA
4435	KNPQEPT	18758	AAGAATCCTCAGGAGCCGACT	33081	AAAAACCCACAAGAACCAACA
4436	KNPRDLG	18759	AAGAATCCTAGGGATTTGGGG	33082	AAAAACCCAAGAGACCTCGGA
4437	KNQPLGY	18760	AAGAATCAGCCTCTGGGTTAT	33083	AAAAACCAACCACTCGGATAC
4438	KNSTSQL	18761	AAGAATTCTACGAGTCAGCTG	33084	AAAAACAGCACAAGCCAACTC
4439	KNVMSGA	18762	AAGAATGTTATGTCTGGTGCT	33085	AAAAACGTCATGAGCGGAGCA
4440	KNYSAAV	18763	AAGAATTATAGTGCGGCTGTT	33086	AAAAACTACAGCGCAGCAGTC
4441	KPAGTDS	18764	AAGCCTGCTGGTACGGATAGT	33087	AAACCAGCAGGAACAGACAGC
4442	KPASNYD	18765	AAGCCTGCGTCTAATTATGAT	33088	AAACCAGCAAGCAACTACGAC
4443	KPATSPG	18766	AAGCCTGCTACGAGTCCGGGT	33089	AAACCAGCAACAAGCCCAGGA
4444	KPAVPVY	18767	AAGCCGGCTGTGCCTGTTTAT	33090	AAACCAGCAGTCCCAGTCTAC

4445	KPDRPPD	18768	AAGCCTGATCGGCCTCCTGAT	33091	AAACCAGACAGACCACCAGAC
4446	KPENSHS	18769	AAGCCGGAGAATAGTCATAGT	33092	AAACCAGAAAACAGCCACAGC
4447	KPFETGR	18770	AAGCCGTTTGAGACTGGGCGT	33093	AAACCATTCGAAACAGGAAGA
4448	KPHPPSF	18771	AAGCCTCATCCGCCGTCTTTT	33094	AAACCACACCCACCAAGCTTC
4449	KPILQSS	18772	AAGCCGATTCTGCAGAGTTCG	33095	AAACCAATCCTCCAAAGCAGC
4450	KPLAQLS	18773	AAGCCGTTGGCGCAGCTTTCT	33096	AAACCACTCGCACAACTCAGC
4451	KPLDHLT	18774	AAGCCGTTGGATCATCTTACG	33097	AAACCACTCGACCACCTCACA
4452	KPLEVEG	18775	AAGCCTTTGGAGGTTGAGGGG	33098	AAACCACTCGAAGTCGAAGGA
4453	KPLQVDP	18776	AAGCCTTTGCAGGTGGATCCT	33099	AAACCACTCCAAGTCGACCCA
4454	KPMAHLE	18777	AAGCCGATGGCGCATCTTGAG	33100	AAACCAATGGCACACCTCGAA
4455	KPMDPTL	18778	AAGCCGATGGATCCTACTCTT	33101	AAACCAATGGACCCAACACTC
4456	KPMSITP	18779	AAGCCGATGTCGATTACTCCT	33102	AAACCAATGAGCATCACACCA
4457	KPNAVSM	18780	AAGCCTAATGCGGTGAGTATG	33103	AAACCAAACGCAGTCAGCATG
4458	KPPILTS	18781	AAGCCGCCTATTCTTACTAGT	33104	AAACCACCAATCCTCACAAGC
4459	KPPLAQD	18782	AAGCCGCCGTTGGCGCAGGAT	33105	AAACCACCACTCGCACAAGAC
4460	KPPREAD	18783	AAGCCTCCGCGGGAGGCTGAT	33106	AAACCACCAAGAGAAGCAGAC
4461	KPRAPSD	18784	AAGCCTAGGGCGCCTTCTGAT	33107	AAACCAAGAGCACCAAGCGAC
4462	KPSGHSS	18785	AAGCCTTCGGGTCATTCGTCT	33108	AAACCAAGCGGACACAGCAGC
4463	KPSGPPT	18786	AAGCCGTCTGGGCCGCCGACT	33109	AAACCAAGCGGACCACCAACA
4464	KPSVPTV	18787	AAGCCGAGTGTGCCGACTGTT	33110	AAACCAAGCGTCCCAACAGTC
4465	KPTGMHL	18788	AAGCCGACGGGTATGCATCTT	33111	AAACCAACAGGAATGCACCTC
4466	KPTPTLM	18789	AAGCCGACTCCGACGCTGATG	33112	AAACCAACACCAACACTCATG
4467	KPTVIPA	18790	AAGCCGACGGTGATTCCGGCT	33113	AAACCAACAGTCATCCCAGCA
4468	KPVGEFT	18791	AAGCCTGTTGGTGAGTTTACG	33114	AAACCAGTCGGAGAATTCACA
4469	KPVPQPD	18792	AAGCCGGTTCCTCAGCCTGAT	33115	AAACCAGTCCCACAACCAGAC
4470	KPVTLDN	18793	AAGCCTGTGACGCTTGATAAT	33116	AAACCAGTCACACTCGACAAC
4471	KPVTPHS	18794	AAGCCTGTGACGCCTCATTCG	33117	AAACCAGTCACACCACACAGC
4472	KPYLPEN	18795	AAGCCTTATTTGCCGGAGAAT	33118	AAACCATACCTCCCAGAAAAC
4473	KQADIPR	18796	AAGCAGGCGGATATTCCGCGT	33119	AAACAAGCAGACATCCCAAGA
4474	KQALTMT	18797	AAGCAGGCGCTGACGATGACT	33120	AAACAAGCACTCACAATGACA
4475	KQDRDRL	18798	AAGCAGGATAGGGATCGTCTT	33121	AAACAAGACAGAGACAGACTC
4476	KQGLTPS	18799	AAGCAGGGTCTGACGCCGTCT	33122	AAACAAGGACTCACACCAAGC
4477	KQGVWPN	18800	AAGCAGGGTGTTTGGCCGAAT	33123	AAACAAGGAGTCTGGCCAAAC
4478	KQIQPKN	18801	AAGCAGATTCAGCCTAAGAAT	33124	AAACAAATCCAACCAAAAAAC
4479	KQKHQFE	18802	AAGCAGAAGCATCAGTTTGAG	33125	AAACAAAAACACCAATTCGAA
4480	KQLPINV	18803	AAGCAGCTGCCGATTAATGTG	33126	AAACAACTCCCAATCAACGTC
4481	KQMLDPT	18804	AAGCAGATGCTTGATCCGACG	33127	AAACAAATGCTCGACCCAACA
4482	KQMNDLA	18805	AAGCAGATGAATGATCTGGCT	33128	AAACAAATGAACGACCTCGCA
4483	KQNVINT	18806	AAGCAGAATGTTATTAATACT	33129	AAACAAAACGTCATCAACACA
4484	KQPPQPP	18807	AAGCAGCCGCCGCAGCCGCCT	33130	AAACAACCACCACAACCACCA
4485	KQREQPM	18808	AAGCAGAGGGAGCAGCCTATG	33131	AAACAAAGAGAACAACCAATG
4486	KQSSHTT	18809	AAGCAGAGTTCTCATACTACG	33132	AAACAAAGCAGCCACACAACA
4487	KQSSTSI	18810	AAGCAGTCTTCGACGTCGATT	33133	AAACAAAGCAGCACAAGCATC
4488	KQTSVTG	18811	AAGCAGACTAGTGTTACTGGT	33134	AAACAAACAAGCGTCACAGGA
4489	KQTTPVL	18812	AAGCAGACGACTCCTGTGTTG	33135	AAACAAACAACACCAGTCCTC

4490	KQVGSMP	18813	AAGCAGGTGGGTTCTATGCCT	33136	AAACAAGTCGGAAGCATGCCA
4491	KQVSSER	18814	AAGCAGGTTTCTTCGGAGAGG	33137	AAACAAGTCAGCAGCGAAAGA
4492	KQVVSVT	18815	AAGCAGGTTGTTTCGGTGACT	33138	AAACAAGTCGTCAGCGTCACA
4493	KQYSSSV	18816	AAGCAGTATTCGTCTAGTGTT	33139	AAACAATACAGCAGCAGCGTC
4494	KRANAIP	18817	AAGAGGGCTAATGCTATTCCT	33140	AAAAGAGCAAACGCAATCCCA
4495	KRAVAAE	18818	AAGAGGGCGGTGGCTGCGGAG	33141	AAAAGAGCAGTCGCAGCAGAA
4496	KRDAAMP	18819	AAGAGGGATGCTGCTATGCCT	33142	AAAAGAGACGCAGCAATGCCA
4497	KRDDMNV	18820	AAGCGTGATGATATGAATGTG	33143	AAAAGAGACGACATGAACGTC
4498	KRDMGAG	18821	AAGAGGGATATGGGTGCTGGT	33144	AAAAGAGACATGGGAGCAGGA
4499	KRDSTSP	18822	AAGCGGGATTCGACTTCTCCT	33145	AAAAGAGACAGCACAAGCCCA
4500	KREFENI	18823	AAGCGGGAGTTTGAGAATATT	33146	AAAAGAGAATTCGAAAACATC
4501	KRESMPI	18824	AAGAGGGAGTCGATGCCTATT	33147	AAAAGAGAAAGCATGCCAATC
4502	KREVLPT	18825	AAGCGTGAGGTTCTTCCTACG	33148	AAAAGAGAAGTCCTCCCAACA
4503	KRFSGVE	18826	AAGCGTTTTTCGGGTGTGGAG	33149	AAAAGATTCAGCGGAGTCGAA
4504	KRHESMS	18827	AAGCGTCATGAGTCTATGTCT	33150	AAAAGACACGAAAGCATGAGC
4505	KRNSLNE	18828	AAGAGGAATAGTCTGAATGAG	33151	AAAAGAAACAGCCTCAACGAA
4506	KRPAEHD	18829	AAGAGGCCGGCGGAGCATGAT	33152	AAAAGACCAGCAGAACACGAC
4507	KRQHPEI	18830	AAGAGGCAGCATCCTGAGATT	33153	AAAAGACAACACCCAGAAATC
4508	KRSLDSP	18831	AAGAGGTCTCTGGATAGTCCG	33154	AAAAGAAGCCTCGACAGCCCA
4509	KRSLTET	18832	AAGCGTTCTCTGACTGAGACG	33155	AAAAGAAGCCTCACAGAAACA
4510	KRTDGLG	18833	AAGAGGACGGATGGGTTGGGT	33156	AAAAGAACAGACGGACTCGGA
4511	KRTSEGV	18834	AAGCGTACGAGTGAGGGGGTG	33157	AAAAGAACAAGCGAAGGAGTC
4512	KSAAIAY	18835	AAGAGTGCGGCGATTGCTTAT	33158	AAAAGCGCAGCAATCGCATAC
4513	KSAEETS	18836	AAGTCTGCTGAGGAGACGTCG	33159	AAAAGCGCAGAAGAAACAAGC
4514	KSALMGP	18837	AAGTCTGCTCTTATGGGTCCG	33160	AAAAGCGCACTCATGGGACCA
4515	KSASLSM	18838	AAGTCTGCGTCTCTTTCTATG	33161	AAAAGCGCAAGCCTCAGCATG
4516	KSASWSE	18839	AAGAGTGCTAGTTGGAGTGAG	33162	AAAAGCGCAAGCTGGAGCGAA
4517	KSDMPFN	18840	AAGTCGGATATGCCTTTTAAT	33163	AAAAGCGACATGCCATTCAAC
4518	KSDPEWP	18841	AAGAGTGATCCGGAGTGGCCG	33164	AAAAGCGACCCAGAATGGCCA
4519	KSDVMFQ	18842	AAGTCTGATGTGATGTTTCAG	33165	AAAAGCGACGTCATGTTCCAA
4520	KSERYAV	18843	AAGTCTGAGCGTTATGCTGTG	33166	AAAAGCGAAAGATACGCAGTC
4521	KSFPVVQ	18844	AAGTCGTTTCCGGTTGTTCAG	33167	AAAAGCTTCCCAGTCGTCCAA
4522	KSFQSTP	18845	AAGAGTTTTCAGTCTACTCCT	33168	AAAAGCTTCCAAAGCACACCA
4523	KSGPVTL	18846	AAGTCTGGTCCTGTTACTCTT	33169	AAAAGCGGACCAGTCACACTC
4524	KSGTAFS	18847	AAGAGTGGTACGGCGTTTTCG	33170	AAAAGCGGAACAGCATTCAGC
4525	KSGVQSP	18848	AAGAGTGGTGTTCAGTCGCCG	33171	AAAAGCGGAGTCCAAAGCCCA
4526	KSIATSG	18849	AAGTCGATTGCTACTAGTGGT	33172	AAAAGCATCGCAACAAGCGGA
4527	KSIEFFA	18850	AAGTCTATTGAGTTTTTTGCG	33173	AAAAGCATCGAATTCTTCGCA
4528	KSIREDP	18851	AAGAGTATTCGTGAGGATCCT	33174	AAAAGCATCAGAGAAGACCCA
4529	KSKDVRY	18852	AAGTCGAAGGATGTGAGGTAT	33175	AAAAGCAAAGACGTCAGATAC
4530	KSMDTTG	18853	AAGTCGATGGATACTACGGGT	33176	AAAAGCATGGACACAACAGGA
4531	KSNACLH	18854	AAGTCGAATGCTTGTTTGCAT	33177	AAAAGCAACGCATGCCTCCAC
4532	KSNDRTD	18855	AAGAGTAATGATCGTACGGAT	33178	AAAAGCAACGACAGAACAGAC
4533	KSNTPAA	18856	AAGTCTAATACTCCTGCGGCG	33179	AAAAGCAACACACCAGCAGCA
4534	KSNTTAD	18857	AAGTCGAATACGACTGCTGAT	33180	AAAAGCAACACAACAGCAGAC

4535	KSPAEIA	18858	AAGAGTCCTGCTGAGATTGCG	33181	AAAAGCCCAGCAGAAATCGCA
4536	KSPDGMV	18859	AAGAGTCCGGATGGTATGGTG	33182	AAAAGCCCAGACGGAATGGTC
4537	KSPDRYH	18860	AAGTCGCCTGATAGGTATCAT	33183	AAAAGCCCAGACAGATACCAC
4538	KSPGVMV	18861	AAGTCTCCGGGTGTGATGGTG	33184	AAAAGCCCAGGAGTCATGGTC
4539	KSPRTPE	18862	AAGTCGCCGCGGACTCCGGAG	33185	AAAAGCCCAAGAACACCAGAA
4540	KSPSHAA	18863	AAGTCTCCTTCGCATGCGGCG	33186	AAAAGCCCAAGCCACGCAGCA
4541	KSPSTFH	18864	AAGTCTCCGTCTACTTTTCAT	33187	AAAAGCCCAAGCACATTCCAC
4542	KSPTLAS	18865	AAGTCTCCTACTCTGGCGTCT	33188	AAAAGCCCAACACTCGCAAGC
4543	KSPVRDT	18866	AAGTCGCCTGTTCGTGATACG	33189	AAAAGCCCAGTCAGAGACACA
4544	KSPVSGN	18867	AAGTCTCCTGTTAGTGGTAAT	33190	AAAAGCCCAGTCAGCGGAAAC
4545	KSPVSSY	18868	AAGTCTCCTGTTTCGTCGTAT	33191	AAAAGCCCAGTCAGCAGCTAC
4546	KSQAEFG	18869	AAGTCTCAGGCTGAGTTTGGG	33192	AAAAGCCAAGCAGAATTCGGA
4547	KSQALTD	18870	AAGTCGCAGGCTCTGACTGAT	33193	AAAAGCCAAGCACTCACAGAC
4548	KSQGSHY	18871	AAGAGTCAGGGGAGTCATTAT	33194	AAAAGCCAAGGAAGCCACTAC
4549	KSQHYPS	18872	AAGAGTCAGCATTATCCGTCT	33195	AAAAGCCAACACTACCCAAGC
4550	KSQSDKV	18873	AAGTCGCAGTCGGATAAGGTT	33196	AAAAGCCAAAGCGACAAAGTC
4551	KSQSGNM	18874	AAGAGTCAGTCGGGTAATATG	33197	AAAAGCCAAAGCGGAAACATG
4552	KSRDNLN	18875	AAGTCTCGGGATAATTTGAAT	33198	AAAAGCAGAGACAACCTCAAC
4553	KSRNLEP	18876	AAGTCTCGGAATCTTGAGCCT	33199	AAAAGCAGAAACCTCGAACCA
4554	KSRTGTE	18877	AAGAGTCGGACTGGGACGGAG	33200	AAAAGCAGAACAGGAACAGAA
4555	KSSAHAW	18878	AAGTCTTCTGCGCATGCTTGG	33201	AAAAGCAGCGCACACGCATGG
4556	KSSDMVV	18879	AAGTCGTCGGATATGGTTGTG	33202	AAAAGCAGCGACATGGTCGTC
4557	KSSHPPV	18880	AAGTCGAGTCATCCTCCTGTT	33203	AAAAGCAGCCACCCACCAGTC
4558	KSSPLTS	18881	AAGAGTAGTCCGTTGACTTCG	33204	AAAAGCAGCCCACTCACAAGC
4559	KSSQQSI	18882	AAGTCGAGTCAGCAGTCTATT	33205	AAAAGCAGCCAACAAAGCATC
4560	KSSSGDK	18883	AAGTCTTCGTCGGGTGATAAG	33206	AAAAGCAGCAGCGGAGACAAA
4561	KSSSGLE	18884	AAGTCTAGTTCTGGTTTGGAG	33207	AAAAGCAGCAGCGGACTCGAA
4562	KSSTAGV	18885	AAGAGTTCGACGGCGGGTGTT	33208	AAAAGCAGCACAGCAGGAGTC
4563	KSSTSGN	18886	AAGTCTTCGACGTCGGGTAAT	33209	AAAAGCAGCACAAGCGGAAAC
4564	KSSYYPA	18887	AAGTCGTCTTATTATCCTGCG	33210	AAAAGCAGCTACTACCCAGCA
4565	KSTHDVP	18888	AAGTCGACGCATGATGTGCCT	33211	AAAAGCACACACGACGTCCCA
4566	KSTPREG	18889	AAGAGTACGCCGCGGGAGGGT	33212	AAAAGCACACCAAGAGAAGGA
4567	KSTSGMP	18890	AAGAGTACTTCGGGGATGCCT	33213	AAAAGCACAAGCGGAATGCCA
4568	KSTVPDL	18891	AAGAGTACTGTTCCTGATCTT	33214	AAAAGCACAGTCCCAGACCTC
4569	KSTVTHF	18892	AAGTCTACTGTGACTCATTTT	33215	AAAAGCACAGTCACACACTTC
4570	KSVAISV	18893	AAGTCTGTGGCGATTTCGGTT	33216	AAAAGCGTCGCAATCAGCGTC
4571	KSVGLSS	18894	AAGTCTGTTGGTCTGTCTAGT	33217	AAAAGCGTCGGACTCAGCAGC
4572	KSVLVES	18895	AAGAGTGTGCTGGTGGAGAGT	33218	AAAAGCGTCCTCGTCGAAAGC
4573	KSYNSPY	18896	AAGTCGTATAATTCTCCTTAT	33219	AAAAGCTACAACAGCCCATAC
4574	KSYPNDH	18897	AAGTCTTATCCGAATGATCAT	33220	AAAAGCTACCCAAACGACCAC
4575	KSYPPAL	18898	AAGAGTTATCCTCCGGCGCTT	33221	AAAAGCTACCCACCAGCACTC
4576	KTADAPR	18899	AAGACGGCGGATGCGCCTCGT	33222	AAAACAGCAGACGCACCAAGA
4577	KTASLGP	18900	AAGACGGCGTCGTTGGGTCCG	33223	AAAACAGCAAGCCTCGGACCA
4578	KTASMPT	18901	AAGACTGCGTCTATGCCTACG	33224	AAAACAGCAAGCATGCCAACA
4579	KTDRTLQ	18902	AAGACGGATCGTACTCTTCAG	33225	AAAACAGACAGAACACTCCAA

4580	KTDSRVP	18903	AAGACGGATAGTAGGGTGCCG	33226	AAAACAGACAGCAGAGTCCCA
4581	KTEFRNP	18904	AAGACGGAGTTTCGGAATCCG	33227	AAAACAGAATTCAGAAACCCA
4582	KTEGSGW	18905	AAGACGGAGGGTTCTGGGTGG	33228	AAAACAGAAGGAAGCGGATGG
4583	KTERTLI	18906	AAGACTGAGAGGACGCTTATT	33229	AAAACAGAAAGAACACTCATC
4584	KTFTEKT	18907	AAGACGTTTACTGAGAAGACG	33230	AAAACATTCACAGAAAAAACA
4585	KTGPPPV	18908	AAGACGGGGCCGCCTCCGGTT	33231	AAAACAGGACCACCACCAGTC
4586	KTGVSSD	18909	AAGACTGGTGTTTCTTCGGAT	33232	AAAACAGGAGTCAGCAGCGAC
4587	KTHGLCL	18910	AAGACGCATGGGCTTTGTCTT	33233	AAAACACACGGACTCTGCCTC
4588	KTIITDL	18911	AAGACGATTATTACTGATTTG	33234	AAAACAATCATCACAGACCTC
4589	KTLPLPE	18912	AAGACGCTTCCTCTTCCTGAG	33235	AAAACACTCCCACTCCCAGAA
4590	KTMTTVP	18913	AAGACGATGACGACGGTTCCT	33236	AAAACAATGACAACAGTCCCA
4591	KTMVPVV	18914	AAGACGATGGTGCCTGTTGTT	33237	AAAACAATGGTCCCAGTCGTC
4592	KTNGHNY	18915	AAGACTAATGGTCATAATTAT	33238	AAAACAAACGGACACAACTAC
4593	KTNPLAQ	18916	AAGACTAATCCTCTGGCGCAG	33239	AAAACAAACCCACTCGCACAA
4594	KTNSEII	18917	AAGACGAATTCTGAGATTATT	33240	AAAACAAACAGCGAAATCATC
4595	KTPDPKK	18918	AAGACTCCTGATCCGAAGAAG	33241	AAAACACCAGACCCAAAAAAA
4596	KTPMVEL	18919	AAGACGCCTATGGTTGAGCTG	33242	AAAACACCAATGGTCGAACTC
4597	KTQLMTS	18920	AAGACTCAGCTGATGACTTCG	33243	AAAACACAACTCATGACAAGC
4598	KTQPGSV	18921	AAGACTCAGCCTGGGTCGGTG	33244	AAAACACAACCAGGAAGCGTC
4599	KTQSILS	18922	AAGACGCAGAGTATTCTTTCG	33245	AAAACACAAAGCATCCTCAGC
4600	KTSEVRW	18923	AAGACGTCTGAGGTGAGGTGG	33246	AAAACAAGCGAAGTCAGATGG
4601	KTSQSHT	18924	AAGACTTCGCAGAGTCATACG	33247	AAAACAAGCCAAAGCCACACA
4602	KTSVTRD	18925	AAGACTTCTGTTACGCGTGAT	33248	AAAACAAGCGTCACAAGAGAC
4603	KTTAPHI	18926	AAGACTACTGCTCCGCATATT	33249	AAAACAACAGCACCACACATC
4604	KTTDRIP	18927	AAGACGACGGATAGGATTCCG	33250	AAAACAACAGACAGAATCCCA
4605	KTTLMTS	18928	AAGACGACTCTTATGACTTCT	33251	AAAACAACACTCATGACAAGC
4606	KTTPVLV	18929	AAGACGACGCCGGTTTTGGTG	33252	AAAACAACACCAGTCCTCGTC
4607	KTTQNSN	18930	AAGACTACGCAGAATTCTAAT	33253	AAAACAACACAAAACAGCAAC
4608	KTTSKPP	18931	AAGACTACGTCTAAGCCTCCT	33254	AAAACAACAAGCAAACCACCA
4609	KTVAMER	18932	AAGACTGTGGCTATGGAGAGG	33255	AAAACAGTCGCAATGGAAAGA
4610	KTVRETS	18933	AAGACGGTTCGGGAGACTAGT	33256	AAAACAGTCAGAGAAACAAGC
4611	KTVTNVL	18934	AAGACTGTGACGAATGTTCTG	33257	AAAACAGTCACAAACGTCCTC
4612	KTVVANP	18935	AAGACTGTGGTGGCTAATCCG	33258	AAAACAGTCGTCGCAAACCCA
4613	KTYGTHA	18936	AAGACTTATGGGACGCATGCT	33259	AAAACATACGGAACACACGCA
4614	KVALATL	18937	AAGGTTGCTCTTGCGACGCTT	33260	AAAGTCGCACTCGCAACACTC
4615	KVAMPVL	18938	AAGGTTGCGATGCCGGTTCTT	33261	AAAGTCGCAATGCCAGTCCTC
4616	KVATSTI	18939	AAGGTTGCTACTTCTACGATT	33262	AAAGTCGCAACAAGCACAATC
4617	KVDSREP	18940	AAGGTGGATTCTCGGGAGCCG	33263	AAAGTCGACAGCAGAGAACCA
4618	KVDVLYN	18941	AAGGTTGATGTTTTGTATAAT	33264	AAAGTCGACGTCCTCTACAAC
4619	KVESMDS	18942	AAGGTGGAGTCGATGGATAGT	33265	AAAGTCGAAAGCATGGACAGC
4620	KVGAGNT	18943	AAGGTTGGGGCGGGTAATACT	33266	AAAGTCGGAGCAGGAAACACA
4621	KVGNNAY	18944	AAGGTGGGTAATAATGCGTAT	33267	AAAGTCGGAAACAACGCATAC
4622	KVGSVYT	18945	AAGGTTGGGTCGGTTTATACT	33268	AAAGTCGGAAGCGTCTACACA
4623	KVLQPHP	18946	AAGGTGCTTCAGCCGCATCCT	33269	AAAGTCCTCCAACCACACCCA
4624	KVNITAF	18947	AAGGTTAATATTACTGCGTTT	33270	AAAGTCAACATCACAGCATTC

4625	KVNLFAG	18948	AAGGTGAATTTGTTTGCTGGG	33271	AAAGTCAACCTCTTCGCAGGA
4626	KVNSVAF	18949	AAGGTGAATTCTGTGGCGTTT	33272	AAAGTCAACAGCGTCGCATTC
4627	KVQERSQ	18950	AAGGTTCAGGAGCGTAGTCAG	33273	AAAGTCCAAGAAAGAAGCCAA
4628	KVSAALS	18951	AAGGTGTCTGCTGCGCTGTCT	33274	AAAGTCAGCGCAGCACTCAGC
4629	KVSGLSM	18952	AAGGTGTCGGGTTTGTCTATG	33275	AAAGTCAGCGGACTCAGCATG
4630	KVSRISD	18953	AAGGTGTCGAGGATTAGTGAT	33276	AAAGTCAGCAGAATCAGCGAC
4631	KVSSTVE	18954	AAGGTTTCTTCTACGGTTGAG	33277	AAAGTCAGCAGCACAGTCGAA
4632	KVTAPNA	18955	AAGGTTACTGCGCCTAATGCT	33278	AAAGTCACAGCACCAAACGCA
4633	KVTGMPV	18956	AAGGTGACTGGGATGCCGGTT	33279	AAAGTCACAGGAATGCCAGTC
4634	KVTGYSE	18957	AAGGTTACTGGGTATTCTGAG	33280	AAAGTCACAGGATACAGCGAA
4635	KVTTPLP	18958	AAGGTTACGACGCCGCTTCCT	33281	AAAGTCACAACACCACTCCCA
4636	KVVAPAL	18959	AAGGTTGTGGCGCCGGCTTTG	33282	AAAGTCGTCGCACCAGCACTC
4637	KVVLREG	18960	AAGGTGGTGTTGCGTGAGGGT	33283	AAAGTCGTCCTCAGAGAAGGA
4638	KVVTAPE	18961	AAGGTGGTTACGGCGCCGGAG	33284	AAAGTCGTCACAGCACCAGAA
4639	KWTDGPA	18962	AAGTGGACTGATGGTCCGGCT	33285	AAATGGACAGACGGACCAGCA
4640	KWVPESP	18963	AAGTGGGTTCCGGAGTCTCCT	33286	AAATGGGTCCCAGAAAGCCCA
4641	KYAHSPT	18964	AAGTATGCTCATAGTCCTACT	33287	AAATACGCACACAGCCCAACA
4642	KYATNAA	18965	AAGTATGCGACGAATGCGGCG	33288	AAATACGCAACAAACGCAGCA
4643	KYDGGQH	18966	AAGTATGATGGGGGGCAGCAT	33289	AAATACGACGGAGGACAACAC
4644	KYGSTVV	18967	AAGTATGGTTCGACGGTGGTG	33290	AAATACGGAAGCACAGTCGTC
4645	KYKDLPA	18968	AAGTATAAGGATTTGCCTGCG	33291	AAATACAAAGACCTCCCAGCA
4646	KYPALSA	18969	AAGTATCCGGCTTTGTCTGCT	33292	AAATACCCAGCACTCAGCGCA
4647	KYRENNV	18970	AAGTATCGTGAGAATAATGTT	33293	AAATACAGAGAAAACAACGTC
4648	KYSKPDT	18971	AAGTATAGTAAGCCGGATACG	33294	AAATACAGCAAACCAGACACA
4649	KYTGRQE	18972	AAGTATACTGGGCGTCAGGAG	33295	AAATACACAGGAAGACAAGAA
4650	KYTLTPN	18973	AAGTATACTCTGACGCCTAAT	33296	AAATACACACTCACACCAAAC
4651	KYVCGPN	18974	AAGTATGTTTGTGGTCCTAAT	33297	AAATACGTCTGCGGACCAAAC
4652	KYVGGPN	18975	AAGTATGTTGGTGGTCCTAAT	33298	AAATACGTCGGAGGACCAAAC
4653	KYVNGVD	18976	AAGTATGTGAATGGTGTTGAT	33299	AAATACGTCAACGGAGTCGAC
4654	KYVTTSP	18977	AAGTATGTTACTACTTCTCCG	33300	AAATACGTCACAACAAGCCCA
4655	LAADVRF	18978	TTGGCTGCTGATGTTCGTTTT	33301	CTCGCAGCAGACGTCAGATTC
4656	LAAGCPV	18979	TTGGCGGCGGGTTGTCCTGTT	33302	CTCGCAGCAGGATGCCCAGTC
4657	LAAGIRF	18980	CTGGCTGCGGGGATTCGTTTT	33303	CTCGCAGCAGGAATCAGATTC
4658	LAAKPLI	18981	CTGGCGGCGAAGCCTCTTATT	33304	CTCGCAGCAAAACCACTCATC
4659	LAANGAH	18982	CTTGCGGCGAATGGGGCTCAT	33305	CTCGCAGCAAACGGAGCACAC
4660	LAAPTSS	18983	CTGGCTGCTCCGACTTCGTCT	33306	CTCGCAGCACCAACAAGCAGC
4661	LAAQDKE	18984	CTGGCGGCGCAGGATAAGGAG	33307	CTCGCAGCACAAGACAAAGAA
4662	LAARMQP	18985	TTGGCTGCGCGGATGCAGCCT	33308	CTCGCAGCAAGAATGCAACCA
4663	LAARRPD	18986	CTGGCGGCGCGTAGGCCGGAT	33309	CTCGCAGCAAGAAGACCAGAC
4664	LAASSRP	18987	CTTGCTGCGAGTAGTAGGCCT	33310	CTCGCAGCAAGCAGCAGACCA
4665	LADKPAM	18988	CTTGCGGATAAGCCGGCTATG	33311	CTCGCAGACAAACCAGCAATG
4666	LADMLKS	18989	CTGGCGGATATGCTGAAGTCT	33312	CTCGCAGACATGCTCAAAAGC
4667	LADRENT	18990	CTGGCGGATAGGGAGAATACG	33313	CTCGCAGACAGAGAAAACACA
4668	LADRRIE	18991	CTTGCTGATCGGAGGATTGAG	33314	CTCGCAGACAGAAGAATCGAA
4669	LAEAVTS	18992	CTTGCTGAGGCTGTGACTTCG	33315	CTCGCAGAAGCAGTCACAAGC

4670	LAEELGR	18993	CTGGCTGAGGAGTTGGGTCGG	33316	CTCGCAGAAGAACTCGGAAGA
4671	LAENSRT	18994	CTGGCTGAGAATTCGAGGACG	33317	CTCGCAGAAAACAGCAGAACA
4672	LAESRGY	18995	CTTGCTGAGTCGAGGGGTTAT	33318	CTCGCAGAAAGCAGAGGATAC
4673	LAEVIYD	18996	TTGGCTGAGGTTATTTATGAT	33319	CTCGCAGAAGTCATCTACGAC
4674	LAGALQE	18997	TTGGCTGGGGCGCTGCAGGAG	33320	CTCGCAGGAGCACTCCAAGAA
4675	LAGDRQW	18998	CTTGCGGGTGATAGGCAGTGG	33321	CTCGCAGGAGACAGACAATGG
4676	LAGHLMP	18999	CTTGCGGGTCATTTGATGCCG	33322	CTCGCAGGACACCTCATGCCA
4677	LAGKGLL	19000	CTTGCGGGTAAGGGTCTGTTG	33323	CTCGCAGGAAAAGGACTCCTC
4678	LAGKNIA	19001	TTGGCGGGGAAGAATATTGCT	33324	CTCGCAGGAAAAAACATCGCA
4679	LAGLGHL	19002	CTGGCGGGTCTGGGTCATCTT	33325	CTCGCAGGACTCGGACACCTC
4680	LAGLVRN	19003	TTGGCGGGTCTGGTTCGGAAT	33326	CTCGCAGGACTCGTCAGAAAC
4681	LAHGTGL	19004	CTTGCGCATGGTACTGGTCTG	33327	CTCGCACACGGAACAGGACTC
4682	LAHKANS	19005	TTGGCTCATAAGGCTAATTCT	33328	CTCGCACACAAAGCAAACAGC
4683	LAHKGIV	19006	CTGGCTCATAAGGGGATTGTT	33329	CTCGCACACAAAGGAATCGTC
4684	LAHPVQF	19007	TTGGCGCATCCTGTGCAGTTT	33330	CTCGCACACCCAGTCCAATTC
4685	LAHSTSV	19008	CTTGCTCATAGTACTTCTGTG	33331	CTCGCACACAGCACAAGCGTC
4686	LAIDPAD	19009	TTGGCTATTGATCCTGCTGAT	33332	CTCGCAATCGACCCAGCAGAC
4687	LAIGPLR	19010	CTTGCTATTGGTCCTCTTCGG	33333	CTCGCAATCGGACCACTCAGA
4688	LAKFAPD	19011	TTGGCGAAGTTTGCTCCGGAT	33334	CTCGCAAAATTCGCACCAGAC
4689	LAKSLQA	19012	CTGGCGAAGTCGTTGCAGGCG	33335	CTCGCAAAAAGCCTCCAAGCA
4690	LALAGSD	19013	TTGGCGCTTGCGGGTTCTGAT	33336	CTCGCACTCGCAGGAAGCGAC
4691	LALGVLR	19014	CTTGCGCTGGGGGTTCTTCGT	33337	CTCGCACTCGGAGTCCTCAGA
4692	LALGVPY	19015	CTGGCGCTGGGTGTGCCGTAT	33338	CTCGCACTCGGAGTCCCATAC
4693	LALKISS	19016	CTGGCGCTGAAGATTTCGAGT	33339	CTCGCACTCAAAATCAGCAGC
4694	LALKSHP	19017	TTGGCGCTTAAGTCGCATCCT	33340	CTCGCACTCAAAAGCCACCCA
4695	LALKSRD	19018	CTTGCGCTTAAGAGTCGGGAT	33341	CTCGCACTCAAAAGCAGAGAC
4696	LALPAHA	19019	TTGGCTTTGCCTGCGCATGCT	33342	CTCGCACTCCCAGCACACGCA
4697	LALRGPG	19020	CTTGCTTTGCGGGGGCCGGGG	33343	CTCGCACTCAGAGGACCAGGA
4698	LALSGNT	19021	CTTGCTTTGTCTGGGAATACT	33344	CTCGCACTCAGCGGAAACACA
4699	LALVTDR	19022	TTGGCTTTGGTTACTGATAGG	33345	CTCGCACTCGTCACAGACAGA
4700	LAMGGIR	19023	TTGGCGATGGGTGGTATTAGG	33346	CTCGCAATGGGAGGAATCAGA
4701	LAMQSRN	19024	CTGGCGATGCAGTCGCGTAAT	33347	CTCGCAATGCAAAGCAGAAAC
4702	LANGNPA	19025	CTGGCGAATGGTAATCCTGCG	33348	CTCGCAAACGGAAACCCAGCA
4703	LANIATK	19026	CTTGCGAATATTGCGACGAAG	33349	CTCGCAAACATCGCAACAAAA
4704	LANKIPP	19027	CTTGCTAATAAGATTCCGCCT	33350	CTCGCAAACAAAATCCCACCA
4705	LANKSMS	19028	TTGGCTAATAAGTCTATGAGT	33351	CTCGCAAACAAAAGCATGAGC
4706	LANPANG	19029	TTGGCTAATCCTGCGAATGGT	33352	CTCGCAAACCCAGCAAACGGA
4707	LANPLGR	19030	CTTGCTAATCCGCTTGGGAGG	33353	CTCGCAAACCCACTCGGAAGA
4708	LANPMSA	19031	CTGGCTAATCCTATGAGTGCT	33354	CTCGCAAACCCAATGAGCGCA
4709	LANSFVA	19032	CTTGCTAATTCTTTTGTTGCG	33355	CTCGCAAACAGCTTCGTCGCA
4710	LANSKSL	19033	CTTGCTAATTCGAAGTCTTTG	33356	CTCGCAAACAGCAAAAGCCTC
4711	LANVRAS	19034	CTTGCTAATGTTAGGGCGAGT	33357	CTCGCAAACGTCAGAGCAAGC
4712	LAPGLAM	19035	TTGGCTCCGGGGCTGGCGATG	33358	CTCGCACCAGGACTCGCAATG
4713	LAPHTSS	19036	TTGGCGCCGCATACTTCGAGT	33359	CTCGCACCACACACAAGCAGC
4714	LAPLSKV	19037	TTGGCTCCTTTGTCGAAGGTG	33360	CTCGCACCACTCAGCAAAGTC

4715	LAPPLRQ	19038	CTGGCGCCTCCTCTGAGGCAG	33361	CTCGCACCACCACTCAGACAA
4716	LAPSYLP	19039	CTTGCGCCGTCGTATTTGCCG	33362	CTCGCACCAAGCTACCTCCCA
4717	LAPTLTP	19040	TTGGCGCCGACTCTTACGCCG	33363	CTCGCACCAACACTCACACCA
4718	LAQGSIS	19041	CTGGCGCAGGGGTCTATTTCG	33364	CTCGCACAAGGAAGCATCAGC
4719	LAQQKDT	19042	CTGGCGCAGCAGAAGGATACG	33365	CTCGCACAACAAAAAGACACA
4720	LAQRPHQ	19043	CTTGCGCAGAGGCCTCATCAG	33366	CTCGCACAAAGACCACACCAA
4721	LAQSSSR	19044	CTGGCGCAGAGTAGTTCTCGT	33367	CTCGCACAAAGCAGCAGCAGA
4722	LAQVSAS	19045	CTGGCTCAGGTTTCGGCTAGT	33368	CTCGCACAAGTCAGCGCAAGC
4723	LARGPGD	19046	CTTGCTCGTGGTCCGGGTGAT	33369	CTCGCAAGAGGACCAGGAGAC
4724	LARLSPT	19047	CTTGCGCGTCTTAGTCCTACT	33370	CTCGCAAGACTCAGCCCAACA
4725	LARQSPE	19048	TTGGCTCGGCAGTCGCCGGAG	33371	CTCGCAAGACAAAGCCCAGAA
4726	LARQTSS	19049	CTGGCGCGGCAGACGTCGTCT	33372	CTCGCAAGACAAACAAGCAGC
4727	LARSPTL	19050	TTGGCGAGGTCTCCTACGCTT	33373	CTCGCAAGAAGCCCAACACTC
4728	LARVNSS	19051	CTGGCTCGTGTGAATTCTAGT	33374	CTCGCAAGAGTCAACAGCAGC
4729	LARVSQT	19052	TTGGCGAGGGTTTCTCAGACG	33375	CTCGCAAGAGTCAGCCAAACA
4730	LASAMKT	19053	CTTGCGTCTGCGATGAAGACT	33376	CTCGCAAGCGCAATGAAAACA
4731	LASAVQS	19054	TTGGCGTCTGCTGTTCAGAGT	33377	CTCGCAAGCGCAGTCCAAAGC
4732	LASDSRA	19055	TTGGCGTCGGATTCTAGGGCT	33378	CTCGCAAGCGACAGCAGAGCA
4733	LASEFIA	19056	CTTGCGTCTGAGTTTATTGCG	33379	CTCGCAAGCGAATTCATCGCA
4734	LASEKVS	19057	CTGGCGTCTGAGAAGGTTAGT	33380	CTCGCAAGCGAAAAAGTCAGC
4735	LASLVSV	19058	CTTGCTAGTTTGGTTTCTGTT	33381	CTCGCAAGCCTCGTCAGCGTC
4736	LASPTDY	19059	CTTGCTTCTCCTACTGATTAT	33382	CTCGCAAGCCCAACAGACTAC
4737	LASQGFN	19060	TTGGCTTCGCAGGGTTTTAAT	33383	CTCGCAAGCCAAGGATTCAAC
4738	LASQGPG	19061	CTGGCGTCTCAGGGGCCTGGT	33384	CTCGCAAGCCAAGGACCAGGA
4739	LASRPAH	19062	CTGGCTTCGAGGCCGGCTCAT	33385	CTCGCAAGCAGACCAGCACAC
4740	LASVNTS	19063	TTGGCGTCTGTGAATACGTCG	33386	CTCGCAAGCGTCAACACAAGC
4741	LATAHRP	19064	CTTGCGACGGCGCATCGTCCT	33387	CTCGCAACAGCACACAGACCA
4742	LATAVVD	19065	CTGGCTACTGCGGTTGTTGAT	33388	CTCGCAACAGCAGTCGTCGAC
4743	LATKSYT	19066	TTGGCTACTAAGTCTTATACG	33389	CTCGCAACAAAAAGCTACACA
4744	LATPPII	19067	TTGGCGACTCCTCCGATTATT	33390	CTCGCAACACCACCAATCATC
4745	LATRQVG	19068	TTGGCGACTCGGCAGGTTGGG	33391	CTCGCAACAAGACAAGTCGGA
4746	LATRVRE	19069	CTTGCGACGCGGGTTCGTGAG	33392	CTCGCAACAAGAGTCAGAGAA
4747	LATSPLH	19070	CTTGCGACTTCTCCGTTGCAT	33393	CTCGCAACAAGCCCACTCCAC
4748	LATSPNH	19071	CTGGCTACGAGTCCTAATCAT	33394	CTCGCAACAAGCCCAAACCAC
4749	LATSRSL	19072	CTGGCGACGAGTCGGAGTCTG	33395	CTCGCAACAAGCAGAAGCCTC
4750	LATTSGA	19073	TTGGCGACGACTTCTGGGGCT	33396	CTCGCAACAACAAGCGGAGCA
4751	LAVEKLP	19074	CTTGCTGTGGAGAAGTTGCCT	33397	CTCGCAGTCGAAAAACTCCCA
4752	LAVGTKG	19075	CTTGCGGTTGGGACTAAGGGG	33398	CTCGCAGTCGGAACAAAAGGA
4753	LAVSPMP	19076	CTGGCGGTGAGTCCGATGCCT	33399	CTCGCAGTCAGCCCAATGCCA
4754	LAVVESL	19077	TTGGCGGTGGTGGAGAGTCTG	33400	CTCGCAGTCGTCGAAAGCCTC
4755	LCRNSHS	19078	CTTTGTAGGAATTCGCATTCT	33401	CTCTGCAGAAACAGCCACAGC
4756	LDARRFF	19079	CTGGATGCTAGGCGTTTTTTT	33402	CTCGACGCAAGAAGATTCTTC
4757	LDDPGGC	19080	CTTGATGATCCGGGTGGTTGT	33403	CTCGACGACCCAGGAGGATGC
4758	LDDSSLL	19081	CTGGATGATTCTTCGCTGTTG	33404	CTCGACGACAGCAGCCTCCTC
4759	LDDVMPG	19082	TTGGATGATGTTATGCCGGGT	33405	CTCGACGACGTCATGCCAGGA

4760	LDERWPT	19083	CTGGATGAGAGGTGGCCGACG	33406	CTCGACGAAAGATGGCCAACA
4761	LDFPASS	19084	CTTGATTTTCCTGCGTCTTCT	33407	CTCGACTTCCCAGCAAGCAGC
4762	LDFREDS	19085	CTTGATTTTAGGGAGGATTCT	33408	CTCGACTTCAGAGAAGACAGC
4763	LDGGSTR	19086	CTGGATGGTGGGAGTACTCGG	33409	CTCGACGGAGGAAGCACAAGA
4764	LDGQMLA	19087	CTTGATGGGCAGATGCTTGCT	33410	CTCGACGGACAAATGCTCGCA
4765	LDGRPLV	19088	CTGGATGGTAGGCCTTTGGTT	33411	CTCGACGGAAGACCACTCGTC
4766	LDIERHS	19089	TTGGATATTGAGCGGCATTCG	33412	CTCGACATCGAAAGACACAGC
4767	LDITNVK	19090	TTGGATATTACGAATGTTAAG	33413	CTCGACATCACAAACGTCAAA
4768	LDKFNSK	19091	CTGGATAAGTTTAATTCGAAG	33414	CTCGACAAATTCAACAGCAAA
4769	LDKKHQS	19092	TTGGATAAGAAGCATCAGTCT	33415	CTCGACAAAAAACACCAAAGC
4770	LDKMRTT	19093	CTTGATAAGATGCGGACTACT	33416	CTCGACAAAATGAGAACAACA
4771	LDKRDIL	19094	CTTGATAAGAGGGATATTCTG	33417	CTCGACAAAAGAGACATCCTC
4772	LDKTSRL	19095	CTGGATAAGACGTCTCGTTTG	33418	CTCGACAAAACAAGCAGACTC
4773	LDLANSM	19096	CTTGATTTGGCGAATAGTATG	33419	CTCGACCTCGCAAACAGCATG
4774	LDLHLQA	19097	TTGGATCTGCATTTGCAGGCG	33420	CTCGACCTCCACCTCCAAGCA
4775	LDLKSVM	19098	TTGGATCTTAAGAGTGTGATG	33421	CTCGACCTCAAAAGCGTCATG
4776	LDLQTTK	19099	CTGGATTTGCAGACGACTAAG	33422	CTCGACCTCCAAACAACAAAA
4777	LDLVAFE	19100	TTGGATTTGGTGGCTTTTGAG	33423	CTCGACCTCGTCGCATTCGAA
4778	LDMRDSG	19101	CTTGATATGCGTGATTCGGGG	33424	CTCGACATGAGAGACAGCGGA
4779	LDMRTQG	19102	CTTGATATGCGTACTCAGGGG	33425	CTCGACATGAGAACACAAGGA
4780	LDNPHHV	19103	CTTGATAATCCTCATCATGTT	33426	CTCGACAACCCACACCACGTC
4781	LDNPVSA	19104	CTTGATAATCCTGTTTCGGCT	33427	CTCGACAACCCAGTCAGCGCA
4782	LDPDARR	19105	CTGGATCCTGATGCTCGTCGG	33428	CTCGACCCAGACGCAAGAAGA
4783	LDPGLKS	19106	CTGGATCCGGGGCTTAAGAGT	33429	CTCGACCCAGGACTCAAAAGC
4784	LDRLSSI	19107	TTGGATCGTCTTAGTTCTATT	33430	CTCGACAGACTCAGCAGCATC
4785	LDRLVTG	19108	CTTGATCGGCTTGTTACGGGT	33431	CTCGACAGACTCGTCACAGGA
4786	LDRMVVG	19109	CTGGATCGTATGGTTGTTGGT	33432	CTCGACAGAATGGTCGTCGGA
4787	LDRPSAW	19110	CTGGATCGGCCGTCGGCTTGG	33433	CTCGACAGACCAAGCGCATGG
4788	LDRRPIQ	19111	TTGGATCGTAGGCCTATTCAG	33434	CTCGACAGAAGACCAATCCAA
4789	LDRRPML	19112	CTTGATCGTCGTCCGATGCTT	33435	CTCGACAGAAGACCAATGCTC
4790	LDRYTPP	19113	CTGGATCGTTATACTCCTCCG	33436	CTCGACAGATACACACCACCA
4791	LDSGRPS	19114	TTGGATAGTGGTCGGCCTAGT	33437	CTCGACAGCGGAAGACCAAGC
4792	LDSLHIP	19115	TTGGATAGTCTGCATATTCCT	33438	CTCGACAGCCTCCACATCCCA
4793	LDSNVTS	19116	TTGGATAGTAATGTTACTTCG	33439	CTCGACAGCAACGTCACAAGC
4794	LDSPAMA	19117	CTGGATAGTCCGGCTATGGCG	33440	CTCGACAGCCCAGCAATGGCA
4795	LDSPPNN	19118	TTGGATTCGCCTCCTAATAAT	33441	CTCGACAGCCCACCAAACAAC
4796	LDSSHGH	19119	TTGGATTCGTCTCATGGTCAT	33442	CTCGACAGCAGCCACGGACAC
4797	LDSSRSS	19120	TTGGATTCGAGTCGTTCTAGT	33443	CTCGACAGCAGCAGAAGCAGC
4798	LDSSWTP	19121	TTGGATTCTTCTTGGACGCCG	33444	CTCGACAGCAGCTGGACACCA
4799	LDSTPRP	19122	TTGGATAGTACTCCGCGGCCT	33445	CTCGACAGCACACCAAGACCA
4800	LDTQAGR	19123	CTTGATACGCAGGCGGGTCGT	33446	CTCGACACACAAGCAGGAAGA
4801	LDTQSRL	19124	TTGGATACTCAGTCTAGGCTG	33447	CTCGACACACAAAGCAGACTC
4802	LDTRGIS	19125	CTGGATACTAGGGGTATTAGT	33448	CTCGACACAAGAGGAATCAGC
4803	LDTRYRY	19126	TTGGATACGCGTTATCGTTAT	33449	CTCGACACAAGATACAGATAC
4804	LDTVQSK	19127	CTGGATACTGTTCAGTCGAAG	33450	CTCGACACAGTCCAAAGCAAA

4805	LDVATSR	19128	CTGGATGTTGCGACTAGTAGG	33451	CTCGACGTCGCAACAAGCAGA
4806	LDVKCDP	19129	CTGGATGTGAAGTGTGATCCT	33452	CTCGACGTCAAATGCGACCCA
4807	LDVLDCK	19130	TTGGATGTTCTTGATTGTAAG	33453	CTCGACGTCCTCGACTGCAAA
4808	LDVNGLR	19131	CTGGATGTTAATGGTTTGCGT	33454	CTCGACGTCAACGGACTCAGA
4809	LDVSQRL	19132	CTTGATGTGTCGCAGCGGCTT	33455	CTCGACGTCAGCCAAAGACTC
4810	LDVVTRV	19133	CTGGATGTGGTTACGCGTGTT	33456	CTCGACGTCGTCACAAGAGTC
4811	LDVYSRE	19134	CTGGATGTGTATAGTCGGGAG	33457	CTCGACGTCTACAGCAGAGAA
4812	LEANLKV	19135	CTTGAGGCTAATCTGAAGGTT	33458	CTCGAAGCAAACCTCAAAGTC
4813	LEAPRAT	19136	CTTGAGGCTCCGAGGGCTACT	33459	CTCGAAGCACCAAGAGCAACA
4814	LEEDKVK	19137	TTGGAGGAGGATAAGGTTAAG	33460	CTCGAAGAAGACAAAGTCAAA
4815	LEFDSKE	19138	CTGGAGTTTGATAGTAAGGAG	33461	CTCGAATTCGACAGCAAAGAA
4816	LEFGSDQ	19139	CTTGAGTTTGGTTCTGATCAG	33462	CTCGAATTCGGAAGCGACCAA
4817	LEFTRIG	19140	CTTGAGTTTACTCGGATTGGT	33463	CTCGAATTCACAAGAATCGGA
4818	LEGTRRD	19141	CTTGAGGGTACGAGGCGGGAT	33464	CTCGAAGGAACAAGAAGAGAC
4819	LEGVRGS	19142	CTTGAGGGTGTTAGGGGTTCG	33465	CTCGAAGGAGTCAGAGGAAGC
4820	LEHLRSA	19143	CTGGAGCATCTTCGTTCTGCG	33466	CTCGAACACCTCAGAAGCGCA
4821	LEHSAHV	19144	TTGGAGCATAGTGCGCATGTT	33467	CTCGAACACAGCGCACACGTC
4822	LEHSVSL	19145	CTGGAGCATAGTGTGAGTCTT	33468	CTCGAACACAGCGTCAGCCTC
4823	LEITGPG	19146	CTGGAGATTACGGGTCCGGGT	33469	CTCGAAATCACAGGACCAGGA
4824	LEKMGLY	19147	CTGGAGAAGATGGGGCTTTAT	33470	CTCGAAAAAATGGGACTCTAC
4825	LEKQTGD	19148	CTGGAGAAGCAGACTGGTGAT	33471	CTCGAAAAACAAACAGGAGAC
4826	LELKPAN	19149	TTGGAGCTTAAGCCTGCGAAT	33472	CTCGAACTCAAACCAGCAAAC
4827	LEMRGLA	19150	CTTGAGATGAGGGGGCTGGCT	33473	CTCGAAATGAGAGGACTCGCA
4828	LENAQTP	19151	CTGGAGAATGCTCAGACTCCT	33474	CTCGAAAACGCACAAACACCA
4829	LENDWRV	19152	CTGGAGAATGATTGGCGTGTT	33475	CTCGAAAACGACTGGAGAGTC
4830	LENHPDR	19153	TTGGAGAATCATCCGGATAGG	33476	CTCGAAAACCACCCAGACAGA
4831	LENNPAL	19154	TTGGAGAATAATCCTGCTTTG	33477	CTCGAAAACAACCCAGCACTC
4832	LENSHLV	19155	CTGGAGAATAGTCATTTGGTG	33478	CTCGAAAACAGCCACCTCGTC
4833	LEPIVRN	19156	CTTGAGCCGATTGTTCGTAAT	33479	CTCGAACCAATCGTCAGAAAC
4834	LEPQTHS	19157	TTGGAGCCGCAGACGCATTCG	33480	CTCGAACCACAAACACACAGC
4835	LEPSHTI	19158	CTGGAGCCGTCGCATACGATT	33481	CTCGAACCAAGCCACACAATC
4836	LEPYKHF	19159	CTGGAGCCGTATAAGCATTTT	33482	CTCGAACCATACAAACACTTC
4837	LEQFSTA	19160	CTTGAGCAGTTTTCGACGGCG	33483	CTCGAACAATTCAGCACAGCA
4838	LEQPPEH	19161	TTGGAGCAGCCTCCTGAGCAT	33484	CTCGAACAACCACCAGAACAC
4839	LEQYNKE	19162	CTTGAGCAGTATAATAAGGAG	33485	CTCGAACAATACAACAAAGAA
4840	LERGSSE	19163	TTGGAGCGGGGTTCGAGTGAG	33486	CTCGAAAGAGGAAGCAGCGAA
4841	LERISSV	19164	TTGGAGAGGATTAGTTCGGTG	33487	CTCGAAAGAATCAGCAGCGTC
4842	LESALSS	19165	TTGGAGTCGGCTCTGTCTTCT	33488	CTCGAAAGCGCACTCAGCAGC
4843	LESAWIG	19166	CTGGAGTCGGCGTGGATTGGG	33489	CTCGAAAGCGCATGGATCGGA
4844	LESKPSP	19167	CTGGAGTCGAAGCCTAGTCCG	33490	CTCGAAAGCAAACCAAGCCCA
4845	LESNNYL	19168	CTGGAGAGTAATAATTATCTG	33491	CTCGAAAGCAACAACTACCTC
4846	LESQTRN	19169	TTGGAGTCTCAGACTAGGAAT	33492	CTCGAAAGCCAAACAAGAAAC
4847	LESRSGM	19170	CTGGAGTCGAGGTCTGGTATG	33493	CTCGAAAGCAGAAGCGGAATG
4848	LESSHTR	19171	CTTGAGTCTTCTCATACGCGG	33494	CTCGAAAGCAGCCACACAAGA
4849	LESSVRV	19172	CTTGAGTCGAGTGTGCGTGTT	33495	CTCGAAAGCAGCGTCAGAGTC

4850	LETASTK	19173	TTGGAGACGGCTTCGACGAAG	33496	CTCGAAACAGCAAGCACAAAA
4851	LETRQIG	19174	CTTGAGACTCGGCAGATTGGG	33497	CTCGAAACAAGACAAATCGGA
4852	LETSDSV	19175	TTGGAGACTTCGGATTCTGTT	33498	CTCGAAACAAGCGACAGCGTC
4853	LEVALRT	19176	TTGGAGGTGGCGTTGAGGACT	33499	CTCGAAGTCGCACTCAGAACA
4854	LEVASNP	19177	CTTGAGGTGGCTAGTAATCCT	33500	CTCGAAGTCGCAAGCAACCCA
4855	LEVTEPW	19178	CTTGAGGTGACGGAGCCGTGG	33501	CTCGAAGTCACAGAACCATGG
4856	LFAISVP	19179	CTTTTTGCTATTTCGGTGCCG	33502	CTCTTCGCAATCAGCGTCCCA
4857	LFANTIS	19180	CTGTTTGCTAATACGATTAGT	33503	CTCTTCGCAAACACAATCAGC
4858	LFDAALP	19181	TTGTTTGATGCGGCGCTTCCG	33504	CTCTTCGACGCAGCACTCCCA
4859	LFDFTKE	19182	CTGTTTGATTTTACGAAGGAG	33505	CTCTTCGACTTCACAAAAGAA
4860	LFDPNRG	19183	CTTTTTGATCCGAATCGGGGG	33506	CTCTTCGACCCAAACAGAGGA
4861	LFDRTAL	19184	CTGTTTGATAGGACGGCTTTG	33507	CTCTTCGACAGAACAGCACTC
4862	LFDSSTT	19185	CTTTTTGATTCGTCTACTACG	33508	CTCTTCGACAGCAGCACAACA
4863	LFELQHR	19186	TTGTTTGAGCTGCAGCATCGG	33509	CTCTTCGAACTCCAACACAGA
4864	LFFTAAP	19187	CTTTTTTTTACGGCGGCTCCG	33510	CTCTTCTTCACAGCAGCACCA
4865	LFGKVSG	19188	CTGTTTGGTAAGGTGAGTGGT	33511	CTCTTCGGAAAAGTCAGCGGA
4866	LFGSRPT	19189	TTGTTTGGGTCGCGTCCGACT	33512	CTCTTCGGAAGCAGACCAACA
4867	LFGTNRS	19190	TTGTTTGGGACGAATCGGAGT	33513	CTCTTCGGAACAAACAGAAGC
4868	LFHESTY	19191	TTGTTTCATGAGTCGACTTAT	33514	CTCTTCCACGAAAGCACATAC
4869	LFHSNDD	19192	CTGTTTCATTCGAATGATGAT	33515	CTCTTCCACAGCAACGACGAC
4870	LFINHGS	19193	CTTTTTATTAATCATGGGTCT	33516	CTCTTCATCAACCACGGAAGC
4871	LFITTTS	19194	CTGTTTATTACTACGACTAGT	33517	CTCTTCATCACAACAACAAGC
4872	LFKHSRE	19195	CTTTTTAAGCATAGTCGTGAG	33518	CTCTTCAAACACAGCAGAGAA
4873	LFLSQVP	19196	CTGTTTCTGTCGCAGGTGCCT	33519	CTCTTCCTCAGCCAAGTCCCA
4874	LFNQQVL	19197	TTGTTTAATCAGCAGGTTCTT	33520	CTCTTCAACCAACAAGTCCTC
4875	LFNSSPE	19198	CTTTTTAATTCTTCGCCTGAG	33521	CTCTTCAACAGCAGCCCAGAA
4876	LFPGSID	19199	CTTTTTCCGGGGTCGATTGAT	33522	CTCTTCCCAGGAAGCATCGAC
4877	LFPTGSL	19200	TTGTTTCCGACTGGTTCTCTT	33523	CTCTTCCCAACAGGAAGCCTC
4878	LFRASDR	19201	TTGTTTCGTGCTTCGGATAGG	33524	CTCTTCAGAGCAAGCGACAGA
4879	LFSESRS	19202	CTGTTTAGTGAGTCTAGGTCG	33525	CTCTTCAGCGAAAGCAGAAGC
4880	LFSGAES	19203	TTGTTTTCGGGTGCTGAGAGT	33526	CTCTTCAGCGGAGCAGAAAGC
4881	LFSMPVS	19204	CTTTTTTCGATGCCGGTGTCT	33527	CTCTTCAGCATGCCAGTCAGC
4882	LFTSADL	19205	TTGTTTACTTCGGCTGATCTT	33528	CTCTTCACAAGCGCAGACCTC
4883	LFTSESI	19206	TTGTTTACTTCTGAGTCGATT	33529	CTCTTCACAAGCGAAAGCATC
4884	LFTSPSM	19207	CTTTTTACTTCTCCTAGTATG	33530	CTCTTCACAAGCCCAAGCATG
4885	LFTTMVP	19208	CTGTTTACTACGATGGTGCCT	33531	CTCTTCACAACAATGGTCCCA
4886	LGAAVNL	19209	TTGGGGGCTGCTGTGAATTTG	33532	CTCGGAGCAGCAGTCAACCTC
4887	LGAGSSV	19210	CTTGGTGCTGGTAGTAGTGTG	33533	CTCGGAGCAGGAAGCAGCGTC
4888	LGALSGP	19211	CTTGGTGCGTTGTCTGGTCCT	33534	CTCGGAGCACTCAGCGGACCA
4889	LGALTHA	19212	TTGGGGGCTCTGACTCATGCT	33535	CTCGGAGCACTCACACACGCA
4890	LGARIQL	19213	CTGGGTGCTAGGATTCAGTTG	33536	CTCGGAGCAAGAATCCAACTC
4891	LGARTAA	19214	TTGGGTGCGCGGACGGCTGCT	33537	CTCGGAGCAAGAACAGCAGCA
4892	LGASSSL	19215	CTTGGTGCTTCTTCGTCTTTG	33538	CTCGGAGCAAGCAGCAGCCTC
4893	LGAYLGP	19216	TTGGGGGCTTATTTGGGGCCG	33539	CTCGGAGCATACCTCGGACCA
4894	LGAYNAQ	19217	TTGGGTGCTTATAATGCTCAG	33540	CTCGGAGCATACAACGCACAA

4895	LGDAGFS	19218	CTTGGTGATGCTGGGTTTTCG	33541	CTCGGAGACGCAGGATTCAGC
4896	LGDHYRH	19219	TTGGGTGATCATTATAGGCAT	33542	CTCGGAGACCACTACAGACAC
4897	LGDPFPP	19220	CTTGGGGATCCTTTTCCTCCT	33543	CTCGGAGACCCATTCCCACCA
4898	LGDRTDF	19221	CTTGGTGATAGGACTGATTTT	33544	CTCGGAGACAGAACAGACTTC
4899	LGDRTHI	19222	CTTGGTGATAGGACGCATATT	33545	CTCGGAGACAGAACACACATC
4900	LGDTAHH	19223	CTTGGGGATACTGCTCATCAT	33546	CTCGGAGACACAGCACACCAC
4901	LGFGATQ	19224	CTTGGTTTTGGGGCGACGCAG	33547	CTCGGATTCGGAGCAACACAA
4902	LGFNVVV	19225	CTGGGTTTTAATGTTGTGGTT	33548	CTCGGATTCAACGTCGTCGTC
4903	LGFNYQD	19226	TTGGGGTTTAATTATCAGGAT	33549	CTCGGATTCAACTACCAAGAC
4904	LGFPSTE	19227	CTGGGGTTTCCTTCTACTGAG	33550	CTCGGATTCCCAAGCACAGAA
4905	LGGDAQI	19228	CTGGGTGGTGATGCTCAGATT	33551	CTCGGAGGAGACGCACAAATC
4906	LGGGRSL	19229	TTGGGGGGGGGGAGGTCGCTG	33552	CTCGGAGGAGGAAGAAGCCTC
4907	LGGSLSM	19230	CTGGGGGGTTCGCTGTCGATG	33553	CTCGGAGGAAGCCTCAGCATG
4908	LGGSYPL	19231	CTGGGGGGGTCTTATCCGCTT	33554	CTCGGAGGAAGCTACCCACTC
4909	LGHATSA	19232	TTGGGGCATGCGACTTCGGCG	33555	CTCGGACACGCAACAAGCGCA
4910	LGHGPGH	19233	TTGGGGCATGGGCCGGGGCAT	33556	CTCGGACACGGACCAGGACAC
4911	LGHSKPP	19234	TTGGGGCATAGTAAGCCTCCT	33557	CTCGGACACAGCAAACCACCA
4912	LGIITHA	19235	CTGGGTATTATTACGCATGCT	33558	CTCGGAATCATCACACACGCA
4913	LGIMKTA	19236	CTTGGTATTATGAAGACTGCT	33559	CTCGGAATCATGAAAACAGCA
4914	LGKLTTV	19237	TTGGGTAAGCTTACGACTGTG	33560	CTCGGAAAACTCACAACAGTC
4915	LGKSLLT	19238	TTGGGTAAGAGTCTTCTGACT	33561	CTCGGAAAAAGCCTCCTCACA
4916	LGKYGIV	19239	TTGGGGAAGTATGGGATTGTG	33562	CTCGGAAAATACGGAATCGTC
4917	LGLNHQT	19240	CTTGGGTTGAATCATCAGACT	33563	CTCGGACTCAACCACCAAACA
4918	LGLPSKG	19241	CTTGGTTTGCCGTCGAAGGGT	33564	CTCGGACTCCCAAGCAAAGGA
4919	LGLRDKD	19242	CTTGGTCTTAGGGATAAGGAT	33565	CTCGGACTCAGAGACAAAGAC
4920	LGLRESS	19243	TTGGGTCTTAGGGAGTCTTCG	33566	CTCGGACTCAGAGAAAGCAGC
4921	LGLSTVH	19244	CTTGGGCTTTCGACGGTTCAT	33567	CTCGGACTCAGCACAGTCCAC
4922	LGLVLNQ	19245	CTGGGTCTTGTTCTTAATCAG	33568	CTCGGACTCGTCCTCAACCAA
4923	LGMLKTE	19246	CTTGGGATGTTGAAGACTGAG	33569	CTCGGAATGCTCAAAACAGAA
4924	LGMMPAS	19247	TTGGGGATGATGCCTGCTTCT	33570	CTCGGAATGATGCCAGCAAGC
4925	LGNHPSV	19248	CTTGGGAATCATCCGAGTGTG	33571	CTCGGAAACCACCCAAGCGTC
4926	LGNPDKM	19249	CTGGGTAATCCGGATAAGATG	33572	CTCGGAAACCCAGACAAAATG
4927	LGNPSPC	19250	CTGGGGAATCCGTCGCCTTGT	33573	CTCGGAAACCCAAGCCCATGC
4928	LGNPVTV	19251	TTGGGTAATCCGGTGACTGTT	33574	CTCGGAAACCCAGTCACAGTC
4929	LGNQRSD	19252	TTGGGTAATCAGCGGTCGGAT	33575	CTCGGAAACCAAAGAAGCGAC
4930	LGPAGMP	19253	CTTGGTCCGGCGGGGATGCCT	33576	CTCGGACCAGCAGGAATGCCA
4931	LGPAGPY	19254	TTGGGTCCTGCGGGGCCTTAT	33577	CTCGGACCAGCAGGACCATAC
4932	LGPFHGE	19255	CTTGGGCCTTTTCATGGTGAG	33578	CTCGGACCATTCCACGGAGAA
4933	LGPGSYP	19256	CTTGGGCCGGGTTCTTATCCG	33579	CTCGGACCAGGAAGCTACCCA
4934	LGPSSKV	19257	CTGGGTCCTTCTTCTAAGGTT	33580	CTCGGACCAAGCAGCAAAGTC
4935	LGPSYTN	19258	CTTGGGCCTAGTTATACGAAT	33581	CTCGGACCAAGCTACACAAAC
4936	LGPTIRS	19259	CTTGGTCCTACTATTAGGTCG	33582	CTCGGACCAACAATCAGAAGC
4937	LGPTKLP	19260	CTGGGTCCGACTAAGCTGCCG	33583	CTCGGACCAACAAAACTCCCA
4938	LGQALRV	19261	TTGGGGCAGGCGCTGCGGGTT	33584	CTCGGACAAGCACTCAGAGTC
4939	LGQKPNE	19262	CTTGGGCAGAAGCCTAATGAG	33585	CTCGGACAAAAACCAAACGAA

4940	LGQSGCR	19263	TTGGGTCAGTCTGGTTGTCGT	33586	CTCGGACAAAGCGGATGCAGA
4941	LGQSGTK	19264	CTTGGTCAGTCTGGTACGAAG	33587	CTCGGACAAAGCGGAACAAAA
4942	LGRALEH	19265	TTGGGTCGTGCGCTGGAGCAT	33588	CTCGGAAGAGCACTCGAACAC
4943	LGRAYSQ	19266	TTGGGGCGGGCGTATAGTCAG	33589	CTCGGAAGAGCATACAGCCAA
4944	LGRERPT	19267	CTTGGTAGGGAGAGGCCTACT	33590	CTCGGAAGAGAAAGACCAACA
4945	LGRIAVN	19268	CTTGGTCGTATTGCGGTGAAT	33591	CTCGGAAGAATCGCAGTCAAC
4946	LGRLNSG	19269	CTTGGTCGGCTGAATTCTGGG	33592	CTCGGAAGACTCAACAGCGGA
4947	LGRPQMD	19270	CTTGGTCGGCCTCAGATGGAT	33593	CTCGGAAGACCACAAATGGAC
4948	LGRSGAL	19271	TTGGGGAGGTCGGGTGCGCTG	33594	CTCGGAAGAAGCGGAGCACTC
4949	LGSAGPP	19272	CTTGGTTCTGCTGGTCCGCCT	33595	CTCGGAAGCGCAGGACCACCA
4950	LGSAGYS	19273	CTGGGTAGTGCGGGGTATTCT	33596	CTCGGAAGCGCAGGATACAGC
4951	LGSAHSP	19274	CTTGGGTCTGCGCATTCTCCT	33597	CTCGGAAGCGCACACAGCCCA
4952	LGSATSG	19275	CTGGGGTCGGCGACTTCTGGG	33598	CTCGGAAGCGCAACAAGCGGA
4953	LGSHYSN	19276	CTTGGTTCTCATTATAGTAAT	33599	CTCGGAAGCCACTACAGCAAC
4954	LGSLTVA	19277	CTTGGTTCTCTTACTGTGGCT	33600	CTCGGAAGCCTCACAGTCGCA
4955	LGSMPLL	19278	TTGGGTTCGATGCCTCTTCTT	33601	CTCGGAAGCATGCCACTCCTC
4956	LGSNHKP	19279	TTGGGGTCTAATCATAAGCCG	33602	CTCGGAAGCAACCACAAACCA
4957	LGSPSPD	19280	CTTGGTTCTCCTTCTCCGGAT	33603	CTCGGAAGCCCAAGCCCAGAC
4958	LGSQVIA	19281	TTGGGTAGTCAGGTTATTGCG	33604	CTCGGAAGCCAAGTCATCGCA
4959	LGSQYAV	19282	TTGGGTTCTCAGTATGCTGTT	33605	CTCGGAAGCCAATACGCAGTC
4960	LGSRSDL	19283	TTGGGGAGTCGGTCGGATCTT	33606	CTCGGAAGCAGAAGCGACCTC
4961	LGSSLRA	19284	CTTGGGTCTTCGTTGCGGGCT	33607	CTCGGAAGCAGCCTCAGAGCA
4962	LGSSLRN	19285	TTGGGTTCTTCGCTGCGGAAT	33608	CTCGGAAGCAGCCTCAGAAAC
4963	LGSSQSR	19286	TTGGGGTCTTCTCAGTCTAGG	33609	CTCGGAAGCAGCCAAAGCAGA
4964	LGSTSAV	19287	CTTGGTTCGACGAGTGCTGTT	33610	CTCGGAAGCACAAGCGCAGTC
4965	LGSVKFS	19288	CTGGGTTCGGTTAAGTTTTCT	33611	CTCGGAAGCGTCAAATTCAGC
4966	LGTALHL	19289	TTGGGGACGGCTTTGCATCTT	33612	CTCGGAACAGCACTCCACCTC
4967	LGTGRLY	19290	TTGGGGACGGGGAGGTTGTAT	33613	CTCGGAACAGGAAGACTCTAC
4968	LGTLNTV	19291	CTGGGTACTCTTAATACTGTG	33614	CTCGGAACACTCAACACAGTC
4969	LGTRASG	19292	CTGGGGACGAGGGCTTCTGGG	33615	CTCGGAACAAGAGCAAGCGGA
4970	LGTRPML	19293	CTGGGTACGCGGCCGATGTTG	33616	CTCGGAACAAGACCAATGCTC
4971	LGTSDVL	19294	CTTGGTACTTCGGATGTGCTT	33617	CTCGGAACAAGCGACGTCCTC
4972	LGTSHVA	19295	TTGGGTACGAGTCATGTGGCT	33618	CTCGGAACAAGCCACGTCGCA
4973	LGTSQTG	19296	TTGGGTACGTCTCAGACGGGT	33619	CTCGGAACAAGCCAAACAGGA
4974	LGTVRVY	19297	CTTGGTACGGTTCGTGTGTAT	33620	CTCGGAACAGTCAGAGTCTAC
4975	LGVAKPA	19298	TTGGGGGTGGCGAAGCCTGCG	33621	CTCGGAGTCGCAAAACCAGCA
4976	LGVDKNA	19299	TTGGGTGTGGATAAGAATGCG	33622	CTCGGAGTCGACAAAAACGCA
4977	LGVEVLK	19300	CTGGGTGTTGAGGTGTTGAAG	33623	CTCGGAGTCGAAGTCCTCAAA
4978	LGVKAAG	19301	CTTGGTGTGAAGGCTGCGGGG	33624	CTCGGAGTCAAAGCAGCAGGA
4979	LGVKSVD	19302	CTTGGGGTGAAGTCTGTTGAT	33625	CTCGGAGTCAAAAGCGTCGAC
4980	LGVLRSS	19303	CTGGGGGTTCTGCGGAGTAGT	33626	CTCGGAGTCCTCAGAAGCAGC
4981	LGVNTSQ	19304	TTGGGGGTTAATACTTCGCAG	33627	CTCGGAGTCAACACAAGCCAA
4982	LGVPPQS	19305	CTTGGGGTGCCGCCTCAGAGT	33628	CTCGGAGTCCCACCACAAAGC
4983	LGVSREL	19306	CTGGGGGTTTCGAGGGAGCTT	33629	CTCGGAGTCAGCAGAGAACTC
4984	LGVSTHM	19307	TTGGGTGTGAGTACGCATATG	33630	CTCGGAGTCAGCACACACATG

4985	LGYNLGE	19308	TTGGGGTATAATTTGGGGGAG	33631	CTCGGATACAACCTCGGAGAA
4986	LGYPPRE	19309	CTTGGGTATCCGCCGCGGGAG	33632	CTCGGATACCCACCAAGAGAA
4987	LGYSTGA	19310	CTTGGGTATTCGACTGGTGCG	33633	CTCGGATACAGCACAGGAGCA
4988	LHAAPAS	19311	CTTCATGCTGCTCCGGCGTCT	33634	CTCCACGCAGCACCAGCAAGC
4989	LHANRTE	19312	CTTCATGCGAATCGGACTGAG	33635	CTCCACGCAAACAGAACAGAA
4990	LHAPEVA	19313	CTGCATGCGCCGGAGGTTGCT	33636	CTCCACGCACCAGAAGTCGCA
4991	LHATSST	19314	TTGCATGCGACTTCTTCTACG	33637	CTCCACGCAACAAGCAGCACA
4992	LHATTGP	19315	CTTCATGCGACGACTGGGCCT	33638	CTCCACGCAACAACAGGACCA
4993	LHEYRSP	19316	TTGCATGAGTATCGTTCTCCT	33639	CTCCACGAATACAGAAGCCCA
4994	LHFGPEG	19317	TTGCATTTTGGTCCTGAGGGG	33640	CTCCACTTCGGACCAGAAGGA
4995	LHGLGSG	19318	TTGCATGGGTTGGGGTCTGGG	33641	CTCCACGGACTCGGAAGCGGA
4996	LHGMPER	19319	CTTCATGGGATGCCGGAGCGG	33642	CTCCACGGAATGCCAGAAAGA
4997	LHIREMA	19320	CTTCATATTCGGGAGATGGCT	33643	CTCCACATCAGAGAAATGGCA
4998	LHKSGFN	19321	CTGCATAAGTCGGGTTTTAAT	33644	CTCCACAAAAGCGGATTCAAC
4999	LHLQGNS	19322	CTGCATCTTCAGGGTAATAGT	33645	CTCCACCTCCAAGGAAACAGC
5000	LHLSRPL	19323	CTTCATTTGTCGCGGCCTTTG	33646	CTCCACCTCAGCAGACCACTC
5001	LHLSTAP	19324	TTGCATCTGTCTACTGCTCCG	33647	CTCCACCTCAGCACAGCACCA
5002	LHMTTTR	19325	TTGCATATGACTACTACTCGT	33648	CTCCACATGACAACAACAAGA
5003	LHNDLIR	19326	TTGCATAATGATCTGATTCGT	33649	CTCCACAACGACCTCATCAGA
5004	LHNIRQQ	19327	TTGCATAATATTCGTCAGCAG	33650	CTCCACAACATCAGACAACAA
5005	LHNKMYD	19328	TTGCATAATAAGATGTATGAT	33651	CTCCACAACAAAATGTACGAC
5006	LHNQAAR	19329	CTGCATAATCAGGCGGCTAGG	33652	CTCCACAACCAAGCAGCAAGA
5007	LHNTAAA	19330	CTGCATAATACTGCTGCTGCT	33653	CTCCACAACACAGCAGCAGCA
5008	LHNTRNM	19331	CTTCATAATACGCGGAATATG	33654	CTCCACAACACAAGAAACATG
5009	LHNTRTV	19332	CTGCATAATACGCGGACTGTG	33655	CTCCACAACACAAGAACAGTC
5010	LHPGSTA	19333	CTGCATCCTGGGTCGACTGCT	33656	CTCCACCCAGGAAGCACAGCA
5011	LHPLSPR	19334	CTTCATCCGCTTTCGCCGCGG	33657	CTCCACCCACTCAGCCCAAGA
5012	LHPVHAP	19335	CTTCATCCGGTGCATGCGCCT	33658	CTCCACCCAGTCCACGCACCA
5013	LHQDRLA	19336	TTGCATCAGGATAGGCTTGCT	33659	CTCCACCAAGACAGACTCGCA
5014	LHQMGNS	19337	CTTCATCAGATGGGGAATTCG	33660	CTCCACCAAATGGGAAACAGC
5015	LHQSYNQ	19338	CTGCATCAGTCGTATAATCAG	33661	CTCCACCAAAGCTACAACCAA
5016	LHRDLPV	19339	CTTCATCGGGATCTTCCTGTG	33662	CTCCACAGAGACCTCCCAGTC
5017	LHRRPSE	19340	TTGCATAGGCGTCCGTCTGAG	33663	CTCCACAGAAGACCAAGCGAA
5018	LHSALTR	19341	TTGCATTCTGCTCTGACGCGT	33664	CTCCACAGCGCACTCACAAGA
5019	LHSASPQ	19342	TTGCATTCTGCTAGTCCTCAG	33665	CTCCACAGCGCAAGCCCACAA
5020	LHSDTRG	19343	CTGCATTCGGATACTCGTGGT	33666	CTCCACAGCGACACAAGAGGA
5021	LHSELTS	19344	TTGCATTCTGAGTTGACTTCG	33667	CTCCACAGCGAACTCACAAGC
5022	LHSGERQ	19345	CTGCATTCTGGGGAGCGTCAG	33668	CTCCACAGCGGAGAAAGACAA
5023	LHSNVTK	19346	TTGCATTCGAATGTGACGAAG	33669	CTCCACAGCAACGTCACAAAA
5024	LHSRADS	19347	CTGCATTCGAGGGCGGATTCG	33670	CTCCACAGCAGAGCAGACAGC
5025	LHSRAIS	19348	CTTCATTCTAGGGCTATTAGT	33671	CTCCACAGCAGAGCAATCAGC
5026	LHSRGTA	19349	TTGCATTCTCGTGGGACTGCT	33672	CTCCACAGCAGAGGAACAGCA
5027	LHSSPQD	19350	CTGCATTCTAGTCCGCAGGAT	33673	CTCCACAGCAGCCCACAAGAC
5028	LHTAKAG	19351	CTTCATACGGCTAAGGCGGGT	33674	CTCCACACAGCAAAAGCAGGA
5029	LHTDWLR	19352	CTTCATACGGATTGGCTTCGG	33675	CTCCACACAGACTGGCTCAGA

5030	LHTPQLS	19353	TTGCATACGCCGCAGCTGAGT	33676	CTCCACACACCACAACTCAGC
5031	LHTSARP	19354	CTGCATACTTCGGCTCGGCCT	33677	CTCCACACAAGCGCAAGACCA
5032	LHVPQPP	19355	TTGCATGTTCCTCAGCCTCCG	33678	CTCCACGTCCCACAACCACCA
5033	LIASHRL	19356	CTTATTGCGAGTCATCGTCTG	33679	CTCATCGCAAGCCACAGACTC
5034	LIASSGV	19357	CTTATTGCTTCGTCTGGTGTG	33680	CTCATCGCAAGCAGCGGAGTC
5035	LIASTTS	19358	CTGATTGCTAGTACTACGTCG	33681	CTCATCGCAAGCACAACAAGC
5036	LIGNVVM	19359	TTGATTGGGAATGTTGTGATG	33682	CTCATCGGAAACGTCGTCATG
5037	LIGRPME	19360	CTTATTGGGCGGCCTATGGAG	33683	CTCATCGGAAGACCAATGGAA
5038	LIGRTIS	19361	CTTATTGGGCGGACTATTTCT	33684	CTCATCGGAAGAACAATCAGC
5039	LIGTASL	19362	TTGATTGGTACGGCGTCGCTG	33685	CTCATCGGAACAGCAAGCCTC
5040	LIGTPVV	19363	CTTATTGGGACGCCTGTTGTG	33686	CTCATCGGAACACCAGTCGTC
5041	LIHASGG	19364	TTGATTCATGCTAGTGGGGGT	33687	CTCATCCACGCAAGCGGAGGA
5042	LIHLSGA	19365	CTGATTCATCTGTCGGGTGCG	33688	CTCATCCACCTCAGCGGAGCA
5043	LIKENVL	19366	CTGATTAAGGAGAATGTTCTG	33689	CTCATCAAAGAAAACGTCCTC
5044	LIKGAAS	19367	TTGATTAAGGGGGCGGCTAGT	33690	CTCATCAAAGGAGCAGCAAGC
5045	LIKGSLD	19368	CTGATTAAGGGGTCTCTGGAT	33691	CTCATCAAAGGAAGCCTCGAC
5046	LIKPSVP	19369	TTGATTAAGCCGTCTGTTCCG	33692	CTCATCAAACCAAGCGTCCCA
5047	LIKSSEP	19370	CTTATTAAGTCTTCGGAGCCT	33693	CTCATCAAAAGCAGCGAACCA
5048	LIKSTLV	19371	CTTATTAAGAGTACGCTTGTT	33694	CTCATCAAAAGCACACTCGTC
5049	LIKTTHG	19372	CTTATTAAGACTACGCATGGT	33695	CTCATCAAAACAACACACGGA
5050	LILPNHS	19373	CTGATTCTGCCTAATCATTCG	33696	CTCATCCTCCCAAACCACAGC
5051	LIMRHDC	19374	TTGATTATGCGGCATGATTGT	33697	CTCATCATGAGACACGACTGC
5052	LINENPH	19375	TTGATTAATGAGAATCCGCAT	33698	CTCATCAACGAAAACCCACAC
5053	LINKISP	19376	TTGATTAATAAGATTTCTCCG	33699	CTCATCAACAAAATCAGCCCA
5054	LINPEMY	19377	CTTATTAATCCGGAGATGTAT	33700	CTCATCAACCCAGAAATGTAC
5055	LIPPHHD	19378	CTTATTCCGCCTCATCATGAT	33701	CTCATCCCACCACACCACGAC
5056	LIPTVMN	19379	CTGATTCCGACTGTGATGAAT	33702	CTCATCCCAACAGTCATGAAC
5057	LIQEVLQ	19380	CTGATTCAGGAGGTTCTTCAG	33703	CTCATCCAAGAAGTCCTCCAA
5058	LIQISQQ	19381	CTTATTCAGATTAGTCAGCAG	33704	CTCATCCAAATCAGCCAACAA
5059	LIQNQGT	19382	CTGATTCAGAATCAGGGTACG	33705	CTCATCCAAAACCAAGGAACA
5060	LIREQNP	19383	TTGATTCGGGAGCAGAATCCT	33706	CTCATCAGAGAACAAAACCCA
5061	LIRLSDN	19384	CTGATTCGTTTGAGTGATAAT	33707	CTCATCAGACTCAGCGACAAC
5062	LIRSDTI	19385	TTGATTCGGTCTGATACTATT	33708	CTCATCAGAAGCGACACAATC
5063	LIRSIPP	19386	TTGATTCGTTCGATTCCGCCG	33709	CTCATCAGAAGCATCCCACCA
5064	LISASHI	19387	TTGATTTCGGCTAGTCATATT	33710	CTCATCAGCGCAAGCCACATC
5065	LISDASS	19388	CTTATTTCGGATGCGAGTTCT	33711	CTCATCAGCGACGCAAGCAGC
5066	LISPTVT	19389	TTGATTTCGCCGACTGTTACG	33712	CTCATCAGCCCAACAGTCACA
5067	LISREVT	19390	CTGATTTCGCGTGAGGTTACT	33713	CTCATCAGCAGAGAAGTCACA
5068	LISRVPD	19391	CTGATTTCTCGTGTGCCGGAT	33714	CTCATCAGCAGAGTCCCAGAC
5069	LITAALA	19392	TTGATTACTGCTGCGCTGGCG	33715	CTCATCACAGCAGCACTCGCA
5070	LITGHST	19393	CTGATTACGGGGCATAGTACT	33716	CTCATCACAGGACACAGCACA
5071	LITPGAS	19394	TTGATTACGCCTGGTGCGAGT	33717	CTCATCACACCAGGAGCAAGC
5072	LITPLPS	19395	TTGATTACGCCTCTGCCTAGT	33718	CTCATCACACCACTCCCAAGC
5073	LITSAAG	19396	TTGATTACGTCTGCGGCTGGT	33719	CTCATCACAAGCGCAGCAGGA
5074	LIVALKG	19397	CTGATTGTGGCTTTGAAGGGT	33720	CTCATCGTCGCACTCAAAGGA

5075	LIVEQAR	19398	TTGATTGTTGAGCAGGCGCGG	33721	CTCATCGTCGAACAAGCAAGA
5076	LIVTENK	19399	CTGATTGTGACTGAGAATAAG	33722	CTCATCGTCACAGAAAACAAA
5077	LKAGSSS	19400	CTGAAGGCTGGTAGTTCGTCT	33723	CTCAAAGCAGGAAGCAGCAGC
5078	LKAGTYG	19401	TTGAAGGCTGGTACGTATGGG	33724	CTCAAAGCAGGAACATACGGA
5079	LKAIPYG	19402	CTGAAGGCGATTCCTTATGGG	33725	CTCAAAGCAATCCCATACGGA
5080	LKAQVEL	19403	CTTAAGGCGCAGGTTGAGCTT	33726	CTCAAAGCACAAGTCGAACTC
5081	LKATITS	19404	TTGAAGGCGACTATTACGTCT	33727	CTCAAAGCAACAATCACAAGC
5082	LKDGRAS	19405	CTGAAGGATGGTAGGGCTTCG	33728	CTCAAAGACGGAAGAGCAAGC
5083	LKDMRLT	19406	CTTAAGGATATGCGTTTGACG	33729	CTCAAAGACATGAGACTCACA
5084	LKDPARL	19407	CTGAAGGATCCGGCGCGTCTT	33730	CTCAAAGACCCAGCAAGACTC
5085	LKDPTAW	19408	TTGAAGGATCCGACTGCTTGG	33731	CTCAAAGACCCAACAGCATGG
5086	LKDSLTC	19409	CTGAAGGATTCTCTGACTTGT	33732	CTCAAAGACAGCCTCACATGC
5087	LKDYGGA	19410	CTGAAGGATTATGGGGGTGCT	33733	CTCAAAGACTACGGAGGAGCA
5088	LKEIAGL	19411	CTGAAGGAGATTGCTGGTCTG	33734	CTCAAAGAAATCGCAGGACTC
5089	LKFSESK	19412	CTGAAGTTTTCTGAGTCTAAG	33735	CTCAAATTCAGCGAAAGCAAA
5090	LKGAVVV	19413	CTGAAGGGGGCTGTGGTTGTT	33736	CTCAAAGGAGCAGTCGTCGTC
5091	LKGDAGY	19414	CTTAAGGGTGATGCTGGGTAT	33737	CTCAAAGGAGACGCAGGATAC
5092	LKGGADT	19415	CTTAAGGGGGGTGCTGATACG	33738	CTCAAAGGAGGAGCAGACACA
5093	LKGMTGL	19416	CTGAAGGGTATGACTGGGCTG	33739	CTCAAAGGAATGACAGGACTC
5094	LKGPNAV	19417	CTGAAGGGTCCGAATGCTGTT	33740	CTCAAAGGACCAAACGCAGTC
5095	LKGYIDS	19418	CTGAAGGGGTATATTGATTCT	33741	CTCAAAGGATACATCGACAGC
5096	LKHQLLA	19419	CTGAAGCATCAGCTGCTTGCT	33742	CTCAAACACCAACTCCTCGCA
5097	LKHSLPD	19420	CTTAAGCATTCTCTGCCTGAT	33743	CTCAAACACAGCCTCCCAGAC
5098	LKIGTVT	19421	TTGAAGATTGGTACTGTTACG	33744	CTCAAAATCGGAACAGTCACA
5099	LKLAPNV	19422	TTGAAGCTTGCTCCTAATGTG	33745	CTCAAACTCGCACCAAACGTC
5100	LKLDEGL	19423	CTGAAGTTGGATGAGGGTCTG	33746	CTCAAACTCGACGAAGGACTC
5101	LKLRASE	19424	CTTAAGTTGCGTGCGTCGGAG	33747	CTCAAACTCAGAGCAAGCGAA
5102	LKMSSTP	19425	TTGAAGATGTCGTCTACGCCG	33748	CTCAAAATGAGCAGCACACCA
5103	LKMVDNV	19426	CTGAAGATGGTTGATAATGTT	33749	CTCAAAATGGTCGACAACGTC
5104	LKNGSMV	19427	CTTAAGAATGGTAGTATGGTG	33750	CTCAAAAACGGAAGCATGGTC
5105	LKNPLPS	19428	TTGAAGAATCCTCTTCCGTCT	33751	CTCAAAAACCCACTCCCAAGC
5106	LKNPSNV	19429	TTGAAGAATCCTAGTAATGTT	33752	CTCAAAAACCCAAGCAACGTC
5107	LKPDMTR	19430	CTGAAGCCTGATATGACGCGG	33753	CTCAAACCAGACATGACAAGA
5108	LKPDRPD	19431	TTGAAGCCTGATCGTCCTGAT	33754	CTCAAACCAGACAGACCAGAC
5109	LKPNEIS	19432	CTGAAGCCGAATGAGATTTCT	33755	CTCAAACCAAACGAAATCAGC
5110	LKPSPIP	19433	CTGAAGCCTTCGCCTATTCCT	33756	CTCAAACCAAGCCCAATCCCA
5111	LKPSSYV	19434	CTGAAGCCGAGTTCGTATGTT	33757	CTCAAACCAAGCAGCTACGTC
5112	LKPVPSL	19435	CTTAAGCCGGTGCCTAGTCTG	33758	CTCAAACCAGTCCCAAGCCTC
5113	LKQIDLG	19436	CTGAAGCAGATTGATCTTGGG	33759	CTCAAACAAATCGACCTCGGA
5114	LKQPTQC	19437	TTGAAGCAGCCTACGCAGTGT	33760	CTCAAACAACCAACACAATGC
5115	LKREFDY	19438	TTGAAGCGGGAGTTTGATTAT	33761	CTCAAAAGAGAATTCGACTAC
5116	LKSATTI	19439	CTTAAGTCTGCGACGACTATT	33762	CTCAAAAGCGCAACAACAATC
5117	LKSGVSP	19440	CTGAAGTCTGGTGTGTCGCCG	33763	CTCAAAAGCGGAGTCAGCCCA
5118	LKSPSTP	19441	CTGAAGTCTCCGAGTACGCCT	33764	CTCAAAAGCCCAAGCACACCA
5119	LKSQLSD	19442	CTGAAGTCGCAGCTGAGTGAT	33765	CTCAAAAGCCAACTCAGCGAC

5120	LKSQSFT	19443	TTGAAGTCGCAGTCGTTTACT	33766	CTCAAAAGCCAAAGCTTCACA
5121	LKSTLMP	19444	CTTAAGTCTACGCTTATGCCT	33767	CTCAAAAGCACACTCATGCCA
5122	LKSTPPG	19445	CTGAAGTCGACTCCTCCGGGG	33768	CTCAAAAGCACACCACCAGGA
5123	LKSTSQV	19446	CTGAAGAGTACGAGTCAGGTT	33769	CTCAAAAGCACAAGCCAAGTC
5124	LKTGRDS	19447	CTTAAGACGGGGCGTGATTCT	33770	CTCAAAACAGGAAGAGACAGC
5125	LKTGYMP	19448	CTGAAGACGGGTTATATGCCG	33771	CTCAAAACAGGATACATGCCA
5126	LKTLLKT	19449	CTGAAGACGCTGCTTAAGACG	33772	CTCAAAACACTCCTCAAAACA
5127	LKTNERV	19450	CTGAAGACGAATGAGCGGGTT	33773	CTCAAAACAAACGAAAGAGTC
5128	LKTSGVI	19451	CTTAAGACTAGTGGTGTGATT	33774	CTCAAAACAAGCGGAGTCATC
5129	LKTSNRD	19452	CTTAAGACTAGTAATCGTGAT	33775	CTCAAAACAAGCAACAGAGAC
5130	LKTTNPP	19453	TTGAAGACGACTAATCCTCCG	33776	CTCAAAACAACAAACCCACCA
5131	LKTVHSD	19454	CTTAAGACTGTTCATTCGGAT	33777	CTCAAAACAGTCCACAGCGAC
5132	LKVEMSP	19455	CTGAAGGTGGAGATGAGTCCG	33778	CTCAAAGTCGAAATGAGCCCA
5133	LKWEHTS	19456	TTGAAGTGGGAGCATACTTCT	33779	CTCAAATGGGAACACACAAGC
5134	LKWGPPD	19457	CTGAAGTGGGGTCCGCCTGAT	33780	CTCAAATGGGGACCACCAGAC
5135	LKYNIPV	19458	CTGAAGTATAATATTCCTGTT	33781	CTCAAATACAACATCCCAGTC
5136	LLAAMGP	19459	TTGCTTGCTGCGATGGGTCCG	33782	CTCCTCGCAGCAATGGGACCA
5137	LLAFEKQ	19460	TTGTTGGCTTTTGAGAAGCAG	33783	CTCCTCGCATTCGAAAAACAA
5138	LLAGHHG	19461	CTTCTGGCGGGTCATCATGGT	33784	CTCCTCGCAGGACACCACGGA
5139	LLARGVN	19462	CTGCTGGCTCGTGGTGTTAAT	33785	CTCCTCGCAAGAGGAGTCAAC
5140	LLATSLT	19463	TTGCTTGCGACTTCGCTGACT	33786	CTCCTCGCAACAAGCCTCACA
5141	LLDGRAR	19464	CTGCTTGATGGTCGTGCGAGG	33787	CTCCTCGACGGAAGAGCAAGA
5142	LLDKERE	19465	CTTTTGGATAAGGAGCGTGAG	33788	CTCCTCGACAAAGAAAGAGAA
5143	LLDQDFF	19466	CTTTTGGATCAGGATTTTTTT	33789	CTCCTCGACCAAGACTTCTTC
5144	LLDTGVP	19467	CTGCTGGATACGGGTGTTCCT	33790	CTCCTCGACACAGGAGTCCCA
5145	LLEKGQS	19468	TTGCTGGAGAAGGGTCAGAGT	33791	CTCCTCGAAAAAGGACAAAGC
5146	LLERSYP	19469	CTTTTGGAGCGTAGTTATCCG	33792	CTCCTCGAAAGAAGCTACCCA
5147	LLEVPIR	19470	CTGCTGGAGGTGCCGATTCGG	33793	CTCCTCGAAGTCCCAATCAGA
5148	LLFKSSS	19471	CTGTTGTTTAAGTCTTCGTCG	33794	CTCCTCTTCAAAAGCAGCAGC
5149	LLGARHL	19472	CTTCTGGGGGCTCGGCATCTT	33795	CTCCTCGGAGCAAGACACCTC
5150	LLGASSA	19473	CTGCTTGGTGCGAGTTCTGCG	33796	CTCCTCGGAGCAAGCAGCGCA
5151	LLGHAAS	19474	CTTCTTGGTCATGCGGCGAGT	33797	CTCCTCGGACACGCAGCAAGC
5152	LLGPDPS	19475	CTGTTGGGTCCTGATCCGTCT	33798	CTCCTCGGACCAGACCCAAGC
5153	LLGPLQG	19476	CTGCTGGGGCCTTTGCAGGGG	33799	CTCCTCGGACCACTCCAAGGA
5154	LLGRLQP	19477	TTGTTGGGTCGTCTGCAGCCT	33800	CTCCTCGGAAGACTCCAACCA
5155	LLGRSTG	19478	CTGTTGGGTCGTTCTACGGGG	33801	CTCCTCGGAAGAAGCACAGGA
5156	LLGSRPS	19479	TTGCTTGGTAGTCGTCCGAGT	33802	CTCCTCGGAAGCAGACCAAGC
5157	LLGVLHP	19480	CTTCTGGGGGTTTTGCATCCG	33803	CTCCTCGGAGTCCTCCACCCA
5158	LLGVTNP	19481	TTGCTTGGGGTGACTAATCCT	33804	CTCCTCGGAGTCACAAACCCA
5159	LLHLGQT	19482	CTTCTTCATCTGGGTCAGACG	33805	CTCCTCCACCTCGGACAAACA
5160	LLHPAPR	19483	TTGCTGCATCCTGCTCCGCGT	33806	CTCCTCCACCCAGCACCAAGA
5161	LLHPEAI	19484	TTGCTTCATCCGGAGGCTATT	33807	CTCCTCCACCCAGAAGCAATC
5162	LLHSSSQ	19485	TTGCTTCATTCGTCGTCTCAG	33808	CTCCTCCACAGCAGCAGCCAA
5163	LLHTQGN	19486	CTTCTGCATACTCAGGGGAAT	33809	CTCCTCCACACACAAGGAAAC
5164	LLHTVSE	19487	CTTCTTCATACGGTGAGTGAG	33810	CTCCTCCACACAGTCAGCGAA

5165	LLHVPRE	19488	CTGCTGCATGTTCCGCGTGAG	33811	CTCCTCCACGTCCCAAGAGAA
5166	LLICGEH	19489	CTGCTTATTTGTGGGGAGCAT	33812	CTCCTCATCTGCGGAGAACAC
5167	LLKGFSV	19490	TTGTTGAAGGGTTTTTCGGTT	33813	CTCCTCAAAGGATTCAGCGTC
5168	LLKPAAP	19491	CTGTTGAAGCCGGCTGCTCCT	33814	CTCCTCAAACCAGCAGCACCA
5169	LLKSPVP	19492	CTTCTGAAGAGTCCTGTGCCT	33815	CTCCTCAAAAGCCCAGTCCCA
5170	LLLAPTS	19493	TTGTTGCTGGCTCCGACTTCG	33816	CTCCTCCTCGCACCAACAAGC
5171	LLLARTV	19494	CTGCTTCTTGCGCGGACGGTT	33817	CTCCTCCTCGCAAGAACAGTC
5172	LLLDDHT	19495	CTGCTTCTTGATGATCATACG	33818	CTCCTCCTCGACGACCACACA
5173	LLLPARG	19496	CTTTTGTTGCCGGCTCGTGGT	33819	CTCCTCCTCCCAGCAAGAGGA
5174	LLLQARA	19497	CTTTTGCTTCAGGCTCGTGCG	33820	CTCCTCCTCCAAGCAAGAGCA
5175	LLLQKGP	19498	TTGTTGTTGCAGAAGGGTCCT	33821	CTCCTCCTCCAAAAAGGACCA
5176	LLLRADG	19499	CTTCTTTTGCGGGCTGATGGT	33822	CTCCTCCTCAGAGCAGACGGA
5177	LLLSVGT	19500	CTGCTGCTGTCTGTTGGTACT	33823	CTCCTCCTCAGCGTCGGAACA
5178	LLLTGVA	19501	CTTCTGCTTACGGGGGTTGCG	33824	CTCCTCCTCACAGGAGTCGCA
5179	LLMPSGL	19502	CTTTTGATGCCGTCGGGGCTT	33825	CTCCTCATGCCAAGCGGACTC
5180	LLNDAYV	19503	TTGCTTAATGATGCTTATGTG	33826	CTCCTCAACGACGCATACGTC
5181	LLNGHEA	19504	TTGTTGAATGGGCATGAGGCT	33827	CTCCTCAACGGACACGAAGCA
5182	LLNMART	19505	CTGTTGAATATGGCTAGGACT	33828	CTCCTCAACATGGCAAGAACA
5183	LLNTSSA	19506	CTGTTGAATACGAGTAGTGCT	33829	CTCCTCAACACAAGCAGCGCA
5184	LLPAERA	19507	TTGTTGCCGGCTGAGAGGGCT	33830	CTCCTCCCAGCAGAAAGAGCA
5185	LLPEYSR	19508	CTTCTTCCTGAGTATTCGCGT	33831	CTCCTCCCAGAATACAGCAGA
5186	LLPGRTD	19509	TTGTTGCCGGGGCGTACTGAT	33832	CTCCTCCCAGGAAGAACAGAC
5187	LLPHEGT	19510	TTGTTGCCGCATGAGGGGACG	33833	CTCCTCCCACACGAAGGAACA
5188	LLPKASS	19511	CTGTTGCCTAAGGCGTCGTCG	33834	CTCCTCCCAAAAGCAAGCAGC
5189	LLPLAPR	19512	CTTTTGCCTCTGGCTCCGAGG	33835	CTCCTCCCACTCGCACCAAGA
5190	LLPNPPT	19513	CTGTTGCCGAATCCGCCTACG	33836	CTCCTCCCAAACCCACCAACA
5191	LLPNQSF	19514	CTTCTGCCTAATCAGAGTTTT	33837	CTCCTCCCAAACCAAAGCTTC
5192	LLPNTPP	19515	CTTTTGCCTAATACGCCTCCG	33838	CTCCTCCCAAACACACCACCA
5193	LLPPRDP	19516	CTGCTTCCTCCGCGTGATCCG	33839	CTCCTCCCACCAAGAGACCCA
5194	LLPPSSS	19517	TTGCTGCCGCCGTCGAGTTCG	33840	CTCCTCCCACCAAGCAGCAGC
5195	LLPQFRS	19518	TTGCTTCCGCAGTTTAGGAGT	33841	CTCCTCCCACAATTCAGAAGC
5196	LLPRTHY	19519	TTGTTGCCGCGTACGCATTAT	33842	CTCCTCCCAAGAACACACTAC
5197	LLPSLAS	19520	CTTCTGCCTTCGTTGGCGTCT	33843	CTCCTCCCAAGCCTCGCAAGC
5198	LLPSRGA	19521	TTGCTGCCGTCGCGTGGGGCT	33844	CTCCTCCCAAGCAGAGGAGCA
5199	LLPTSKL	19522	TTGCTGCCTACTAGTAAGCTG	33845	CTCCTCCCAACAAGCAAACTC
5200	LLPVLSE	19523	CTTCTGCCTGTGTTGTCTGAG	33846	CTCCTCCCAGTCCTCAGCGAA
5201	LLQPSVP	19524	CTTCTTCAGCCGTCGGTTCCT	33847	CTCCTCCAACCAAGCGTCCCA
5202	LLQQPEW	19525	CTGCTTCAGCAGCCTGAGTGG	33848	CTCCTCCAACAACCAGAATGG
5203	LLQRSLS	19526	CTTCTTCAGCGTTCTCTTTCT	33849	CTCCTCCAAAGAAGCCTCAGC
5204	LLQTLKP	19527	CTTCTGCAGACGCTTAAGCCG	33850	CTCCTCCAAACACTCAAACCA
5205	LLRGAVA	19528	CTTCTGCGTGGGGCGGTGGCG	33851	CTCCTCAGAGGAGCAGTCGCA
5206	LLRGDAA	19529	CTGCTGAGGGGTGATGCGGCG	33852	CTCCTCAGAGGAGACGCAGCA
5207	LLRKDEA	19530	TTGTTGCGTAAGGATGAGGCT	33853	CTCCTCAGAAAAGACGAAGCA
5208	LLRNNPH	19531	CTGCTTCGGAATAATCCGCAT	33854	CTCCTCAGAAACAACCCACAC
5209	LLRNVLP	19532	CTTTTGCGTAATGTGCTGCCT	33855	CTCCTCAGAAACGTCCTCCCA

5210	LLRSQSA	19533	TTGCTTAGGTCGCAGAGTGCG	33856	CTCCTCAGAAGCCAAAGCGCA
5211	LLRTPSS	19534	CTTCTTAGGACTCCTTCTTCT	33857	CTCCTCAGAACACCAAGCAGC
5212	LLRVPNP	19535	CTGTTGCGGGTTCCGAATCCG	33858	CTCCTCAGAGTCCCAAACCCA
5213	LLSAADR	19536	CTTCTTAGTGCTGCGGATCGG	33859	CTCCTCAGCGCAGCAGACAGA
5214	LLSAPYT	19537	CTGCTGTCGGCGCCGTATACT	33860	CTCCTCAGCGCACCATACACA
5215	LLSASTS	19538	CTGCTGAGTGCTTCTACTTCG	33861	CTCCTCAGCGCAAGCACAAGC
5216	LLSDSAR	19539	CTTTTGTCTGATAGTGCTAGG	33862	CTCCTCAGCGACAGCGCAAGA
5217	LLSFTTD	19540	CTGTTGTCGTTTACTACGGAT	33863	CTCCTCAGCTTCACAACAGAC
5218	LLSGALQ	19541	CTGTTGTCGGGTGCGCTTCAG	33864	CTCCTCAGCGGAGCACTCCAA
5219	LLSGRVT	19542	CTTTTGAGTGGGCGGGTTACT	33865	CTCCTCAGCGGAAGAGTCACA
5220	LLSKGHS	19543	CTTCTTTCTAAGGGTCATTCG	33866	CTCCTCAGCAAAGGACACAGC
5221	LLSMRTP	19544	TTGCTGAGTATGCGTACGCCT	33867	CTCCTCAGCATGAGAACACCA
5222	LLSPDEY	19545	CTTTTGTCTCCTGATGAGTAT	33868	CTCCTCAGCCCAGACGAATAC
5223	LLSPGPL	19546	CTGCTTAGTCCTGGTCCTCTT	33869	CTCCTCAGCCCAGGACCACTC
5224	LLSRVHD	19547	CTGCTGAGTCGTGTGCATGAT	33870	CTCCTCAGCAGAGTCCACGAC
5225	LLSTAVS	19548	CTTCTTTCTACGGCTGTTAGT	33871	CTCCTCAGCACAGCAGTCAGC
5226	LLSTDGS	19549	CTGCTGTCTACTGATGGGTCG	33872	CTCCTCAGCACAGACGGAAGC
5227	LLSVHEM	19550	CTGCTTTCTGTTCATGAGATG	33873	CTCCTCAGCGTCCACGAAATG
5228	LLTDECT	19551	CTTCTTACTGATGAGTGTACG	33874	CTCCTCACAGACGAATGCACA
5229	LLTDRRL	19552	CTTCTGACTGATCGGCGTCTG	33875	CTCCTCACAGACAGAAGACTC
5230	LLTHFSS	19553	TTGCTGACGCATTTTTCTTCG	33876	CTCCTCACACACTTCAGCAGC
5231	LLTIGKP	19554	TTGTTGACTATTGGGAAGCCG	33877	CTCCTCACAATCGGAAAACCA
5232	LLTLSEV	19555	CTGTTGACTCTGTCTGAGGTG	33878	CTCCTCACACTCAGCGAAGTC
5233	LLTLSTP	19556	CTGCTGACGCTGAGTACTCCG	33879	CTCCTCACACTCAGCACACCA
5234	LLTNAIP	19557	CTTCTTACTAATGCTATTCCG	33880	CTCCTCACAAACGCAATCCCA
5235	LLTPYNP	19558	CTGTTGACTCCGTATAATCCT	33881	CTCCTCACACCATACAACCCA
5236	LLTRSTE	19559	CTGTTGACTCGTTCTACTGAG	33882	CTCCTCACAAGAAGCACAGAA
5237	LLVHKVV	19560	TTGCTGGTTCATAAGGTTGTT	33883	CTCCTCGTCCACAAAGTCGTC
5238	LLVRHRD	19561	CTTCTGGTGAGGCATCGTGAT	33884	CTCCTCGTCAGACACAGAGAC
5239	LLVRNTD	19562	CTTCTGGTGCGTAATACTGAT	33885	CTCCTCGTCAGAAACACAGAC
5240	LLVSENS	19563	CTTTTGGTTTCTGAGAATTCT	33886	CTCCTCGTCAGCGAAAACAGC
5241	LLVTDKM	19564	TTGCTGGTTACTGATAAGATG	33887	CTCCTCGTCACAGACAAAATG
5242	LLVVPSR	19565	TTGTTGGTGGTGCCTTCGCGT	33888	CTCCTCGTCGTCCCAAGCAGA
5243	LLYAERP	19566	TTGCTTTATGCGGAGCGTCCT	33889	CTCCTCTACGCAGAAAGACCA
5244	LLYQNSS	19567	TTGTTGTATCAGAATTCGTCG	33890	CTCCTCTACCAAAACAGCAGC
5245	LLYSTDK	19568	CTTCTTTATAGTACTGATAAG	33891	CTCCTCTACAGCACAGACAAA
5246	LMAHSQL	19569	CTGATGGCTCATTCTCAGCTT	33892	CTCATGGCACACAGCCAACTC
5247	LMAIHKP	19570	CTTATGGCTATTCATAAGCCG	33893	CTCATGGCAATCCACAAACCA
5248	LMATRVP	19571	TTGATGGCTACTCGTGTGCCT	33894	CTCATGGCAACAAGAGTCCCA
5249	LMDSRKY	19572	TTGATGGATTCTCGTAAGTAT	33895	CTCATGGACAGCAGAAAATAC
5250	LMEATFK	19573	TTGATGGAGGCTACTTTTAAG	33896	CTCATGGAAGCAACATTCAAA
5251	LMEHIIE	19574	CTGATGGAGCATATTATTGAG	33897	CTCATGGAACACATCATCGAA
5252	LMENHMA	19575	TTGATGGAGAATCATATGGCT	33898	CTCATGGAAAACCACATGGCA
5253	LMGQGRT	19576	TTGATGGGGCAGGGTAGGACG	33899	CTCATGGGACAAGGAAGAACA
5254	LMGQVAG	19577	CTGATGGGGCAGGTTGCTGGG	33900	CTCATGGGACAAGTCGCAGGA

5255	LMKPSAG	19578	CTTATGAAGCCTAGTGCTGGT	33901	CTCATGAAACCAAGCGCAGGA
5256	LMKRVET	19579	TTGATGAAGCGTGTGGAGACT	33902	CTCATGAAAAGAGTCGAAACA
5257	LMLARND	19580	CTGATGCTTGCTCGTAATGAT	33903	CTCATGCTCGCAAGAAACGAC
5258	LMLRSSQ	19581	CTGATGCTGCGTTCTTCGCAG	33904	CTCATGCTCAGAAGCAGCCAA
5259	LMNGGST	19582	CTGATGAATGGTGGGTCGACT	33905	CTCATGAACGGAGGAAGCACA
5260	LMNSAIA	19583	TTGATGAATTCGGCGATTGCT	33906	CTCATGAACAGCGCAATCGCA
5261	LMPSMRP	19584	CTTATGCCTTCGATGCGTCCT	33907	CTCATGCCAAGCATGAGACCA
5262	LMQPKSA	19585	TTGATGCAGCCGAAGTCTGCT	33908	CTCATGCAACCAAAAAGCGCA
5263	LMRISTA	19586	CTGATGAGGATTTCTACTGCG	33909	CTCATGAGAATCAGCACAGCA
5264	LMRPAEL	19587	TTGATGCGGCCGGCGGAGCTT	33910	CTCATGAGACCAGCAGAACTC
5265	LMRTNPD	19588	TTGATGCGTACTAATCCGGAT	33911	CTCATGAGAACAAACCCAGAC
5266	LMSLTTV	19589	TTGATGTCGCTGACGACTGTT	33912	CTCATGAGCCTCACAACAGTC
5267	LMSPQSP	19590	CTTATGTCGCCTCAGAGTCCG	33913	CTCATGAGCCCACAAAGCCCA
5268	LMSQELR	19591	CTTATGTCGCAGGAGCTGCGT	33914	CTCATGAGCCAAGAACTCAGA
5269	LMSQTQR	19592	CTGATGTCTCAGACTCAGCGT	33915	CTCATGAGCCAAACACAAAGA
5270	LMSSKPP	19593	CTTATGTCTTCTAAGCCTCCT	33916	CTCATGAGCAGCAAACCACCA
5271	LMSTAEP	19594	CTGATGTCTACGGCTGAGCCT	33917	CTCATGAGCACAGCAGAACCA
5272	LMSTASP	19595	TTGATGTCGACGGCTTCGCCT	33918	CTCATGAGCACAGCAAGCCCA
5273	LMTGITI	19596	TTGATGACTGGTATTACGATT	33919	CTCATGACAGGAATCACAATC
5274	LMTGVPL	19597	TTGATGACTGGTGTTCCTTTG	33920	CTCATGACAGGAGTCCCACTC
5275	LMTNAQL	19598	TTGATGACTAATGCTCAGCTG	33921	CTCATGACAAACGCACAACTC
5276	LMTNPVP	19599	TTGATGACTAATCCTGTTCCG	33922	CTCATGACAAACCCAGTCCCA
5277	LMTSGHK	19600	CTGATGACTTCGGGTCATAAG	33923	CTCATGACAAGCGGACACAAA
5278	LMTSNGA	19601	TTGATGACTTCTAATGGGGCG	33924	CTCATGACAAGCAACGGAGCA
5279	LMTTHVD	19602	CTTATGACTACGCATGTTGAT	33925	CTCATGACAACACACGTCGAC
5280	LMVESHV	19603	CTGATGGTTGAGTCTCATGTT	33926	CTCATGGTCGAAAGCCACGTC
5281	LMVGRKL	19604	CTTATGGTGGGTCGTAAGTTG	33927	CTCATGGTCGGAAGAAAACTC
5282	LNANALA	19605	CTGAATGCGAATGCGTTGGCT	33928	CTCAACGCAAACGCACTCGCA
5283	LNAPGRT	19606	CTGAATGCGCCGGGTCGTACT	33929	CTCAACGCACCAGGAAGAACA
5284	LNAPNPM	19607	CTTAATGCGCCTAATCCTATG	33930	CTCAACGCACCAAACCCAATG
5285	LNAQVST	19608	CTGAATGCTCAGGTGAGTACG	33931	CTCAACGCACAAGTCAGCACA
5286	LNASTKT	19609	CTTAATGCTTCGACTAAGACT	33932	CTCAACGCAAGCACAAAAACA
5287	LNATDGK	19610	CTTAATGCTACGGATGGGAAG	33933	CTCAACGCAACAGACGGAAAA
5288	LNDDAWS	19611	CTTAATGATGATGCGTGGTCG	33934	CTCAACGACGACGCATGGAGC
5289	LNDVLTQ	19612	CTTAATGATGTTTTGACGCAG	33935	CTCAACGACGTCCTCACACAA
5290	LNEITRS	19613	CTTAATGAGATTACGCGGAGT	33936	CTCAACGAAATCACAAGAAGC
5291	LNELQFQ	19614	CTTAATGAGTTGCAGTTTCAG	33937	CTCAACGAACTCCAATTCCAA
5292	LNERPRS	19615	CTGAATGAGAGGCCGCGTAGT	33938	CTCAACGAAAGACCAAGAAGC
5293	LNGEYLK	19616	TTGAATGGTGAGTATTTGAAG	33939	CTCAACGGAGAATACCTCAAA
5294	LNGFTAT	19617	CTGAATGGTTTTACTGCGACG	33940	CTCAACGGATTCACAGCAACA
5295	LNGRRAE	19618	TTGAATGGTCGTAGGGCTGAG	33941	CTCAACGGAAGAAGAGCAGAA
5296	LNGSYIQ	19619	TTGAATGGGTCTTATATTCAG	33942	CTCAACGGAAGCTACATCCAA
5297	LNHEKDG	19620	CTTAATCATGAGAAGGATGGT	33943	CTCAACCACGAAAAAGACGGA
5298	LNHNPGL	19621	CTGAATCATAATCCTGGTTTG	33944	CTCAACCACAACCCAGGACTC
5299	LNHNSLR	19622	CTGAATCATAATAGTTTGCGT	33945	CTCAACCACAACAGCCTCAGA

5300	LNHTRPL	19623	TTGAATCATACGAGGCCGTTG	33946	CTCAACCACACAAGACCACTC
5301	LNIPSDP	19624	TTGAATATTCCTAGTGATCCT	33947	CTCAACATCCCAAGCGACCCA
5302	LNITTSG	19625	CTTAATATTACGACTTCGGGT	33948	CTCAACATCACAACAAGCGGA
5303	LNKEFAS	19626	TTGAATAAGGAGTTTGCGAGT	33949	CTCAACAAAGAATTCGCAAGC
5304	LNKNSPV	19627	TTGAATAAGAATTCGCCGGTG	33950	CTCAACAAAAACAGCCCAGTC
5305	LNKQPFV	19628	CTTAATAAGCAGCCGTTTGTG	33951	CTCAACAAACAACCATTCGTC
5306	LNKRAPD	19629	TTGAATAAGCGTGCTCCTGAT	33952	CTCAACAAAAGAGCACCAGAC
5307	LNKSSTG	19630	CTTAATAAGTCTTCGACGGGT	33953	CTCAACAAAAGCAGCACAGGA
5308	LNLARPA	19631	CTTAATCTGGCGAGGCCGGCG	33954	CTCAACCTCGCAAGACCAGCA
5309	LNLELYD	19632	CTGAATTTGGAGTTGTATGAT	33955	CTCAACCTCGAACTCTACGAC
5310	LNLGRPD	19633	CTGAATCTGGGGAGGCCGGAT	33956	CTCAACCTCGGAAGACCAGAC
5311	LNLHAPT	19634	CTTAATCTGCATGCGCCGACG	33957	CTCAACCTCCACGCACCAACA
5312	LNLPNHG	19635	TTGAATCTTCCGAATCATGGT	33958	CTCAACCTCCCAAACCACGGA
5313	LNLQSQS	19636	CTGAATCTTCAGTCTCAGAGT	33959	CTCAACCTCCAAAGCCAAAGC
5314	LNLSGLV	19637	CTTAATCTTAGTGGGCTTGTT	33960	CTCAACCTCAGCGGACTCGTC
5315	LNLTSVS	19638	TTGAATCTTACGTCGGTTAGT	33961	CTCAACCTCACAAGCGTCAGC
5316	LNMSEPR	19639	CTGAATATGTCTGAGCCGCGT	33962	CTCAACATGAGCGAACCAAGA
5317	LNMSPTG	19640	TTGAATATGAGTCCTACGGGT	33963	CTCAACATGAGCCCAACAGGA
5318	LNNHQFS	19641	TTGAATAATCATCAGTTTAGT	33964	CTCAACAACCACCAATTCAGC
5319	LNNLPSR	19642	TTGAATAATCTGCCGAGTCGT	33965	CTCAACAACCTCCCAAGCAGA
5320	LNPAARI	19643	CTTAATCCGGCTGCGCGTATT	33966	CTCAACCCAGCAGCAAGAATC
5321	LNPAKAS	19644	CTTAATCCTGCGAAGGCTAGT	33967	CTCAACCCAGCAAAAGCAAGC
5322	LNPHENG	19645	CTTAATCCTCATGAGAATGGG	33968	CTCAACCCACACGAAAACGGA
5323	LNPSRVP	19646	CTTAATCCTTCTAGGGTGCCG	33969	CTCAACCCAAGCAGAGTCCCA
5324	LNPVNVM	19647	TTGAATCCTGTTAATGTGATG	33970	CTCAACCCAGTCAACGTCATG
5325	LNQGNMT	19648	TTGAATCAGGGTAATATGACG	33971	CTCAACCAAGGAAACATGACA
5326	LNQHVPV	19649	TTGAATCAGCATGTTCCTGTT	33972	CTCAACCAACACGTCCCAGTC
5327	LNQSRST	19650	TTGAATCAGTCGCGGTCTACT	33973	CTCAACCAAAGCAGAAGCACA
5328	LNQSVRV	19651	CTGAATCAGTCGGTGAGGGTT	33974	CTCAACCAAAGCGTCAGAGTC
5329	LNRADVD	19652	TTGAATCGTGCTGATGTTGAT	33975	CTCAACAGAGCAGACGTCGAC
5330	LNRDMSY	19653	CTGAATAGGGATATGTCTTAT	33976	CTCAACAGAGACATGAGCTAC
5331	LNREQAS	19654	CTTAATCGGGAGCAGGCGTCT	33977	CTCAACAGAGAACAAGCAAGC
5332	LNRSSMP	19655	CTGAATAGGTCGAGTATGCCG	33978	CTCAACAGAAGCAGCATGCCA
5333	LNRTNPD	19656	CTTAATCGGACGAATCCGGAT	33979	CTCAACAGAACAAACCCAGAC
5334	LNRVTPS	19657	CTTAATCGGGTTACTCCGTCG	33980	CTCAACAGAGTCACACCAAGC
5335	LNSDAPY	19658	CTGAATTCGGATGCTCCGTAT	33981	CTCAACAGCGACGCACCATAC
5336	LNSLGTF	19659	TTGAATAGTCTGGGTACGTTT	33982	CTCAACAGCCTCGGAACATTC
5337	LNSPLIA	19660	CTGAATTCGCCTCTTATTGCG	33983	CTCAACAGCCCACTCATCGCA
5338	LNSQPGL	19661	CTTAATAGTCAGCCTGGTTTG	33984	CTCAACAGCCAACCAGGACTC
5339	LNSQRFG	19662	TTGAATAGTCAGCGGTTTGGT	33985	CTCAACAGCCAAAGATTCGGA
5340	LNSSHDA	19663	CTGAATTCTTCGCATGATGCT	33986	CTCAACAGCAGCCACGACGCA
5341	LNSSRSA	19664	CTGAATAGTTCTCGTTCTGCT	33987	CTCAACAGCAGCAGAAGCGCA
5342	LNSSSHG	19665	CTGAATTCGTCTTCGCATGGG	33988	CTCAACAGCAGCAGCCACGGA
5343	LNSTNPH	19666	TTGAATTCGACGAATCCGCAT	33989	CTCAACAGCACAAACCCACAC
5344	LNSVRNN	19667	CTTAATTCGGTTAGGAATAAT	33990	CTCAACAGCGTCAGAAACAAC

5345	LNTAALP	19668	CTTAATACGGCTGCTTTGCCG	33991	CTCAACACAGCAGCACTCCCA
5346	LNTHSYV	19669	CTGAATACTCATTCTTATGTG	33992	CTCAACACACACAGCTACGTC
5347	LNTKPFS	19670	CTGAATACTAAGCCGTTTTCG	33993	CTCAACACAAAACCATTCAGC
5348	LNTRQQT	19671	CTTAATACGAGGCAGCAGACT	33994	CTCAACACAAGACAACAAACA
5349	LNTRSLS	19672	TTGAATACGCGGTCTCTTTCT	33995	CTCAACACAAGAAGCCTCAGC
5350	LNVEVER	19673	CTTAATGTGGAGGTGGAGCGG	33996	CTCAACGTCGAAGTCGAAAGA
5351	LNVKSGL	19674	CTTAATGTTAAGTCTGGGCTG	33997	CTCAACGTCAAAAGCGGACTC
5352	LNVNIAP	19675	TTGAATGTTAATATTGCGCCG	33998	CTCAACGTCAACATCGCACCA
5353	LNVRESV	19676	TTGAATGTGCGTGAGAGTGTG	33999	CTCAACGTCAGAGAAAGCGTC
5354	LNVRRVA	19677	CTGAATGTGCGGAGGGTGGCT	34000	CTCAACGTCAGAAGAGTCGCA
5355	LNVRTDR	19678	CTTAATGTGCGTACGGATCGT	34001	CTCAACGTCAGAACAGACAGA
5356	LNVSGNA	19679	CTTAATGTGTCGGGGAATGCG	34002	CTCAACGTCAGCGGAAACGCA
5357	LNVSSTG	19680	CTTAATGTGTCTAGTACGGGT	34003	CTCAACGTCAGCAGCACAGGA
5358	LNVVSTY	19681	TTGAATGTTGTTAGTACTTAT	34004	CTCAACGTCGTCAGCACATAC
5359	LNYDPMT	19682	CTTAATTATGATCCGATGACG	34005	CTCAACTACGACCCAATGACA
5360	LNYGPAL	19683	CTGAATTATGGGCCGGCTCTG	34006	CTCAACTACGGACCAGCACTC
5361	LNYHASV	19684	CTTAATTATCATGCGAGTGTG	34007	CTCAACTACCACGCAAGCGTC
5362	LPAGNTS	19685	TTGCCTGCGGGTAATACGTCT	34008	CTCCCAGCAGGAAACACAAGC
5363	LPAGNYH	19686	CTTCCTGCGGGTAATTATCAT	34009	CTCCCAGCAGGAAACTACCAC
5364	LPANNSI	19687	CTGCCTGCTAATAATTCGATT	34010	CTCCCAGCAAACAACAGCATC
5365	LPAPKPA	19688	TTGCCTGCTCCTAAGCCTGCG	34011	CTCCCAGCACCAAAACCAGCA
5366	LPARLAT	19689	CTTCCTGCGCGTTTGGCTACT	34012	CTCCCAGCAAGACTCGCAACA
5367	LPASGAA	19690	TTGCCTGCGTCTGGGGCTGCG	34013	CTCCCAGCAAGCGGAGCAGCA
5368	LPATRSI	19691	TTGCCGGCGACGAGGTCTATT	34014	CTCCCAGCAACAAGAAGCATC
5369	LPAVCGP	19692	CTGCCGGCTGTGTGTGGTCCG	34015	CTCCCAGCAGTCTGCGGACCA
5370	LPDKSLM	19693	CTGCCTGATAAGTCGCTTATG	34016	CTCCCAGACAAAAGCCTCATG
5371	LPDMSRE	19694	CTGCCGGATATGTCTCGTGAG	34017	CTCCCAGACATGAGCAGAGAA
5372	LPDPRPD	19695	CTGCCGGATCCTAGGCCTGAT	34018	CTCCCAGACCCAAGACCAGAC
5373	LPDTIRS	19696	CTTCCGGATACGATTCGTAGT	34019	CTCCCAGACACAATCAGAAGC
5374	LPDTRTL	19697	CTTCCTGATACGAGGACGCTT	34020	CTCCCAGACACAAGAACACTC
5375	LPDVARY	19698	TTGCCGGATGTGGCTAGGTAT	34021	CTCCCAGACGTCGCAAGATAC
5376	LPEAGVP	19699	TTGCCTGAGGCTGGGGTTCCG	34022	CTCCCAGAAGCAGGAGTCCCA
5377	LPEISPH	19700	TTGCCTGAGATTTCGCCGCAT	34023	CTCCCAGAAATCAGCCCACAC
5378	LPENTPY	19701	CTGCCGGAGAATACGCCTTAT	34024	CTCCCAGAAAACACACCATAC
5379	LPEQTVI	19702	CTTCCGGAGCAGACGGTTATT	34025	CTCCCAGAACAAACAGTCATC
5380	LPERVGL	19703	CTGCCGGAGCGGGTTGGTCTG	34026	CTCCCAGAAAGAGTCGGACTC
5381	LPETGMS	19704	CTGCCTGAGACTGGTATGAGT	34027	CTCCCAGAAACAGGAATGAGC
5382	LPFATSP	19705	CTTCCGTTTGCTACTTCTCCT	34028	CTCCCATTCGCAACAAGCCCA
5383	LPGATIE	19706	TTGCCGGGGGCGACTATTGAG	34029	CTCCCAGGAGCAACAATCGAA
5384	LPGKVTT	19707	CTTCCGGGTAAGGTTACGACG	34030	CTCCCAGGAAAAGTCACAACA
5385	LPGRAAP	19708	TTGCCGGGTCGTGCTGCGCCT	34031	CTCCCAGGAAGAGCAGCACCA
5386	LPGTPRG	19709	CTTCCGGGGACTCCGCGGGGT	34032	CTCCCAGGAACACCAAGAGGA
5387	LPGTVGV	19710	CTTCCTGGTACTGTGGGTGTT	34033	CTCCCAGGAACAGTCGGAGTC
5388	LPGWPLD	19711	TTGCCGGGTTGGCCTCTGGAT	34034	CTCCCAGGATGGCCACTCGAC
5389	LPHPSQN	19712	CTGCCGCATCCTTCGCAGAAT	34035	CTCCCACACCCAAGCCAAAAC

5390	LPHRPNS	19713	CTTCCTCATCGTCCGAATAGT	34036	CTCCCACACAGACCAAACAGC
5391	LPHSTPM	19714	TTGCCTCATTCTACTCCGATG	34037	CTCCCACACAGCACACCAATG
5392	LPIATSK	19715	TTGCCTATTGCTACGTCTAAG	34038	CTCCCAATCGCAACAAGCAAA
5393	LPIGKQV	19716	TTGCCTATTGGTAAGCAGGTG	34039	CTCCCAATCGGAAAACAAGTC
5394	LPILTSH	19717	CTGCCTATTTTGACGTCTCAT	34040	CTCCCAATCCTCACAAGCCAC
5395	LPILTSS	19718	CTGCCTATTCTTACTAGTAGT	34041	CTCCCAATCCTCACAAGCAGC
5396	LPINHKF	19719	CTGCCTATTAATCATAAGTTT	34042	CTCCCAATCAACCACAAATTC
5397	LPIPVDA	19720	TTGCCTATTCCGGTTGATGCG	34043	CTCCCAATCCCAGTCGACGCA
5398	LPISLQP	19721	TTGCCGATTTCTCTTCAGCCT	34044	CTCCCAATCAGCCTCCAACCA
5399	LPITYAD	19722	TTGCCTATTACTTATGCGGAT	34045	CTCCCAATCACATACGCAGAC
5400	LPKASTS	19723	CTGCCGAAGGCGTCGACGTCG	34046	CTCCCAAAAGCAAGCACAAGC
5401	LPKFRDQ	19724	CTTCCTAAGTTTCGTGATCAG	34047	CTCCCAAAATTCAGAGACCAA
5402	LPKIDNT	19725	CTTCCTAAGATTGATAATACT	34048	CTCCCAAAAATCGACAACACA
5403	LPKNYDA	19726	CTGCCTAAGAATTATGATGCT	34049	CTCCCAAAAAACTACGACGCA
5404	LPKSSDA	19727	CTGCCTAAGTCTAGTGATGCT	34050	CTCCCAAAAAGCAGCGACGCA
5405	LPKVVAT	19728	CTTCCTAAGGTGGTTGCTACG	34051	CTCCCAAAAGTCGTCGCAACA
5406	LPLAQQP	19729	CTGCCGTTGGCTCAGCAGCCT	34052	CTCCCACTCGCACAACAACCA
5407	LPLAVYD	19730	TTGCCTCTTGCTGTGTATGAT	34053	CTCCCACTCGCAGTCTACGAC
5408	LPLGNRM	19731	TTGCCGCTTGGTAATCGTATG	34054	CTCCCACTCGGAAACAGAATG
5409	LPLHRSS	19732	CTGCCTCTTCATAGGAGTTCT	34055	CTCCCACTCCACAGAAGCAGC
5410	LPLHSPR	19733	TTGCCTTTGCATAGTCCTAGG	34056	CTCCCACTCCACAGCCCAAGA
5411	LPLIFTE	19734	CTGCCGCTGATTTTTACTGAG	34057	CTCCCACTCATCTTCACAGAA
5412	LPLKGAD	19735	CTTCCGTTGAAGGGGGCGGAT	34058	CTCCCACTCAAAGGAGCAGAC
5413	LPLMKPG	19736	CTTCCTCTGATGAAGCCGGGG	34059	CTCCCACTCATGAAACCAGGA
5414	LPLNFDR	19737	CTGCCGTTGAATTTTGATCGT	34060	CTCCCACTCAACTTCGACAGA
5415	LPLNKSH	19738	CTTCCGCTGAATAAGTCTCAT	34061	CTCCCACTCAACAAAAGCCAC
5416	LPLNTYT	19739	TTGCCGTTGAATACTTATACT	34062	CTCCCACTCAACACATACACA
5417	LPLPPYV	19740	TTGCCTCTTCCTCCGTATGTT	34063	CTCCCACTCCCACCATACGTC
5418	LPLPTSG	19741	CTGCCTTTGCCGACGAGTGGT	34064	CTCCCACTCCCAACAAGCGGA
5419	LPLREPK	19742	CTGCCTCTGCGGGAGCCTAAG	34065	CTCCCACTCAGAGAACCAAAA
5420	LPLRMSD	19743	CTGCCGCTTCGGATGTCTGAT	34066	CTCCCACTCAGAATGAGCGAC
5421	LPLSPMH	19744	TTGCCGTTGTCGCCGATGCAT	34067	CTCCCACTCAGCCCAATGCAC
5422	LPMDLVA	19745	CTGCCTATGGATCTTGTGGCG	34068	CTCCCAATGGACCTCGTCGCA
5423	LPMMAHL	19746	TTGCCTATGATGGCTCATCTT	34069	CTCCCAATGATGGCACACCTC
5424	LPMSHLP	19747	CTTCCGATGAGTCATCTGCCG	34070	CTCCCAATGAGCCACCTCCCA
5425	LPNAYMH	19748	TTGCCTAATGCTTATATGCAT	34071	CTCCCAAACGCATACATGCAC
5426	LPNEPSD	19749	TTGCCGAATGAGCCGAGTGAT	34072	CTCCCAAACGAACCAAGCGAC
5427	LPNHISP	19750	TTGCCGAATCATATTTCGCCG	34073	CTCCCAAACCACATCAGCCCA
5428	LPNLRDQ	19751	CTGCCGAATCTGCGTGATCAG	34074	CTCCCAAACCTCAGAGACCAA
5429	LPNNSRD	19752	TTGCCGAATAATTCGAGGGAT	34075	CTCCCAAACAACAGCAGAGAC
5430	LPNPRSD	19753	CTTCCGAATCCGCGTAGTGAT	34076	CTCCCAAACCCAAGAAGCGAC
5431	LPNSVFT	19754	CTTCCGAATTCTGTTTTTACG	34077	CTCCCAAACAGCGTCTTCACA
5432	LPPAAHR	19755	CTTCCTCCTGCTGCGCATAGG	34078	CTCCCACCAGCAGCACACAGA
5433	LPPAHAH	19756	CTGCCTCCGGCTCATGCTCAT	34079	CTCCCACCAGCACACGCACAC
5434	LPPCLTN	19757	CTTCCGCCGTGTCTTACGAAT	34080	CTCCCACCATGCCTCACAAAC

5435	LPPEHRG	19758	CTGCCTCCGGAGCATCGGGGT	34081	CTCCCACCAGAACACAGAGGA
5436	LPPETFP	19759	CTTCCTCCGGAGACGTTTCCT	34082	CTCCCACCAGAAACATTCCCA
5437	LPPGPAT	19760	TTGCCGCCTGGGCCTGCTACG	34083	CTCCCACCAGGACCAGCAACA
5438	LPPHGNV	19761	CTGCCGCCGCATGGGAATGTG	34084	CTCCCACCACACGGAAACGTC
5439	LPPHGSA	19762	TTGCCGCCTCATGGTTCGGCT	34085	CTCCCACCACACGGAAGCGCA
5440	LPPHGYA	19763	CTTCCTCCGCATGGTTATGCT	34086	CTCCCACCACACGGATACGCA
5441	LPPLVQY	19764	TTGCCTCCGCTTGTTCAGTAT	34087	CTCCCACCACTCGTCCAATAC
5442	LPPNGHR	19765	CTTCCGCCTAATGGGCATCGG	34088	CTCCCACCAAACGGACACAGA
5443	LPPNKFM	19766	TTGCCGCCTAATAAGTTTATG	34089	CTCCCACCAAACAAATTCATG
5444	LPPRDDR	19767	TTGCCGCCGCGGGATGATCGT	34090	CTCCCACCAAGAGACGACAGA
5445	LPPRSSY	19768	CTGCCTCCTAGGTCTTCGTAT	34091	CTCCCACCAAGAAGCAGCTAC
5446	LPPSHAM	19769	CTGCCGCCTAGTCATGCTATG	34092	CTCCCACCAAGCCACGCAATG
5447	LPPSIDN	19770	TTGCCTCCGTCGATTGATAAT	34093	CTCCCACCAAGCATCGACAAC
5448	LPPYRGP	19771	CTGCCGCCTTATCGGGGGCCT	34094	CTCCCACCATACAGAGGACCA
5449	LPPYSPA	19772	CTGCCGCCGTATTCTCCTGCG	34095	CTCCCACCATACAGCCCAGCA
5450	LPQPGAA	19773	TTGCCGCAGCCTGGGGCTGCT	34096	CTCCCACAACCAGGAGCAGCA
5451	LPQRTSH	19774	TTGCCGCAGCGTACGTCTCAT	34097	CTCCCACAAAGAACAAGCCAC
5452	LPREPLT	19775	TTGCCGCGGGAGCCGTTGACT	34098	CTCCCAAGAGAACCACTCACA
5453	LPRFPVD	19776	TTGCCGAGGTTTCCTGTGGAT	34099	CTCCCAAGATTCCCAGTCGAC
5454	LPRGMTS	19777	CTTCCGAGGGGTATGACTTCT	34100	CTCCCAAGAGGAATGACAAGC
5455	LPRHQQT	19778	CTGCCGCGTCATCAGCAGACG	34101	CTCCCAAGACACCAACAAACA
5456	LPRIPTG	19779	TTGCCGAGGATTCCTACTGGT	34102	CTCCCAAGAATCCCAACAGGA
5457	LPRLMAP	19780	TTGCCTCGGCTGATGGCGCCT	34103	CTCCCAAGACTCATGGCACCA
5458	LPRQAAL	19781	CTTCCGCGTCAGGCTGCGCTG	34104	CTCCCAAGACAAGCAGCACTC
5459	LPRSQFI	19782	CTGCCTCGTTCTCAGTTTATT	34105	CTCCCAAGAAGCCAATTCATC
5460	LPRVNAG	19783	CTGCCGCGTGTTAATGCTGGG	34106	CTCCCAAGAGTCAACGCAGGA
5461	LPSADRV	19784	CTTCCGAGTGCTGATCGTGTT	34107	CTCCCAAGCGCAGACAGAGTC
5462	LPSCIGP	19785	CTTCCTTCTTGTATTGGTCCT	34108	CTCCCAAGCTGCATCGGACCA
5463	LPSFNGS	19786	CTGCCTTCGTTTAATGGGTCG	34109	CTCCCAAGCTTCAACGGAAGC
5464	LPSILLP	19787	CTTCCTAGTATTTTGTTGCCG	34110	CTCCCAAGCATCCTCCTCCCA
5465	LPSIPRT	19788	CTTCCGTCTATTCCTCGGACT	34111	CTCCCAAGCATCCCAAGAACA
5466	LPSMSLS	19789	TTGCCGAGTATGTCTTTGTCT	34112	CTCCCAAGCATGAGCCTCAGC
5467	LPSNAVS	19790	CTGCCTAGTAATGCTGTTTCG	34113	CTCCCAAGCAACGCAGTCAGC
5468	LPSNTRL	19791	TTGCCTTCTAATACGAGGCTG	34114	CTCCCAAGCAACACAAGACTC
5469	LPSPPGV	19792	CTTCCTAGTCCTCCGGGTGTG	34115	CTCCCAAGCCCACCAGGAGTC
5470	LPSPPIS	19793	TTGCCGTCGCCTCCTATTTCT	34116	CTCCCAAGCCCACCAATCAGC
5471	LPSQLIG	19794	TTGCCTTCTCAGCTTATTGGT	34117	CTCCCAAGCCAACTCATCGGA
5472	LPSRAFS	19795	CTTCCTTCTCGGGCTTTTTCG	34118	CTCCCAAGCAGAGCATTCAGC
5473	LPSSTPN	19796	CTGCCGAGTAGTACGCCGAAT	34119	CTCCCAAGCAGCACACCAAAC
5474	LPSSVYT	19797	TTGCCTTCTTCTGTTTATACG	34120	CTCCCAAGCAGCGTCTACACA
5475	LPSTCGK	19798	CTTCCTAGTACGTGTGGGAAG	34121	CTCCCAAGCACATGCGGAAAA
5476	LPSTGGL	19799	CTTCCTTCGACTGGGGGTCTG	34122	CTCCCAAGCACAGGAGGACTC
5477	LPSTPPR	19800	TTGCCTAGTACTCCTCCGAGG	34123	CTCCCAAGCACACCACCAAGA
5478	LPSYNAS	19801	CTGCCTTCGTATAATGCGTCT	34124	CTCCCAAGCTACAACGCAAGC
5479	LPTHLEA	19802	CTTCCGACGCATTTGGAGGCG	34125	CTCCCAACACACCTCGAAGCA

5480	LPTINAV	19803	TTGCCGACTATTAATGCTGTG	34126	CTCCCAACAATCAACGCAGTC
5481	LPTKEAV	19804	CTGCCTACTAAGGAGGCTGTG	34127	CTCCCAACAAAAGAAGCAGTC
5482	LPTLRIP	19805	CTGCCTACTCTGCGGATTCCT	34128	CTCCCAACACTCAGAATCCCA
5483	LPTLSYV	19806	TTGCCTACTCTTTCGTATGTT	34129	CTCCCAACACTCAGCTACGTC
5484	LPTMHNT	19807	CTGCCGACTATGCATAATACT	34130	CTCCCAACAATGCACAACACA
5485	LPTNKGI	19808	TTGCCGACGAATAAGGGTATT	34131	CTCCCAACAAACAAAGGAATC
5486	LPTNYAA	19809	CTGCCTACTAATTATGCTGCG	34132	CTCCCAACAAACTACGCAGCA
5487	LPTPFSS	19810	CTGCCGACGCCGTTTAGTTCT	34133	CTCCCAACACCATTCAGCAGC
5488	LPTPLTS	19811	CTTCCTACGCCGTTGACTAGT	34134	CTCCCAACACCACTCACAAGC
5489	LPTSPSA	19812	TTGCCGACGAGTCCGAGTGCG	34135	CTCCCAACAAGCCCAAGCGCA
5490	LPTSTSI	19813	CTGCCTACTTCTACTTCTATT	34136	CTCCCAACAAGCACAAGCATC
5491	LPTSVVL	19814	CTGCCTACTAGTGTTGTTCTG	34137	CTCCCAACAAGCGTCGTCCTC
5492	LPVGDPL	19815	CTGCCGGTGGGGGATCCTCTG	34138	CTCCCAGTCGGAGACCCACTC
5493	LPVNIVG	19816	TTGCCTGTTAATATTGTGGGT	34139	CTCCCAGTCAACATCGTCGGA
5494	LPVSDRY	19817	CTTCCTGTGAGTGATAGGTAT	34140	CTCCCAGTCAGCGACAGATAC
5495	LPVSSRH	19818	CTGCCTGTGAGTTCTCGTCAT	34141	CTCCCAGTCAGCAGCAGACAC
5496	LPVSTRH	19819	CTGCCGGTTTCTACGCGGCAT	34142	CTCCCAGTCAGCACAAGACAC
5497	LPVVNAS	19820	CTGCCTGTTGTTAATGCTAGT	34143	CTCCCAGTCGTCAACGCAAGC
5498	LPYTVGT	19821	TTGCCTTATACTGTTGGTACG	34144	CTCCCATACACAGTCGGAACA
5499	LQARTLN	19822	CTGCAGGCTCGTACGCTTAAT	34145	CTCCAAGCAAGAACACTCAAC
5500	LQASKAD	19823	CTTCAGGCGTCTAAGGCTGAT	34146	CTCCAAGCAAGCAAAGCAGAC
5501	LQASNDI	19824	CTTCAGGCTTCTAATGATATT	34147	CTCCAAGCAAGCAACGACATC
5502	LQATRGA	19825	CTTCAGGCGACTCGGGGGGCT	34148	CTCCAAGCAACAAGAGGAGCA
5503	LQDAVCN	19826	CTTCAGGATGCGGTGTGTAAT	34149	CTCCAAGACGCAGTCTGCAAC
5504	LQDPRSP	19827	CTTCAGGATCCTCGTAGTCCG	34150	CTCCAAGACCCAAGAAGCCCA
5505	LQDVSMG	19828	TTGCAGGATGTTTCGATGGGG	34151	CTCCAAGACGTCAGCATGGGA
5506	LQEKSWE	19829	TTGCAGGAGAAGAGTTGGGAG	34152	CTCCAAGAAAAAAGCTGGGAA
5507	LQEPGNL	19830	TTGCAGGAGCCGGGTAATTTG	34153	CTCCAAGAACCAGGAAACCTC
5508	LQFSPPS	19831	CTTCAGTTTAGTCCGCCTAGT	34154	CTCCAATTCAGCCCACCAAGC
5509	LQGAFAS	19832	TTGCAGGGGGCGTTTGCTTCG	34155	CTCCAAGGAGCATTCGCAAGC
5510	LQGSRQI	19833	TTGCAGGGGTCGCGTCAGATT	34156	CTCCAAGGAAGCAGACAAATC
5511	LQGWHAQ	19834	CTTCAGGGGTGGCATGCTCAG	34157	CTCCAAGGATGGCACGCACAA
5512	LQHHSNG	19835	TTGCAGCATCATTCTAATGGG	34158	CTCCAACACCACAGCAACGGA
5513	LQHLQPS	19836	CTGCAGCATCTGCAGCCGTCG	34159	CTCCAACACCTCCAACCAAGC
5514	LQKMVPL	19837	TTGCAGAAGATGGTTCCGTTG	34160	CTCCAAAAAATGGTCCCACTC
5515	LQKPTMS	19838	TTGCAGAAGCCGACGATGTCT	34161	CTCCAAAAACCAACAATGAGC
5516	LQKPTSA	19839	CTGCAGAAGCCTACTTCTGCT	34162	CTCCAAAAACCAACAAGCGCA
5517	LQLNQQK	19840	CTTCAGTTGAATCAGCAGAAG	34163	CTCCAACTCAACCAACAAAAA
5518	LQLRQTS	19841	TTGCAGTTGCGGCAGACTAGT	34164	CTCCAACTCAGACAAACAAGC
5519	LQLTRGE	19842	CTTCAGTTGACTCGTGGTGAG	34165	CTCCAACTCACAAGAGGAGAA
5520	LQMARGG	19843	TTGCAGATGGCGAGGGGGGGT	34166	CTCCAAATGGCAAGAGGAGGA
5521	LQMRPMT	19844	CTGCAGATGCGTCCTATGACT	34167	CTCCAAATGAGACCAATGACA
5522	LQNGCKS	19845	CTTCAGAATGGTTGTAAGTCT	34168	CTCCAAAACGGATGCAAAAGC
5523	LQNTSSS	19846	CTTCAGAATACGAGTAGTTCG	34169	CTCCAAAACACAAGCAGCAGC
5524	LQPFKHQ	19847	CTTCAGCCTTTTAAGCATCAG	34170	CTCCAACCATTCAAACACCAA

5525	LQPREPV	19848	TTGCAGCCTCGTGAGCCTGTT	34171	CTCCAACCAAGAGAACCAGTC
5526	LQPSSRT	19849	TTGCAGCCTAGTTCGCGTACG	34172	CTCCAACCAAGCAGCAGAACA
5527	LQPTGEA	19850	CTTCAGCCGACTGGTGAGGCT	34173	CTCCAACCAACAGGAGAAGCA
5528	LQQTGLR	19851	CTGCAGCAGACGGGGTTGCGT	34174	CTCCAACAAACAGGACTCAGA
5529	LQRANMV	19852	CTTCAGCGTGCGAATATGGTG	34175	CTCCAAAGAGCAAACATGGTC
5530	LQREAHT	19853	CTTCAGCGTGAGGCTCATACG	34176	CTCCAAAGAGAAGCACACACA
5531	LQRSRGP	19854	TTGCAGCGTTCGAGGGGGCCG	34177	CTCCAAAGAAGCAGAGGACCA
5532	LQSARAP	19855	CTTCAGTCTGCTCGTGCTCCT	34178	CTCCAAAGCGCAAGAGCACCA
5533	LQSFSSP	19856	TTGCAGTCTTTTTCGTCTCCG	34179	CTCCAAAGCTTCAGCAGCCCA
5534	LQSGPQP	19857	CTGCAGAGTGGTCCTCAGCCG	34180	CTCCAAAGCGGACCACAACCA
5535	LQSPENE	19858	CTTCAGTCTCCTGAGAATGAG	34181	CTCCAAAGCCCAGAAAACGAA
5536	LQSYTPP	19859	CTGCAGAGTTATACGCCGCCG	34182	CTCCAAAGCTACACACCACCA
5537	LQTGRFS	19860	TTGCAGACTGGGCGTTTTTCT	34183	CTCCAAACAGGAAGATTCAGC
5538	LQTKSSS	19861	TTGCAGACTAAGTCGTCTTCT	34184	CTCCAAACAAAAAGCAGCAGC
5539	LQTVDID	19862	TTGCAGACGGTGGATATTGAT	34185	CTCCAAACAGTCGACATCGAC
5540	LQVDSNV	19863	TTGCAGGTGGATTCTAATGTG	34186	CTCCAAGTCGACAGCAACGTC
5541	LQVPSSL	19864	TTGCAGGTTCCTTCTTCTCTG	34187	CTCCAAGTCCCAAGCAGCCTC
5542	LQVSGLD	19865	TTGCAGGTGTCGGGGCTGGAT	34188	CTCCAAGTCAGCGGACTCGAC
5543	LQYATSD	19866	CTGCAGTATGCTACTTCGGAT	34189	CTCCAATACGCAACAAGCGAC
5544	LRAAEIS	19867	CTGCGTGCGGCTGAGATTTCG	34190	CTCAGAGCAGCAGAAATCAGC
5545	LRAANAL	19868	CTTCGTGCGGCGAATGCTCTT	34191	CTCAGAGCAGCAAACGCACTC
5546	LRADGKA	19869	CTGCGTGCTGATGGGAAGGCG	34192	CTCAGAGCAGACGGAAAAGCA
5547	LRAGTAQ	19870	CTTCGTGCGGGGACGGCGCAG	34193	CTCAGAGCAGGAACAGCACAA
5548	LRAGTSS	19871	TTGCGTGCTGGTACGTCTAGT	34194	CTCAGAGCAGGAACAAGCAGC
5549	LRAILEE	19872	CTTCGGGCGATTCTTGAGGAG	34195	CTCAGAGCAATCCTCGAAGAA
5550	LRALTGS	19873	CTTCGTGCTCTGACGGGGAGT	34196	CTCAGAGCACTCACAGGAAGC
5551	LRAQNDA	19874	TTGCGTGCTCAGAATGATGCT	34197	CTCAGAGCACAAAACGACGCA
5552	LRATNSL	19875	CTGCGGGCGACGAATTCTTTG	34198	CTCAGAGCAACAAACAGCCTC
5553	LRDGQRP	19876	CTTAGGGATGGTCAGCGTCCT	34199	CTCAGAGACGGACAAAGACCA
5554	LRDGRAS	19877	CTTCGGGATGGGCGTGCTTCT	34200	CTCAGAGACGGAAGAGCAAGC
5555	LRDHGGH	19878	TTGCGGGATCATGGTGGTCAT	34201	CTCAGAGACCACGGAGGACAC
5556	LRDRDFK	19879	CTTCGGGATCGGGATTTTAAG	34202	CTCAGAGACAGAGACTTCAAA
5557	LRDRDVL	19880	CTGAGGGATCGTGATGTGCTT	34203	CTCAGAGACAGAGACGTCCTC
5558	LRDSNKN	19881	CTTCGGGATTCGAATAAGAAT	34204	CTCAGAGACAGCAACAAAAAC
5559	LRDSVQV	19882	TTGCGGGATAGTGTGCAGGTG	34205	CTCAGAGACAGCGTCCAAGTC
5560	LREHGPV	19883	TTGAGGGAGCATGGGCCTGTT	34206	CTCAGAGAACACGGACCAGTC
5561	LREMPLP	19884	TTGAGGGAGATGCCTCTGCCT	34207	CTCAGAGAAATGCCACTCCCA
5562	LRENMSN	19885	TTGAGGGAGAATATGTCGAAT	34208	CTCAGAGAAAACATGAGCAAC
5563	LREPTGF	19886	CTTCGTGAGCCTACTGGGTTT	34209	CTCAGAGAACCAACAGGATTC
5564	LREPVIQ	19887	CTTCGTGAGCCGGTGATTCAG	34210	CTCAGAGAACCAGTCATCCAA
5565	LRESQRI	19888	TTGCGTGAGTCTCAGCGGATT	34211	CTCAGAGAAAGCCAAAGAATC
5566	LRFPGTP	19889	TTGAGGTTTCCTGGTACGCCT	34212	CTCAGATTCCCAGGAACACCA
5567	LRFQSTP	19890	CTTCGTTTTCAGTCTACTCCG	34213	CTCAGATTCCAAAGCACACCA
5568	LRGAIAP	19891	CTGAGGGGTGCGATTGCTCCG	34214	CTCAGAGGAGCAATCGCACCA
5569	LRGDASE	19892	TTGCGGGGTGATGCGAGTGAG	34215	CTCAGAGGAGACGCAAGCGAA

5570	LRGESSP	19893	CTTAGGGGGGAGAGTAGTCCG	34216	CTCAGAGGAGAAAGCAGCCCA
5571	LRGGMDP	19894	CTGCGTGGGGGTATGGATCCG	34217	CTCAGAGGAGGAATGGACCCA
5572	LRGNVEA	19895	TTGAGGGGTAATGTGGAGGCG	34218	CTCAGAGGAAACGTCGAAGCA
5573	LRGPTTV	19896	CTGAGGGGGCCTACTACGGTG	34219	CTCAGAGGACCAACAACAGTC
5574	LRGQLSN	19897	CTGAGGGGTCAGCTTTCGAAT	34220	CTCAGAGGACAACTCAGCAAC
5575	LRGRSSE	19898	TTGCGTGGGCGTTCGAGTGAG	34221	CTCAGAGGAAGAAGCAGCGAA
5576	LRGSLEH	19899	CTGAGGGGGTCGCTTGAGCAT	34222	CTCAGAGGAAGCCTCGAACAC
5577	LRGTMES	19900	TTGCGTGGGACTATGGAGAGT	34223	CTCAGAGGAACAATGGAAAGC
5578	LRHDSNA	19901	TTGCGGCATGATTCTAATGCG	34224	CTCAGACACGACAGCAACGCA
5579	LRISTSD	19902	CTTCGTATTTCGACTAGTGAT	34225	CTCAGAATCAGCACAAGCGAC
5580	LRKEYLG	19903	TTGCGTAAGGAGTATCTTGGT	34226	CTCAGAAAAGAATACCTCGGA
5581	LRLDDQA	19904	TTGCGGTTGGATGATCAGGCT	34227	CTCAGACTCGACGACCAAGCA
5582	LRLHQES	19905	CTGCGGCTGCATCAGGAGTCG	34228	CTCAGACTCCACCAAGAAAGC
5583	LRLKNDA	19906	TTGCGGTTGAAGAATGATGCT	34229	CTCAGACTCAAAAACGACGCA
5584	LRLPPAE	19907	TTGCGTCTGCCTCCTGCTGAG	34230	CTCAGACTCCCACCAGCAGAA
5585	LRLSDNR	19908	TTGCGGCTTTCTGATAATCGG	34231	CTCAGACTCAGCGACAACAGA
5586	LRLTGRP	19909	TTGAGGCTTACGGGGCGTCCT	34232	CTCAGACTCACAGGAAGACCA
5587	LRLVREP	19910	TTGCGTCTGGTTCGTGAGCCG	34233	CTCAGACTCGTCAGAGAACCA
5588	LRNAASV	19911	CTTAGGAATGCTGCGTCTGTG	34234	CTCAGAAACGCAGCAAGCGTC
5589	LRNADGA	19912	CTTAGGAATGCTGATGGTGCG	34235	CTCAGAAACGCAGACGGAGCA
5590	LRNLNSY	19913	CTGAGGAATCTGAATTCGTAT	34236	CTCAGAAACCTCAACAGCTAC
5591	LRNNPLA	19914	TTGCGTAATAATCCTTTGGCG	34237	CTCAGAAACAACCCACTCGCA
5592	LRNRPSE	19915	TTGAGGAATCGGCCTAGTGAG	34238	CTCAGAAACAGACCAAGCGAA
5593	LRNSSVV	19916	TTGAGGAATTCTTCGGTTGTG	34239	CTCAGAAACAGCAGCGTCGTC
5594	LRNTPMS	19917	CTGCGTAATACTCCTATGTCT	34240	CTCAGAAACACACCAATGAGC
5595	LRNTVLG	19918	TTGCGGAATACTGTTTTGGGT	34241	CTCAGAAACACAGTCCTCGGA
5596	LRNVAEH	19919	TTGCGTAATGTGGCGGAGCAT	34242	CTCAGAAACGTCGCAGAACAC
5597	LRPNGYT	19920	TTGCGTCCGAATGGTTATACT	34243	CTCAGACCAAACGGATACACA
5598	LRPPAFP	19921	TTGCGTCCGCCTGCGTTTCCG	34244	CTCAGACCACCAGCATTCCCA
5599	LRPPAGL	19922	TTGAGGCCGCCGGCTGGGTTG	34245	CTCAGACCACCAGCAGGACTC
5600	LRPPQNN	19923	CTGCGTCCTCCTCAGAATAAT	34246	CTCAGACCACCACAAAACAAC
5601	LRPRPSD	19924	TTGCGTCCGCGTCCGAGTGAT	34247	CTCAGACCAAGACCAAGCGAC
5602	LRPSFSP	19925	TTGCGGCCTAGTTTTAGTCCG	34248	CTCAGACCAAGCTTCAGCCCA
5603	LRPSSIS	19926	CTTCGTCCTTCTAGTATTAGT	34249	CTCAGACCAAGCAGCATCAGC
5604	LRPSSQT	19927	CTGAGGCCTTCTTCTCAGACT	34250	CTCAGACCAAGCAGCCAAACA
5605	LRPSVRE	19928	TTGCGTCCTTCTGTTCGGGAG	34251	CTCAGACCAAGCGTCAGAGAA
5606	LRPTTMP	19929	CTGCGGCCGACGACTATGCCT	34252	CTCAGACCAACAACAATGCCA
5607	LRQGYSQ	19930	TTGCGGCAGGGTTATAGTCAG	34253	CTCAGACAAGGATACAGCCAA
5608	LRQSTPP	19931	TTGAGGCAGTCTACTCCGCCT	34254	CTCAGACAAAGCACACCACCA
5609	LRRPEEL	19932	CTGCGTAGGCCTGAGGAGCTT	34255	CTCAGAAGACCAGAAGAACTC
5610	LRSDTKY	19933	CTTCGGAGTGATACGAAGTAT	34256	CTCAGAAGCGACACAAAATAC
5611	LRSDVQF	19934	CTGAGGTCGGATGTGCAGTTT	34257	CTCAGAAGCGACGTCCAATTC
5612	LRSDWVE	19935	TTGCGTTCTGATTGGGTTGAG	34258	CTCAGAAGCGACTGGGTCGAA
5613	LRSESCA	19936	CTGAGGTCTGAGTCGTGTGCG	34259	CTCAGAAGCGAAAGCTGCGCA
5614	LRSGAIQ	19937	CTGCGGTCGGGTGCTATTCAG	34260	CTCAGAAGCGGAGCAATCCAA

5615	LRSGTLA	19938	TTGAGGTCTGGGACGCTGGCT	34261	CTCAGAAGCGGAACACTCGCA
5616	LRSLTDA	19939	CTGCGGTCGCTGACTGATGCG	34262	CTCAGAAGCCTCACAGACGCA
5617	LRSMQTP	19940	CTTCGGTCGATGCAGACTCCG	34263	CTCAGAAGCATGCAAACACCA
5618	LRSPHFD	19941	TTGAGGTCTCCGCATTTTGAT	34264	CTCAGAAGCCCACACTTCGAC
5619	LRSPLSP	19942	CTGAGGAGTCCGCTGTCTCCG	34265	CTCAGAAGCCCACTCAGCCCA
5620	LRSPPTA	19943	CTGCGGTCTCCTCCTACTGCG	34266	CTCAGAAGCCCACCAACAGCA
5621	LRSQERH	19944	TTGCGGTCTCAGGAGCGGCAT	34267	CTCAGAAGCCAAGAAAGACAC
5622	LRSQGPL	19945	TTGCGTTCTCAGGGGCCGCTG	34268	CTCAGAAGCCAAGGACCACTC
5623	LRSSLDW	19946	CTGAGGAGTTCGCTGGATTGG	34269	CTCAGAAGCAGCCTCGACTGG
5624	LRSSSPG	19947	CTGCGGAGTTCTTCGCCTGGG	34270	CTCAGAAGCAGCAGCCCAGGA
5625	LRSSTTP	19948	CTTCGGTCTTCGACTACTCCT	34271	CTCAGAAGCAGCACAACACCA
5626	LRSTSAY	19949	TTGCGTTCTACTTCGGCGTAT	34272	CTCAGAAGCACAAGCGCATAC
5627	LRSVNDS	19950	TTGCGGTCTGTTAATGATTCG	34273	CTCAGAAGCGTCAACGACAGC
5628	LRTADVA	19951	TTGCGGACGGCTGATGTTGCG	34274	CTCAGAACAGCAGACGTCGCA
5629	LRTASPP	19952	CTTAGGACTGCTTCGCCTCCT	34275	CTCAGAACAGCAAGCCCACCA
5630	LRTASST	19953	TTGCGTACGGCTTCGTCGACT	34276	CTCAGAACAGCAAGCAGCACA
5631	LRTDILS	19954	CTTAGGACGGATATTCTGTCT	34277	CTCAGAACAGACATCCTCAGC
5632	LRTGYLD	19955	CTGAGGACTGGGTATCTTGAT	34278	CTCAGAACAGGATACCTCGAC
5633	LRTLNAA	19956	CTTAGGACGCTTAATGCGGCG	34279	CTCAGAACACTCAACGCAGCA
5634	LRTNDSQ	19957	CTTCGTACGAATGATAGTCAG	34280	CTCAGAACAAACGACAGCCAA
5635	LRTPERL	19958	CTGAGGACGCCGGAGAGGTTG	34281	CTCAGAACACCAGAAAGACTC
5636	LRTPNGP	19959	TTGCGGACTCCGAATGGTCCT	34282	CTCAGAACACCAAACGGACCA
5637	LRTREAG	19960	CTTCGTACGCGTGAGGCGGGT	34283	CTCAGAACAAGAGAAGCAGGA
5638	LRTSQDR	19961	CTGCGTACTTCTCAGGATCGT	34284	CTCAGAACAAGCCAAGACAGA
5639	LRTTLPL	19962	CTTCGGACTACTCTTCCGTTG	34285	CTCAGAACAACACTCCCACTC
5640	LRTVNSA	19963	CTGCGTACGGTGAATAGTGCG	34286	CTCAGAACAGTCAACAGCGCA
5641	LRVDLLQ	19964	CTTCGTGTTGATCTTCTGCAG	34287	CTCAGAGTCGACCTCCTCCAA
5642	LRVDSPV	19965	CTTCGGGTTGATTCGCCGGTT	34288	CTCAGAGTCGACAGCCCAGTC
5643	LRVDVAT	19966	CTTAGGGTTGATGTTGCTACT	34289	CTCAGAGTCGACGTCGCAACA
5644	LRVGGSY	19967	CTTCGTGTGGGTGGGTCGTAT	34290	CTCAGAGTCGGAGGAAGCTAC
5645	LRVGTEQ	19968	TTGCGTGTGGGTACTGAGCAG	34291	CTCAGAGTCGGAACAGAACAA
5646	LRVLDAS	19969	CTGAGGGTGCTGGATGCTAGT	34292	CTCAGAGTCCTCGACGCAAGC
5647	LRVNPMV	19970	CTGCGTGTGAATCCGATGGTT	34293	CTCAGAGTCAACCCAATGGTC
5648	LRVNVEV	19971	CTTCGTGTTAATGTGGAGGTT	34294	CTCAGAGTCAACGTCGAAGTC
5649	LRVPPMS	19972	TTGCGTGTTCCGCCTATGTCT	34295	CTCAGAGTCCCACCAATGAGC
5650	LRVPPNN	19973	TTGCGGGTGCCGCCTAATAAT	34296	CTCAGAGTCCCACCAAACAAC
5651	LRVTSHP	19974	TTGAGGGTTACTTCTCATCCG	34297	CTCAGAGTCACAAGCCACCCA
5652	LSAAPSN	19975	CTTAGTGCGGCTCCTAGTAAT	34298	CTCAGCGCAGCACCAAGCAAC
5653	LSAATTK	19976	CTTAGTGCGGCGACTACTAAG	34299	CTCAGCGCAGCAACAACAAAA
5654	LSAFVKE	19977	CTTAGTGCGTTTGTTAAGGAG	34300	CTCAGCGCATTCGTCAAAGAA
5655	LSAGARA	19978	TTGAGTGCGGGTGCTCGGGCT	34301	CTCAGCGCAGGAGCAAGAGCA
5656	LSALNVK	19979	TTGTCTGCTCTGAATGTGAAG	34302	CTCAGCGCACTCAACGTCAAA
5657	LSAQRGA	19980	CTGTCGGCTCAGCGGGGGGCT	34303	CTCAGCGCACAAAGAGGAGCA
5658	LSARHMP	19981	CTGTCGGCTAGGCATATGCCG	34304	CTCAGCGCAAGACACATGCCA
5659	LSARPDL	19982	CTGTCGGCGCGGCCGGATTTG	34305	CTCAGCGCAAGACCAGACCTC

5660	LSARPHL	19983	CTGTCTGCGAGGCCGCATTTG	34306	CTCAGCGCAAGACCACACCTC
5661	LSASANS	19984	TTGTCGGCTTCTGCGAATAGT	34307	CTCAGCGCAAGCGCAAACAGC
5662	LSASHVV	19985	TTGTCTGCGAGTCATGTGGTG	34308	CTCAGCGCAAGCCACGTCGTC
5663	LSASWTS	19986	CTTTCGGCGTCTTGGACTAGT	34309	CTCAGCGCAAGCTGGACAAGC
5664	LSAYAQG	19987	TTGTCGGCGTATGCTCAGGGT	34310	CTCAGCGCATACGCACAAGGA
5665	LSCGSME	19988	TTGTCTTGTGGGTCGATGGAG	34311	CTCAGCTGCGGAAGCATGGAA
5666	LSDAHSW	19989	CTTTCGGATGCTCATTCGTGG	34312	CTCAGCGACGCACACAGCTGG
5667	LSDAVAE	19990	TTGTCGGATGCGGTTGCGGAG	34313	CTCAGCGACGCAGTCGCAGAA
5668	LSDERTH	19991	CTGTCTGATGAGCGTACTCAT	34314	CTCAGCGACGAAAGAACACAC
5669	LSDFQNP	19992	CTGAGTGATTTTCAGAATCCG	34315	CTCAGCGACTTCCAAAACCCA
5670	LSDHHGL	19993	CTGTCTGATCATCATGGGTTG	34316	CTCAGCGACCACCACGGACTC
5671	LSDKGHP	19994	CTGTCGGATAAGGGTCATCCG	34317	CTCAGCGACAAAGGACACCCA
5672	LSDLQGN	19995	CTTAGTGATTTGCAGGGGAAT	34318	CTCAGCGACCTCCAAGGAAAC
5673	LSDLTSW	19996	CTGTCTGATTTGACTTCGTGG	34319	CTCAGCGACCTCACAAGCTGG
5674	LSDPTEI	19997	CTTTCTGATCCTACTGAGATT	34320	CTCAGCGACCCAACAGAAATC
5675	LSDRSVL	19998	TTGTCTGATCGGTCTGTTTTG	34321	CTCAGCGACAGAAGCGTCCTC
5676	LSEAPVH	19999	CTTTCTGAGGCTCCGGTGCAT	34322	CTCAGCGAAGCACCAGTCCAC
5677	LSEFSRA	20000	CTTTCTGAGTTTTCTCGGGCG	34323	CTCAGCGAATTCAGCAGAGCA
5678	LSEGCIL	20001	CTTAGTGAGGGGTGTATTTTG	34324	CTCAGCGAAGGATGCATCCTC
5679	LSEGLQK	20002	CTTTCGGAGGGGTTGCAGAAG	34325	CTCAGCGAAGGACTCCAAAAA
5680	LSEPMPF	20003	TTGTCTGAGCCGATGCCTTTT	34326	CTCAGCGAACCAATGCCATTC
5681	LSEQTRY	20004	CTGTCTGAGCAGACGCGGTAT	34327	CTCAGCGAACAAACAAGATAC
5682	LSERGDM	20005	TTGTCTGAGCGGGGGGATATG	34328	CTCAGCGAAAGAGGAGACATG
5683	LSERPVL	20006	CTTTCGGAGCGGCCGGTTCTG	34329	CTCAGCGAAAGACCAGTCCTC
5684	LSESNQV	20007	CTGTCTGAGTCTAATCAGGTT	34330	CTCAGCGAAAGCAACCAAGTC
5685	LSESYVV	20008	CTTTCTGAGAGTTATGTTGTG	34331	CTCAGCGAAAGCTACGTCGTC
5686	LSFGTTT	20009	TTGAGTTTTGGGACGACTACG	34332	CTCAGCTTCGGAACAACAACA
5687	LSFKTQL	20010	TTGAGTTTTAAGACGCAGCTG	34333	CTCAGCTTCAAAACACAACTC
5688	LSFSAES	20011	TTGTCGTTTAGTGCTGAGTCG	34334	CTCAGCTTCAGCGCAGAAAGC
5689	LSFSTSG	20012	CTGAGTTTTTCGACGTCTGGG	34335	CTCAGCTTCAGCACAAGCGGA
5690	LSGAAGL	20013	CTTTCTGGGGCGGCTGGTCTT	34336	CTCAGCGGAGCAGCAGGACTC
5691	LSGAIPP	20014	TTGTCTGGTGCTATTCCGCCG	34337	CTCAGCGGAGCAATCCCACCA
5692	LSGANSG	20015	TTGTCGGGGGCTAATTCGGGT	34338	CTCAGCGGAGCAAACAGCGGA
5693	LSGEQAL	20016	CTTTCGGGGGAGCAGGCGTTG	34339	CTCAGCGGAGAACAAGCACTC
5694	LSGGEPP	20017	TTGAGTGGGGGTGAGCCTCCG	34340	CTCAGCGGAGGAGAACCACCA
5695	LSGGQIS	20018	CTTTCGGGGGGTCAGATTTCT	34341	CTCAGCGGAGGACAAATCAGC
5696	LSGHHIV	20019	CTGTCTGGTCATCATATTGTG	34342	CTCAGCGGACACCACATCGTC
5697	LSGIAGI	20020	TTGTCGGGTATTGCTGGTATT	34343	CTCAGCGGAATCGCAGGAATC
5698	LSGPSSL	20021	CTGAGTGGTCCTTCGTCTCTG	34344	CTCAGCGGACCAAGCAGCCTC
5699	LSGTPGI	20022	CTGTCTGGTACGCCGGGGATT	34345	CTCAGCGGAACACCAGGAATC
5700	LSGVAIQ	20023	TTGTCTGGTGTTGCTATTCAG	34346	CTCAGCGGAGTCGCAATCCAA
5701	LSHDVLT	20024	TTGTCGCATGATGTGCTTACG	34347	CTCAGCCACGACGTCCTCACA
5702	LSHGMLG	20025	TTGAGTCATGGGATGCTTGGG	34348	CTCAGCCACGGAATGCTCGGA
5703	LSHKLTE	20026	TTGTCGCATAAGCTGACGGAG	34349	CTCAGCCACAAACTCACAGAA
5704	LSHLGFP	20027	CTGTCGCATCTGGGTTTTCCT	34350	CTCAGCCACCTCGGATTCCCA

5705	LSHPMGY	20028	CTGTCTCATCCTATGGGGTAT	34351	CTCAGCCACCCAATGGGATAC
5706	LSHSIPR	20029	TTGTCTCATTCTATTCCTCGG	34352	CTCAGCCACAGCATCCCAAGA
5707	LSHTTNG	20030	TTGTCGCATACGACTAATGGT	34353	CTCAGCCACACAACAAACGGA
5708	LSHVTTA	20031	TTGTCTCATGTGACGACGGCG	34354	CTCAGCCACGTCACAACAGCA
5709	LSILSGI	20032	CTTTCTATTTTGTCGGGGATT	34355	CTCAGCATCCTCAGCGGAATC
5710	LSIPSGP	20033	CTTTCGATTCCTAGTGGTCCT	34356	CTCAGCATCCCAAGCGGACCA
5711	LSKEPFM	20034	TTGTCTAAGGAGCCTTTTATG	34357	CTCAGCAAAGAACCATTCATG
5712	LSKGFMG	20035	CTTTCGAAGGGGTTTATGGGG	34358	CTCAGCAAAGGATTCATGGGA
5713	LSKGNAA	20036	CTGTCGAAGGGTAATGCTGCT	34359	CTCAGCAAAGGAAACGCAGCA
5714	LSKTLEE	20037	CTTAGTAAGACGTTGGAGGAG	34360	CTCAGCAAAACACTCGAAGAA
5715	LSLGASA	20038	CTGTCGCTGGGGGCTTCTGCT	34361	CTCAGCCTCGGAGCAAGCGCA
5716	LSLGPHS	20039	TTGTCTCTTGGGCCGCATAGT	34362	CTCAGCCTCGGACCACACAGC
5717	LSLGVDS	20040	CTGTCTCTTGGGGTGGATAGT	34363	CTCAGCCTCGGAGTCGACAGC
5718	LSLHPAP	20041	CTTAGTTTGCATCCGGCGCCT	34364	CTCAGCCTCCACCCAGCACCA
5719	LSLKHLK	20042	TTGTCTCTTAAGCATCTGAAG	34365	CTCAGCCTCAAACACCTCAAA
5720	LSLPQSM	20043	CTTAGTCTGCCGCAGTCGATG	34366	CTCAGCCTCCCACAAAGCATG
5721	LSLPRSD	20044	CTTTCGCTTCCTCGTTCGGAT	34367	CTCAGCCTCCCAAGAAGCGAC
5722	LSLPYNR	20045	CTTTCGTTGCCTTATAATCGT	34368	CTCAGCCTCCCATACAACAGA
5723	LSLQTVP	20046	CTTTCTCTTCAGACGGTTCCT	34369	CTCAGCCTCCAAACAGTCCCA
5724	LSLSKGS	20047	TTGTCTTTGTCTAAGGGTTCG	34370	CTCAGCCTCAGCAAAGGAAGC
5725	LSLSPVV	20048	TTGTCTCTGAGTCCTGTTGTT	34371	CTCAGCCTCAGCCCAGTCGTC
5726	LSLVKHD	20049	CTGTCGCTTGTGAAGCATGAT	34372	CTCAGCCTCGTCAAACACGAC
5727	LSMARTP	20050	CTTTCTATGGCTAGGACTCCT	34373	CTCAGCATGGCAAGAACACCA
5728	LSMNPNG	20051	CTGTCGATGAATCCTAATGGT	34374	CTCAGCATGAACCCAAACGGA
5729	LSMNVQY	20052	TTGTCGATGAATGTTCAGTAT	34375	CTCAGCATGAACGTCCAATAC
5730	LSMQRTV	20053	CTGAGTATGCAGAGGACTGTG	34376	CTCAGCATGCAAAGAACAGTC
5731	LSMRSET	20054	TTGTCTATGCGTTCGGAGACG	34377	CTCAGCATGAGAAGCGAAACA
5732	LSMSKTP	20055	TTGAGTATGTCTAAGACGCCT	34378	CTCAGCATGAGCAAAACACCA
5733	LSNEGSY	20056	CTGTCGAATGAGGGTAGTTAT	34379	CTCAGCAACGAAGGAAGCTAC
5734	LSNGRYS	20057	CTTTCTAATGGGCGGTATTCG	34380	CTCAGCAACGGAAGATACAGC
5735	LSNHPFS	20058	CTGAGTAATCATCCGTTTAGT	34381	CTCAGCAACCACCCATTCAGC
5736	LSNHVIT	20059	CTGTCTAATCATGTGATTACG	34382	CTCAGCAACCACGTCATCACA
5737	LSNMQQK	20060	CTTTCGAATATGCAGCAGAAG	34383	CTCAGCAACATGCAACAAAAA
5738	LSNPAKT	20061	CTGTCTAATCCGGCGAAGACT	34384	CTCAGCAACCCAGCAAAAACA
5739	LSNPTRS	20062	CTTTCGAATCCGACGAGGAGT	34385	CTCAGCAACCCAACAAGAAGC
5740	LSNRKGE	20063	CTGTCTAATCGTAAGGGTGAG	34386	CTCAGCAACAGAAAAGGAGAA
5741	LSNRQIT	20064	TTGTCGAATCGTCAGATTACT	34387	CTCAGCAACAGACAAATCACA
5742	LSNSAIL	20065	CTGTCGAATTCTGCGATTCTG	34388	CTCAGCAACAGCGCAATCCTC
5743	LSNSKGP	20066	CTTTCTAATTCGAAGGGGCCT	34389	CTCAGCAACAGCAAAGGACCA
5744	LSNSRHD	20067	CTTTCTAATTCTCGTCATGAT	34390	CTCAGCAACAGCAGACACGAC
5745	LSNSSRM	20068	CTGAGTAATTCTAGTAGGATG	34391	CTCAGCAACAGCAGCAGAATG
5746	LSPAVTR	20069	CTGTCTCCTGCTGTTACGCGT	34392	CTCAGCCCAGCAGTCACAAGA
5747	LSPCPSN	20070	TTGAGTCCTTGTCCGAGTAAT	34393	CTCAGCCCATGCCCAAGCAAC
5748	LSPFSVV	20071	CTGTCTCCGTTTTCGGTTGTT	34394	CTCAGCCCATTCAGCGTCGTC
5749	LSPGIAQ	20072	CTGAGTCCGGGGATTGCGCAG	34395	CTCAGCCCAGGAATCGCACAA

5750	LSPHRTS	20073	CTTTCTCCGCATAGGACGTCT	34396	CTCAGCCCACACAGAACAAGC
5751	LSPKFVL	20074	CTTAGTCCTAAGTTTGTGCTG	34397	CTCAGCCCAAAATTCGTCCTC
5752	LSPNGPN	20075	CTTTCTCCGAATGGGCCGAAT	34398	CTCAGCCCAAACGGACCAAAC
5753	LSPPDRL	20076	CTTTCGCCTCCGGATAGGTTG	34399	CTCAGCCCACCAGACAGACTC
5754	LSPPPVD	20077	CTGTCTCCGCCTCCTGTTGAT	34400	CTCAGCCCACCACCAGTCGAC
5755	LSPPTPH	20078	CTGTCTCCTCCTACGCCTCAT	34401	CTCAGCCCACCAACACCACAC
5756	LSPRTVH	20079	TTGAGTCCTAGGACTGTGCAT	34402	CTCAGCCCAAGAACAGTCCAC
5757	LSPSFTS	20080	TTGAGTCCGTCGTTTACGAGT	34403	CTCAGCCCAAGCTTCACAAGC
5758	LSPSSLF	20081	TTGTCGCCTTCGTCGCTTTTT	34404	CTCAGCCCAAGCAGCCTCTTC
5759	LSPSSLG	20082	TTGTCGCCGTCTAGTCTGGGG	34405	CTCAGCCCAAGCAGCCTCGGA
5760	LSPSSRG	20083	CTTTCTCCGAGTTCTCGTGGT	34406	CTCAGCCCAAGCAGCAGAGGA
5761	LSPSTDF	20084	CTGTCGCCGAGTACTGATTTT	34407	CTCAGCCCAAGCACAGACTTC
5762	LSPSVTK	20085	CTGTCTCCTTCTGTTACGAAG	34408	CTCAGCCCAAGCGTCACAAAA
5763	LSPTRTQ	20086	TTGAGTCCTACGCGTACTCAG	34409	CTCAGCCCAACAAGAACACAA
5764	LSPTVAY	20087	CTGTCTCCGACTGTTGCTTAT	34410	CTCAGCCCAACAGTCGCATAC
5765	LSPVPVA	20088	TTGAGTCCTGTTCCTGTGGCG	34411	CTCAGCCCAGTCCCAGTCGCA
5766	LSPVQAA	20089	CTTAGTCCTGTTCAGGCGGCG	34412	CTCAGCCCAGTCCAAGCAGCA
5767	LSQAIQS	20090	CTGTCGCAGGCGATTCAGTCT	34413	CTCAGCCAAGCAATCCAAAGC
5768	LSQAKNV	20091	TTGAGTCAGGCGAAGAATGTT	34414	CTCAGCCAAGCAAAAAACGTC
5769	LSQALLD	20092	CTTTCTCAGGCTCTGCTTGAT	34415	CTCAGCCAAGCACTCCTCGAC
5770	LSQANER	20093	TTGAGTCAGGCGAATGAGAGG	34416	CTCAGCCAAGCAAACGAAAGA
5771	LSQDLTV	20094	CTGTCGCAGGATCTGACTGTG	34417	CTCAGCCAAGACCTCACAGTC
5772	LSQGSAP	20095	CTTTCTCAGGGGTCTGCTCCT	34418	CTCAGCCAAGGAAGCGCACCA
5773	LSQHAST	20096	CTTAGTCAGCATGCTAGTACT	34419	CTCAGCCAACACGCAAGCACA
5774	LSQHMRP	20097	CTTTCGCAGCATATGCGTCCT	34420	CTCAGCCAACACATGAGACCA
5775	LSQKTGI	20098	CTGTCTCAGAAGACTGGTATT	34421	CTCAGCCAAAAAACAGGAATC
5776	LSQLIQG	20099	CTTTCTCAGCTTATTCAGGGT	34422	CTCAGCCAACTCATCCAAGGA
5777	LSQLTPS	20100	CTTTCGCAGTTGACTCCGTCT	34423	CTCAGCCAACTCACACCAAGC
5778	LSQLTSQ	20101	TTGTCTCAGCTGACTTCTCAG	34424	CTCAGCCAACTCACAAGCCAA
5779	LSQLVSS	20102	CTGTCGCAGCTTGTTTCGAGT	34425	CTCAGCCAACTCGTCAGCAGC
5780	LSQPLNM	20103	TTGTCTCAGCCGCTGAATATG	34426	CTCAGCCAACCACTCAACATG
5781	LSQSFAS	20104	CTTAGTCAGTCTTTTGCGAGT	34427	CTCAGCCAAAGCTTCGCAAGC
5782	LSQTARA	20105	CTGTCTCAGACTGCTCGTGCT	34428	CTCAGCCAAACAGCAAGAGCA
5783	LSQVHKF	20106	CTTTCTCAGGTTCATAAGTTT	34429	CTCAGCCAAGTCCACAAATTC
5784	LSQVQAG	20107	TTGTCTCAGGTGCAGGCTGGT	34430	CTCAGCCAAGTCCAAGCAGGA
5785	LSRDLEL	20108	TTGTCGCGTGATTTGGAGCTG	34431	CTCAGCAGAGACCTCGAACTC
5786	LSRGPTP	20109	TTGAGTCGGGGGCCGACTCCG	34432	CTCAGCAGAGGACCAACACCA
5787	LSRGQVP	20110	CTGTCTCGGGGGCAGGTTCCT	34433	CTCAGCAGAGGACAAGTCCCA
5788	LSRLGPS	20111	CTTTCGAGGCTTGGTCCGTCT	34434	CTCAGCAGACTCGGACCAAGC
5789	LSRLPSS	20112	CTTAGTAGGCTTCCTAGTTCT	34435	CTCAGCAGACTCCCAAGCAGC
5790	LSRLSTD	20113	TTGAGTAGGCTTTCTACTGAT	34436	CTCAGCAGACTCAGCACAGAC
5791	LSRNVTE	20114	TTGTCGCGTAATGTGACGGAG	34437	CTCAGCAGAAACGTCACAGAA
5792	LSRQTGY	20115	TTGAGTCGTCAGACGGGTTAT	34438	CTCAGCAGACAAACAGGATAC
5793	LSRSSAA	20116	TTGAGTAGGAGTTCTGCGGCT	34439	CTCAGCAGAAGCAGCGCAGCA
5794	LSRSVST	20117	TTGAGTCGTTCTGTGAGTACT	34440	CTCAGCAGAAGCGTCAGCACA

5795	LSRTTAD	20118	CTGTCGCGTACTACTGCTGAT	34441	CTCAGCAGAACAACAGCAGAC
5796	LSRVAVL	20119	CTGTCTAGGGTGGCGGTTCTT	34442	CTCAGCAGAGTCGCAGTCCTC
5797	LSSANST	20120	CTGTCGAGTGCGAATTCGACG	34443	CTCAGCAGCGCAAACAGCACA
5798	LSSAQRA	20121	TTGTCTTCGGCGCAGAGGGCT	34444	CTCAGCAGCGCACAAAGAGCA
5799	LSSDSPV	20122	CTGTCGTCTGATAGTCCTGTG	34445	CTCAGCAGCGACAGCCCAGTC
5800	LSSECAP	20123	TTGTCGAGTGAGTGTGCTCCT	34446	CTCAGCAGCGAATGCGCACCA
5801	LSSGMSR	20124	CTTTCGAGTGGTATGTCGCGT	34447	CTCAGCAGCGGAATGAGCAGA
5802	LSSGRPP	20125	CTTAGTTCTGGGCGTCCTCCT	34448	CTCAGCAGCGGAAGACCACCA
5803	LSSHSTS	20126	CTTTCTTCTCATAGTACGTCT	34449	CTCAGCAGCCACAGCACAAGC
5804	LSSIQTY	20127	TTGTCGTCTATTCAGACTTAT	34450	CTCAGCAGCATCCAAACATAC
5805	LSSISHN	20128	CTTAGTTCGATTTCGCATAAT	34451	CTCAGCAGCATCAGCCACAAC
5806	LSSKPYA	20129	TTGTCGAGTAAGCCGTATGCG	34452	CTCAGCAGCAAACCATACGCA
5807	LSSLAMV	20130	CTTAGTAGTCTTGCGATGGTT	34453	CTCAGCAGCCTCGCAATGGTC
5808	LSSLKGN	20131	CTGTCTTCGCTGAAGGGTAAT	34454	CTCAGCAGCCTCAAAGGAAAC
5809	LSSLKLA	20132	CTTTCTTCTCTGAAGCTTGCT	34455	CTCAGCAGCCTCAAACTCGCA
5810	LSSLMHS	20133	CTGTCGTCGCTTATGCATAGT	34456	CTCAGCAGCCTCATGCACAGC
5811	LSSLNPS	20134	CTTAGTTCTTTGAATCCTAGT	34457	CTCAGCAGCCTCAACCCAAGC
5812	LSSLPKI	20135	CTGTCGTCTCTTCCGAAGATT	34458	CTCAGCAGCCTCCCAAAAATC
5813	LSSMRST	20136	CTGTCGTCTATGCGTTCTACT	34459	CTCAGCAGCATGAGAAGCACA
5814	LSSMTND	20137	CTGAGTAGTATGACTAATGAT	34460	CTCAGCAGCATGACAAACGAC
5815	LSSNSLD	20138	CTGTCTAGTAATTCGCTGGAT	34461	CTCAGCAGCAACAGCCTCGAC
5816	LSSPAGS	20139	TTGAGTAGTCCTGCGGGGTCG	34462	CTCAGCAGCCCAGCAGGAAGC
5817	LSSPGSM	20140	CTTTCGAGTCCTGGGTCTATG	34463	CTCAGCAGCCCAGGAAGCATG
5818	LSSPMDS	20141	TTGTCTAGTCCTATGGATTCG	34464	CTCAGCAGCCCAATGGACAGC
5819	LSSQCIN	20142	CTGTCTTCTCAGTGTATTAAT	34465	CTCAGCAGCCAATGCATCAAC
5820	LSSQHTS	20143	TTGTCGTCTCAGCATACGAGT	34466	CTCAGCAGCCAACACACAAGC
5821	LSSQPKF	20144	CTGTCGTCGCAGCCTAAGTTT	34467	CTCAGCAGCCAACCAAAATTC
5822	LSSRSTT	20145	TTGAGTAGTAGGAGTACGACG	34468	CTCAGCAGCAGAAGCACAACA
5823	LSSSCER	20146	CTTTCGTCGTCGTGTGAGCGT	34469	CTCAGCAGCAGCTGCGAAAGA
5824	LSSSLEY	20147	CTGAGTTCTTCTCTTGAGTAT	34470	CTCAGCAGCAGCCTCGAATAC
5825	LSSSRPS	20148	CTGTCTTCGAGTAGGCCGTCG	34471	CTCAGCAGCAGCAGACCAAGC
5826	LSSSVVF	20149	CTTTCGAGTTCGGTTGTGTTT	34472	CTCAGCAGCAGCGTCGTCTTC
5827	LSSTSKA	20150	CTGTCGTCTACGTCTAAGGCG	34473	CTCAGCAGCACAAGCAAAGCA
5828	LSSVATP	20151	CTGAGTTCGGTTGCGACTCCG	34474	CTCAGCAGCGTCGCAACACCA
5829	LSSVFRT	20152	CTTTCGTCTGTTTTTCGGACT	34475	CTCAGCAGCGTCTTCAGAACA
5830	LSSVHAV	20153	CTGTCTAGTGTGCATGCGGTT	34476	CTCAGCAGCGTCCACGCAGTC
5831	LSSVRLS	20154	CTTTCTTCGGTGCGTCTGTCG	34477	CTCAGCAGCGTCAGACTCAGC
5832	LSTAVIR	20155	TTGTCTACTGCTGTGACTAGG	34478	CTCAGCACAGCAGTCACAAGA
5833	LSTEDLL	20156	TTGAGTACTGAGGATCTTCTT	34479	CTCAGCACAGAAGACCTCCTC
5834	LSTFPVA	20157	CTGTCGACTTTTCCTGTTGCT	34480	CTCAGCACATTCCCAGTCGCA
5835	LSTFQGG	20158	CTTTCGACTTTTCAGGGTGGG	34481	CTCAGCACATTCCAAGGAGGA
5836	LSTGSRQ	20159	CTGTCTACGGGGTCGAGGCAG	34482	CTCAGCACAGGAAGCAGACAA
5837	LSTGTMD	20160	TTGAGTACGGGTACTATGGAT	34483	CTCAGCACAGGAACAATGGAC
5838	LSTIHPS	20161	TTGTCTACGATTCATCCTTCG	34484	CTCAGCACAATCCACCCAAGC
5839	LSTKGTM	20162	CTGTCGACTAAGGGGACTATG	34485	CTCAGCACAAAAGGAACAATG

5840	LSTLENE	20163	CTGAGTACGCTTGAGAATGAG	34486	CTCAGCACACTCGAAAACGAA
5841	LSTLLTA	20164	CTTTCGACTCTTTTGACGGCT	34487	CTCAGCACACTCCTCACAGCA
5842	LSTLPKD	20165	CTGTCTACTCTGCCTAAGGAT	34488	CTCAGCACACTCCCAAAAGAC
5843	LSTMSSL	20166	TTGAGTACGATGTCTTCTCTG	34489	CTCAGCACAATGAGCAGCCTC
5844	LSTMTAY	20167	CTTAGTACGATGACTGCTTAT	34490	CTCAGCACAATGACAGCATAC
5845	LSTNMPP	20168	TTGTCTACGAATATGCCGCCG	34491	CTCAGCACAAACATGCCACCA
5846	LSTPHLT	20169	CTTTCGACTCCTCATCTGACG	34492	CTCAGCACACCACACCTCACA
5847	LSTPHMA	20170	TTGTCTACGCCGCATATGGCG	34493	CTCAGCACACCACACATGGCA
5848	LSTPSQP	20171	CTTAGTACTCCTTCGCAGCCT	34494	CTCAGCACACCAAGCCAACCA
5849	LSTRSLP	20172	CTTAGTACGAGGTCTCTGCCT	34495	CTCAGCACAAGAAGCCTCCCA
5850	LSTRSPL	20173	CTTAGTACGAGGTCTCCGCTG	34496	CTCAGCACAAGAAGCCCACTC
5851	LSTSHSV	20174	CTTTCGACTTCGCATTCGGTT	34497	CTCAGCACAAGCCACAGCGTC
5852	LSTVRMV	20175	CTTTCTACGGTGAGGATGGTT	34498	CTCAGCACAGTCAGAATGGTC
5853	LSVDEMV	20176	TTGAGTGTTGATGAGATGGTT	34499	CTCAGCGTCGACGAAATGGTC
5854	LSVGRTE	20177	CTGAGTGTGGGTCGGACGGAG	34500	CTCAGCGTCGGAAGAACAGAA
5855	LSVHGLK	20178	CTTTCTGTTCATGGGCTGAAG	34501	CTCAGCGTCCACGGACTCAAA
5856	LSVNSSL	20179	CTTTCGGTGAATAGTTCTTTG	34502	CTCAGCGTCAACAGCAGCCTC
5857	LSVPMPD	20180	CTTAGTGTGCCTATGCCTGAT	34503	CTCAGCGTCCCAATGCCAGAC
5858	LSVPRAP	20181	TTGTCTGTGCCTCGGGCTCCT	34504	CTCAGCGTCCCAAGAGCACCA
5859	LSVRGHI	20182	CTGTCGGTTAGGGGGCATATT	34505	CTCAGCGTCAGAGGACACATC
5860	LSVRSIG	20183	CTGTCTGTGCGGTCTATTGGG	34506	CTCAGCGTCAGAAGCATCGGA
5861	LSVSLTA	20184	TTGAGTGTTTCTCTTACGGCG	34507	CTCAGCGTCAGCCTCACAGCA
5862	LSVSPLS	20185	TTGAGTGTTTCTCCTTTGAGT	34508	CTCAGCGTCAGCCCACTCAGC
5863	LSVYTAD	20186	CTGAGTGTGTATACTGCGGAT	34509	CTCAGCGTCTACACAGCAGAC
5864	LSYGRPV	20187	CTTTCTTATGGTCGTCCTGTG	34510	CTCAGCTACGGAAGACCAGTC
5865	LSYPRND	20188	TTGTCTTATCCGAGGAATGAT	34511	CTCAGCTACCCAAGAAACGAC
5866	LTAPRQA	20189	CTGACTGCTCCTAGGCAGGCG	34512	CTCACAGCACCAAGACAAGCA
5867	LTAPTSQ	20190	CTTACGGCGCCTACGAGTCAG	34513	CTCACAGCACCAACAAGCCAA
5868	LTASIGN	20191	TTGACTGCGAGTATTGGGAAT	34514	CTCACAGCAAGCATCGGAAAC
5869	LTASIKA	20192	CTGACGGCGAGTATTAAGGCT	34515	CTCACAGCAAGCATCAAAGCA
5870	LTAVPLS	20193	CTTACTGCGGTGCCGCTGTCG	34516	CTCACAGCAGTCCCACTCAGC
5871	LTDENVC	20194	CTTACGGATGAGAATGTGTGT	34517	CTCACAGACGAAAACGTCTGC
5872	LTDITNR	20195	CTTACGGATATTACGAATCGG	34518	CTCACAGACATCACAAACAGA
5873	LTDLDQM	20196	TTGACGGATTTGGATCAGATG	34519	CTCACAGACCTCGACCAAATG
5874	LTDLRLV	20197	CTGACGGATCTTCGTCTGGTG	34520	CTCACAGACCTCAGACTCGTC
5875	LTDLSAS	20198	CTTACTGATCTGAGTGCTAGT	34521	CTCACAGACCTCAGCGCAAGC
5876	LTDSLRT	20199	CTTACGGATTCGCTTCGTACG	34522	CTCACAGACAGCCTCAGAACA
5877	LTDTRVT	20200	CTTACTGATACTAGGGTTACG	34523	CTCACAGACACAAGAGTCACA
5878	LTEMRPG	20201	CTTACTGAGATGCGTCCGGGG	34524	CTCACAGAAATGAGACCAGGA
5879	LTETRAG	20202	CTTACTGAGACTCGTGCTGGG	34525	CTCACAGAAACAAGAGCAGGA
5880	LTEVRTY	20203	CTTACTGAGGTGCGGACGTAT	34526	CTCACAGAAGTCAGAACATAC
5881	LTEWSKE	20204	CTTACTGAGTGGTCTAAGGAG	34527	CTCACAGAATGGAGCAAAGAA
5882	LTFGATS	20205	CTTACTTTTGGTGCTACTTCG	34528	CTCACATTCGGAGCAACAAGC
5883	LTFSAGL	20206	TTGACGTTTTCGGCTGGTTTG	34529	CTCACATTCAGCGCAGGACTC
5884	LTGAFKS	20207	CTGACTGGGGCGTTTAAGAGT	34530	CTCACAGGAGCATTCAAAAGC

5885	LTGEFRD	20208	TTGACGGGTGAGTTTCGTGAT	34531	CTCACAGGAGAATTCAGAGAC
5886	LTGFSNQ	20209	CTGACTGGTTTTTCTAATCAG	34532	CTCACAGGATTCAGCAACCAA
5887	LTGGLYG	20210	CTTACTGGGGGGTTGTATGGG	34533	CTCACAGGAGGACTCTACGGA
5888	LTGGQVA	20211	CTGACTGGTGGTCAGGTGGCT	34534	CTCACAGGAGGACAAGTCGCA
5889	LTGMIKY	20212	CTTACGGGGATGATTAAGTAT	34535	CTCACAGGAATGATCAAATAC
5890	LTGNRPA	20213	CTTACTGGTAATCGTCCTGCT	34536	CTCACAGGAAACAGACCAGCA
5891	LTGPCTS	20214	CTTACGGGTCCTTGTACGTCT	34537	CTCACAGGACCATGCACAAGC
5892	LTGQIRV	20215	TTGACTGGTCAGATTAGGGTT	34538	CTCACAGGACAAATCAGAGTC
5893	LTGRGGS	20216	TTGACTGGGCGTGGGGGTTCG	34539	CTCACAGGAAGAGGAGGAAGC
5894	LTGSSHV	20217	CTGACTGGTAGTAGTCATGTG	34540	CTCACAGGAAGCAGCCACGTC
5895	LTGTLRM	20218	CTTACTGGGACGCTTAGGATG	34541	CTCACAGGAACACTCAGAATG
5896	LTHAVPT	20219	CTTACTCATGCTGTGCCTACG	34542	CTCACACACGCAGTCCCAACA
5897	LTHKLDA	20220	TTGACTCATAAGCTGGATGCT	34543	CTCACACACAAACTCGACGCA
5898	LTHPAVH	20221	CTTACTCATCCGGCTGTGCAT	34544	CTCACACACCCAGCAGTCCAC
5899	LTHVPTA	20222	TTGACTCATGTTCCTACGGCG	34545	CTCACACACGTCCCAACAGCA
5900	LTIGHVP	20223	TTGACTATTGGTCATGTGCCT	34546	CTCACAATCGGACACGTCCCA
5901	LTIPSAQ	20224	CTTACGATTCCGTCTGCGCAG	34547	CTCACAATCCCAAGCGCACAA
5902	LTKGSVQ	20225	CTTACGAAGGGTAGTGTTCAG	34548	CTCACAAAAGGAAGCGTCCAA
5903	LTKSSHA	20226	TTGACTAAGTCGAGTCATGCT	34549	CTCACAAAAAGCAGCCACGCA
5904	LTKTVGS	20227	CTGACTAAGACTGTGGGGTCG	34550	CTCACAAAAACAGTCGGAAGC
5905	LTLAIGA	20228	CTGACTCTGGCTATTGGGGCT	34551	CTCACACTCGCAATCGGAGCA
5906	LTLGPRS	20229	TTGACTCTGGGTCCTCGTTCT	34552	CTCACACTCGGACCAAGAAGC
5907	LTLQKGT	20230	TTGACTCTGCAGAAGGGTACG	34553	CTCACACTCCAAAAAGGAACA
5908	LTLQPIA	20231	CTTACGTTGCAGCCGATTGCT	34554	CTCACACTCCAACCAATCGCA
5909	LTLTGSS	20232	CTGACGCTGACTGGTTCTTCT	34555	CTCACACTCACAGGAAGCAGC
5910	LTLTSAH	20233	TTGACTCTGACGTCGGCTCAT	34556	CTCACACTCACAAGCGCACAC
5911	LTLVHAE	20234	CTGACGTTGGTTCATGCTGAG	34557	CTCACACTCGTCCACGCAGAA
5912	LTMGSAS	20235	TTGACTATGGGTTCGGCGTCT	34558	CTCACAATGGGAAGCGCAAGC
5913	LTMIQRD	20236	CTTACGATGATTCAGCGGGAT	34559	CTCACAATGATCCAAAGAGAC
5914	LTMRPPS	20237	TTGACTATGAGGCCGCCGAGT	34560	CTCACAATGAGACCACCAAGC
5915	LTMSRAL	20238	TTGACGATGTCGAGGGCTCTT	34561	CTCACAATGAGCAGAGCACTC
5916	LTNAHHL	20239	CTTACGAATGCTCATCATCTT	34562	CTCACAAACGCACACCACCTC
5917	LTNARPA	20240	TTGACGAATGCGCGTCCGGCG	34563	CTCACAAACGCAAGACCAGCA
5918	LTNEAHR	20241	CTTACTAATGAGGCTCATCGG	34564	CTCACAAACGAAGCACACAGA
5919	LTNKPIC	20242	TTGACTAATAAGCCGATTTGT	34565	CTCACAAACAAACCAATCTGC
5920	LTNMRTT	20243	CTTACGAATATGCGTACTACT	34566	CTCACAAACATGAGAACAACA
5921	LTNNEQV	20244	CTGACGAATAATGAGCAGGTT	34567	CTCACAAACAACGAACAAGTC
5922	LTNRQNQ	20245	TTGACTAATCGTCAGAATCAG	34568	CTCACAAACAGACAAAACCAA
5923	LTPALGP	20246	TTGACGCCTGCGTTGGGTCCT	34569	CTCACACCAGCACTCGGACCA
5924	LTPARTY	20247	CTTACTCCGGCTAGGACGTAT	34570	CTCACACCAGCAAGAACATAC
5925	LTPGRGV	20248	CTGACTCCTGGTCGGGGGGTG	34571	CTCACACCAGGAAGAGGAGTC
5926	LTPHVMD	20249	CTGACGCCGCATGTTATGGAT	34572	CTCACACCACACGTCATGGAC
5927	LTPINSA	20250	TTGACTCCGATTAATTCTGCT	34573	CTCACACCAATCAACAGCGCA
5928	LTPKSIS	20251	CTTACGCCGAAGTCGATTTCT	34574	CTCACACCAAAAAGCATCAGC
5929	LTPLLGS	20252	TTGACGCCGCTTCTTGGTAGT	34575	CTCACACCACTCCTCGGAAGC

5930	LTPLMSD	20253	TTGACGCCGCTGATGTCTGAT	34576	CTCACACCACTCATGAGCGAC
5931	LTPRLPA	20254	TTGACTCCTCGGTTGCCTGCT	34577	CTCACACCAAGACTCCCAGCA
5932	LTPSGHW	20255	CTTACGCCTTCTGGTCATTGG	34578	CTCACACCAAGCGGACACTGG
5933	LTPSGYN	20256	CTGACGCCTTCGGGGTATAAT	34579	CTCACACCAAGCGGATACAAC
5934	LTPSQPY	20257	CTGACTCCGTCGCAGCCTTAT	34580	CTCACACCAAGCCAACCATAC
5935	LTPSVKG	20258	CTGACGCCTTCGGTTAAGGGT	34581	CTCACACCAAGCGTCAAAGGA
5936	LTPSVPH	20259	TTGACTCCTAGTGTTCCGCAT	34582	CTCACACCAAGCGTCCCACAC
5937	LTPTKME	20260	CTGACTCCTACGAAGATGGAG	34583	CTCACACCAACAAAAATGGAA
5938	LTPVSPD	20261	CTTACTCCTGTTTCGCCGGAT	34584	CTCACACCAGTCAGCCCAGAC
5939	LTQKTPY	20262	CTTACGCAGAAGACTCCGTAT	34585	CTCACACAAAAAACACCATAC
5940	LTQLRVT	20263	CTTACTCAGTTGAGGGTTACT	34586	CTCACACAACTCAGAGTCACA
5941	LTQSHPA	20264	CTGACTCAGTCTCATCCGGCT	34587	CTCACACAAAGCCACCCAGCA
5942	LTRKETD	20265	CTTACTCGGAAGGAGACTGAT	34588	CTCACAAGAAAAGAAACAGAC
5943	LTRPDDT	20266	CTGACTAGGCCTGATGATACG	34589	CTCACAAGACCAGACGACACA
5944	LTRQHSD	20267	CTTACTCGGCAGCATTCTGAT	34590	CTCACAAGACAACACAGCGAC
5945	LTRSPPA	20268	CTGACTCGGTCTCCGCCTGCT	34591	CTCACAAGAAGCCCACCAGCA
5946	LTSAPGR	20269	TTGACGAGTGCTCCGGGGCGT	34592	CTCACAAGCGCACCAGGAAGA
5947	LTSGKSQ	20270	CTGACTTCTGGTAAGTCGCAG	34593	CTCACAAGCGGAAAAAGCCAA
5948	LTSGPLR	20271	CTGACGTCTGGGCCGCTTCGG	34594	CTCACAAGCGGACCACTCAGA
5949	LTSHAQY	20272	CTTACGTCGCATGCGCAGTAT	34595	CTCACAAGCCACGCACAATAC
5950	LTSKHLP	20273	TTGACTAGTAAGCATTTGCCG	34596	CTCACAAGCAAACACCTCCCA
5951	LTSKQGS	20274	TTGACTAGTAAGCAGGGTTCG	34597	CTCACAAGCAAACAAGGAAGC
5952	LTSLKSA	20275	TTGACTTCTCTGAAGAGTGCT	34598	CTCACAAGCCTCAAAAGCGCA
5953	LTSLRTE	20276	TTGACTTCTCTTCGTACGGAG	34599	CTCACAAGCCTCAGAACAGAA
5954	LTSLYGV	20277	CTGACTTCGCTTTATGGTGTT	34600	CTCACAAGCCTCTACGGAGTC
5955	LTSNEMS	20278	CTTACTAGTAATGAGATGAGT	34601	CTCACAAGCAACGAAATGAGC
5956	LTSNRAL	20279	CTGACGTCGAATAGGGCTTTG	34602	CTCACAAGCAACAGAGCACTC
5957	LTSRTVP	20280	CTTACTAGTCGGACGGTGCCT	34603	CTCACAAGCAGAACAGTCCCA
5958	LTSTAQS	20281	TTGACGTCTACGGCTCAGAGT	34604	CTCACAAGCACAGCACAAAGC
5959	LTSTNGM	20282	TTGACTAGTACTAATGGGATG	34605	CTCACAAGCACAAACGGAATG
5960	LTSTRLS	20283	TTGACTAGTACTCGTCTTAGT	34606	CTCACAAGCACAAGACTCAGC
5961	LTTARPL	20284	CTTACGACTGCGCGGCCTCTT	34607	CTCACAACAGCAAGACCACTC
5962	LTTGAYG	20285	CTTACGACGGGTGCTTATGGG	34608	CTCACAACAGGAGCATACGGA
5963	LTTIRDV	20286	CTTACGACTATTAGGGATGTG	34609	CTCACAACAATCAGAGACGTC
5964	LTTKAAN	20287	TTGACGACTAAGGCTGCGAAT	34610	CTCACAACAAAAGCAGCAAAC
5965	LTTKNMA	20288	CTTACTACGAAGAATATGGCG	34611	CTCACAACAAAAAACATGGCA
5966	LTTKRLD	20289	CTGACGACTAAGCGGCTTGAT	34612	CTCACAACAAAAAGACTCGAC
5967	LTTKSQD	20290	CTTACGACTAAGAGTCAGGAT	34613	CTCACAACAAAAAGCCAAGAC
5968	LTTLHSK	20291	TTGACTACGCTTCATTCTAAG	34614	CTCACAACACTCCACAGCAAA
5969	LTTMNAF	20292	CTGACGACGATGAATGCGTTT	34615	CTCACAACAATGAACGCATTC
5970	LTTMRSN	20293	TTGACTACGATGAGGTCGAAT	34616	CTCACAACAATGAGAAGCAAC
5971	LTTMSKA	20294	TTGACTACTATGTCGAAGGCG	34617	CTCACAACAATGAGCAAAGCA
5972	LTTPLPH	20295	CTTACGACTCCTCTTCCGCAT	34618	CTCACAACACCACTCCCACAC
5973	LTTQEHW	20296	TTGACTACGCAGGAGCATTGG	34619	CTCACAACACAAGAACACTGG
5974	LTTRPAF	20297	CTGACTACTAGGCCTGCTTTT	34620	CTCACAACAAGACCAGCATTC

5975	LTTRSSP	20298	CTGACGACGCGGTCGAGTCCG	34621	CTCACAACAAGAAGCAGCCCA
5976	LTTSLKP	20299	TTGACTACGTCGCTTAAGCCT	34622	CTCACAACAAGCCTCAAACCA
5977	LTTSSFT	20300	TTGACTACGAGTTCTTTTACG	34623	CTCACAACAAGCAGCTTCACA
5978	LTTTINN	20301	TTGACTACTACTATTAATAAT	34624	CTCACAACAACAATCAACAAC
5979	LTTTPAK	20302	TTGACTACGACGCCGGCTAAG	34625	CTCACAACAACACCAGCAAAA
5980	LTVGATI	20303	CTTACGGTGGGGGCTACGATT	34626	CTCACAGTCGGAGCAACAATC
5981	LTVQETQ	20304	TTGACTGTGCAGGAGACTCAG	34627	CTCACAGTCCAAGAAACACAA
5982	LTVSAVK	20305	CTTACGGTGTCGGCTGTGAAG	34628	CTCACAGTCAGCGCAGTCAAA
5983	LTVSNLP	20306	CTTACTGTGTCTAATCTGCCT	34629	CTCACAGTCAGCAACCTCCCA
5984	LTVTWAE	20307	CTTACTGTTACTTGGGCTGAG	34630	CTCACAGTCACATGGGCAGAA
5985	LTVVPSG	20308	TTGACGGTGGTTCCTAGTGGT	34631	CTCACAGTCGTCCCAAGCGGA
5986	LTYFVEE	20309	CTGACGTATTTTGTGGAGGAG	34632	CTCACATACTTCGTCGAAGAA
5987	LTYPGSQ	20310	CTTACGTATCCTGGTAGTCAG	34633	CTCACATACCCAGGAAGCCAA
5988	LTYRGGE	20311	TTGACTTATCGTGGTGGGGAG	34634	CTCACATACAGAGGAGGAGAA
5989	LTYSPQT	20312	CTTACTTATAGTCCGCAGACG	34635	CTCACATACAGCCCACAAACA
5990	LTYSRSD	20313	TTGACGTATTCTCGGAGTGAT	34636	CTCACATACAGCAGAAGCGAC
5991	LVAKMTP	20314	TTGGTTGCTAAGATGACTCCG	34637	CTCGTCGCAAAAATGACACCA
5992	LVARGGA	20315	TTGGTGGCGCGTGGGGGTGCT	34638	CTCGTCGCAAGAGGAGGAGCA
5993	LVATQAP	20316	CTGGTTGCGACGCAGGCGCCT	34639	CTCGTCGCAACACAAGCACCA
5994	LVAVSTT	20317	CTTGTGGCTGTTAGTACGACT	34640	CTCGTCGCAGTCAGCACAACA
5995	LVDSRTM	20318	CTTGTGGATTCGCGGACTATG	34641	CTCGTCGACAGCAGAACAATG
5996	LVEGLID	20319	CTGGTTGAGGGGCTGATTGAT	34642	CTCGTCGAAGGACTCATCGAC
5997	LVENRRE	20320	TTGGTTGAGAATCGTCGTGAG	34643	CTCGTCGAAAACAGAAGAGAA
5998	LVEPMKH	20321	CTGGTGGAGCCTATGAAGCAT	34644	CTCGTCGAACCAATGAAACAC
5999	LVETKGS	20322	CTTGTGGAGACGAAGGGTAGT	34645	CTCGTCGAAACAAAAGGAAGC
6000	LVETLTH	20323	TTGGTTGAGACGTTGACTCAT	34646	CTCGTCGAAACACTCACACAC
6001	LVGESHI	20324	CTGGTTGGTGAGTCGCATATT	34647	CTCGTCGGAGAAAGCCACATC
6002	LVGHPTP	20325	CTGGTGGGTCATCCTACGCCT	34648	CTCGTCGGACACCCAACACCA
6003	LVGHTGS	20326	CTGGTGGGTCATACTGGTTCT	34649	CTCGTCGGACACACAGGAAGC
6004	LVGQVAV	20327	TTGGTGGGTCAGGTTGCGGTT	34650	CTCGTCGGACAAGTCGCAGTC
6005	LVGRACC	20328	TTGGTTGGGCGTGCTTGTTGT	34651	CTCGTCGGAAGAGCATGCTGC
6006	LVGRLST	20329	TTGGTTGGTCGGCTGTCTACG	34652	CTCGTCGGAAGACTCAGCACA
6007	LVGSPPS	20330	CTGGTTGGTTCTCCTCCTTCT	34653	CTCGTCGGAAGCCCACCAAGC
6008	LVHLMTD	20331	CTGGTGCATTTGATGACTGAT	34654	CTCGTCCACCTCATGACAGAC
6009	LVHNRTS	20332	TTGGTTCATAATCGGACGTCT	34655	CTCGTCCACAACAGAACAAGC
6010	LVHYSPD	20333	CTTGTTCATTATTCTCCGGAT	34656	CTCGTCCACTACAGCCCAGAC
6011	LVIPGPG	20334	CTGGTTATTCCGGGGCCTGGT	34657	CTCGTCATCCCAGGACCAGGA
6012	LVKESPT	20335	CTTGTGAAGGAGAGTCCTACG	34658	CTCGTCAAAGAAAGCCCAACA
6013	LVKGGPN	20336	CTTGTTAAGGGTGGGCCTAAT	34659	CTCGTCAAAGGAGGACCAAAC
6014	LVKQTTL	20337	CTTGTGAAGCAGACTACGCTG	34660	CTCGTCAAACAAACAACACTC
6015	LVKSVDQ	20338	CTGGTGAAGTCGGTTGATCAG	34661	CTCGTCAAAAGCGTCGACCAA
6016	LVLGPPA	20339	CTGGTTCTTGGGCCTCCTGCG	34662	CTCGTCCTCGGACCACCAGCA
6017	LVLGSKS	20340	CTTGTTTTGGGTAGTAAGTCT	34663	CTCGTCCTCGGAAGCAAAAGC
6018	LVLNNDG	20341	TTGGTTCTGAATAATGATGGG	34664	CTCGTCCTCAACAACGACGGA
6019	LVLPARQ	20342	CTTGTGCTTCCGGCGAGGCAG	34665	CTCGTCCTCCCAGCAAGACAA

6020	LVLPQKS	20343	TTGGTGCTGCCGCAGAAGAGT	34666	CTCGTCCTCCCACAAAAAAGC
6021	LVLSNAS	20344	CTGGTTTTGTCGAATGCGTCG	34667	CTCGTCCTCAGCAACGCAAGC
6022	LVMSPAP	20345	CTGGTGATGAGTCCGGCTCCT	34668	CTCGTCATGAGCCCAGCACCA
6023	LVMSTRA	20346	TTGGTTATGTCTACGAGGGCG	34669	CTCGTCATGAGCACAAGAGCA
6024	LVMTSGS	20347	CTTGTTATGACGTCGGGGAGT	34670	CTCGTCATGACAAGCGGAAGC
6025	LVNDCCT	20348	CTGGTGAATGATTGTTGTACT	34671	CTCGTCAACGACTGCTGCACA
6026	LVNETTR	20349	CTGGTGAATGAGACGACTCGT	34672	CTCGTCAACGAAACAACAAGA
6027	LVNKLGP	20350	CTTGTTAATAAGTTGGGGCCT	34673	CTCGTCAACAAACTCGGACCA
6028	LVNKSYN	20351	CTGGTTAATAAGAGTTATAAT	34674	CTCGTCAACAAAAGCTACAAC
6029	LVNPGTR	20352	CTTGTGAATCCTGGGACGCGG	34675	CTCGTCAACCCAGGAACAAGA
6030	LVNSKDS	20353	TTGGTTAATTCTAAGGATTCG	34676	CTCGTCAACAGCAAAGACAGC
6031	LVNTPTE	20354	TTGGTGAATACTCCTACGGAG	34677	CTCGTCAACACACCAACAGAA
6032	LVPARSG	20355	CTGGTGCCTGCGCGGTCTGGT	34678	CTCGTCCCAGCAAGAAGCGGA
6033	LVPGLTG	20356	CTGGTTCCTGGGCTGACGGGG	34679	CTCGTCCCAGGACTCACAGGA
6034	LVPGMIT	20357	TTGGTTCCTGGTATGATTACT	34680	CTCGTCCCAGGAATGATCACA
6035	LVPGVHS	20358	CTGGTGCCGGGTGTTCATTCT	34681	CTCGTCCCAGGAGTCCACAGC
6036	LVPHSNF	20359	TTGGTTCCTCATAGTAATTTT	34682	CTCGTCCCACACAGCAACTTC
6037	LVPKHMN	20360	CTTGTGCCTAAGCATATGAAT	34683	CTCGTCCCAAAACACATGAAC
6038	LVPLLPA	20361	TTGGTTCCGTTGCTTCCGGCT	34684	CTCGTCCCACTCCTCCCAGCA
6039	LVPLPHS	20362	TTGGTTCCGCTTCCTCATTCG	34685	CTCGTCCCACTCCCACACAGC
6040	LVPLYTE	20363	CTTGTTCCGCTGTATACTGAG	34686	CTCGTCCCACTCTACACAGAA
6041	LVPNFQP	20364	TTGGTTCCGAATTTTCAGCCT	34687	CTCGTCCCAAACTTCCAACCA
6042	LVPNSAE	20365	CTGGTGCCGAATAGTGCGGAG	34688	CTCGTCCCAAACAGCGCAGAA
6043	LVPRAAD	20366	CTTGTTCCGCGGGCTGCGGAT	34689	CTCGTCCCAAGAGCAGCAGAC
6044	LVPRNSL	20367	CTTGTGCCGCGTAATAGTCTT	34690	CTCGTCCCAAGAAACAGCCTC
6045	LVPSIQT	20368	TTGGTTCCTTCGATTCAGACT	34691	CTCGTCCCAAGCATCCAAACA
6046	LVPSLEQ	20369	TTGGTTCCGAGTTTGGAGCAG	34692	CTCGTCCCAAGCCTCGAACAA
6047	LVPVSLS	20370	CTTGTGCCTGTGAGTTTGAGT	34693	CTCGTCCCAGTCAGCCTCAGC
6048	LVQLDVA	20371	TTGGTTCAGTTGGATGTGGCG	34694	CTCGTCCAACTCGACGTCGCA
6049	LVQSLGM	20372	CTGGTGCAGTCGCTGGGGATG	34695	CTCGTCCAAAGCCTCGGAATG
6050	LVRAMDT	20373	CTTGTGAGGGCTATGGATACG	34696	CTCGTCAGAGCAATGGACACA
6051	LVRGASH	20374	CTTGTGCGTGGGGCTAGTCAT	34697	CTCGTCAGAGGAGCAAGCCAC
6052	LVRHDNL	20375	CTTGTTCGGCATGATAATTTG	34698	CTCGTCAGACACGACAACCTC
6053	LVRNGLS	20376	CTTGTTCGTAATGGGCTTTCG	34699	CTCGTCAGAAACGGACTCAGC
6054	LVRPSPA	20377	CTGGTGCGTCCGTCTCCTGCT	34700	CTCGTCAGACCAAGCCCAGCA
6055	LVSGHHM	20378	CTTGTTTCGGGTCATCATATG	34701	CTCGTCAGCGGACACCACATG
6056	LVSGNRV	20379	CTTGTGTCGGGTAATCGTGTG	34702	CTCGTCAGCGGAAACAGAGTC
6057	LVSGTDR	20380	CTTGTTAGTGGGACTGATAGG	34703	CTCGTCAGCGGAACAGACAGA
6058	LVSHPRP	20381	TTGGTTTCTCATCCTCGGCCT	34704	CTCGTCAGCCACCCAAGACCA
6059	LVSHRSA	20382	TTGGTTTCTCATCGGTCGGCT	34705	CTCGTCAGCCACAGAAGCGCA
6060	LVSKDES	20383	CTGGTTAGTAAGGATGAGAGT	34706	CTCGTCAGCAAAGACGAAAGC
6061	LVSPARP	20384	CTTGTTAGTCCGGCTCGGCCG	34707	CTCGTCAGCCCAGCAAGACCA
6062	LVSPEEG	20385	CTGGTTTCTCCTGAGGAGGGG	34708	CTCGTCAGCCCAGAAGAAGGA
6063	LVSPSLT	20386	CTGGTTTCGCCTTCTTTGACT	34709	CTCGTCAGCCCAAGCCTCACA
6064	LVSSKHP	20387	CTGGTGTCGTCTAAGCATCCG	34710	CTCGTCAGCAGCAAACACCCA

6065	LVSSPRT	20388	CTTGTGTCGTCGCCTCGGACT	34711	CTCGTCAGCAGCCCAAGAACA
6066	LVSTMTE	20389	CTTGTTTCGACGATGACTGAG	34712	CTCGTCAGCACAATGACAGAA
6067	LVTAGPL	20390	CTTGTGACTGCGGGTCCGTTG	34713	CTCGTCACAGCAGGACCACTC
6068	LVTAPTP	20391	CTTGTTACTGCGCCGACTCCT	34714	CTCGTCACAGCACCAACACCA
6069	LVTAQHP	20392	TTGGTTACTGCTCAGCATCCG	34715	CTCGTCACAGCACAACACCCA
6070	LVTGDAS	20393	CTGGTTACGGGGGATGCTAGT	34716	CTCGTCACAGGAGACGCAAGC
6071	LVTHNYA	20394	CTGGTGACGCATAATTATGCT	34717	CTCGTCACACACAACTACGCA
6072	LVTMRPV	20395	CTTGTGACGATGAGGCCGGTT	34718	CTCGTCACAATGAGACCAGTC
6073	LVTNAHS	20396	TTGGTGACGAATGCGCATAGT	34719	CTCGTCACAAACGCACACAGC
6074	LVTPGDR	20397	CTTGTGACTCCTGGGGATAGG	34720	CTCGTCACACCAGGAGACAGA
6075	LVTQSNE	20398	CTGGTTACTCAGTCTAATGAG	34721	CTCGTCACACAAAGCAACGAA
6076	LVTYTPM	20399	CTTGTGACTTATACTCCTATG	34722	CTCGTCACATACACACCAATG
6077	LVVAAHL	20400	TTGGTGGTGGCTGCGCATTTG	34723	CTCGTCGTCGCAGCACACCTC
6078	LVVAERI	20401	TTGGTGGTGGCGGAGAGGATT	34724	CTCGTCGTCGCAGAAAGAATC
6079	LVVDEMT	20402	TTGGTTGTTGATGAGATGACG	34725	CTCGTCGTCGACGAAATGACA
6080	LVVNRMD	20403	CTTGTTGTTAATCGTATGGAT	34726	CTCGTCGTCAACAGAATGGAC
6081	LVVPGNG	20404	CTTGTGGTTCCTGGTAATGGT	34727	CTCGTCGTCCCAGGAAACGGA
6082	LVYGHDH	20405	CTGGTGTATGGTCATGATCAT	34728	CTCGTCTACGGACACGACCAC
6083	LVYTSTS	20406	TTGGTTTATACTTCGACGTCG	34729	CTCGTCTACACAAGCACAAGC
6084	LWDLGNP	20407	CTGTGGGATCTTGGTAATCCG	34730	CTCTGGGACCTCGGAAACCCA
6085	LWETSTD	20408	TTGTGGGAGACTTCTACTGAT	34731	CTCTGGGAAACAAGCACAGAC
6086	LWGDGTL	20409	CTGTGGGGGGATGGTACGTTG	34732	CTCTGGGGAGACGGAACACTC
6087	LWNKPDD	20410	CTGTGGAATAAGCCTGATGAT	34733	CTCTGGAACAAACCAGACGAC
6088	LWNSNTA	20411	TTGTGGAATTCTAATACTGCT	34734	CTCTGGAACAGCAACACAGCA
6089	LWQSEVD	20412	CTGTGGCAGTCTGAGGTGGAT	34735	CTCTGGCAAAGCGAAGTCGAC
6090	LWRADDA	20413	CTGTGGCGTGCGGATGATGCT	34736	CTCTGGAGAGCAGACGACGCA
6091	LWRSSTT	20414	TTGTGGAGGTCGTCTACGACG	34737	CTCTGGAGAAGCAGCACAACA
6092	LWTAERD	20415	CTTTGGACGGCTGAGCGTGAT	34738	CTCTGGACAGCAGAAAGAGAC
6093	LWTGSGP	20416	TTGTGGACTGGTTCGGGTCCT	34739	CTCTGGACAGGAAGCGGACCA
6094	LWTNQPS	20417	CTTTGGACGAATCAGCCGAGT	34740	CTCTGGACAAACCAACCAAGC
6095	LYANSKP	20418	CTTTATGCTAATTCTAAGCCT	34741	CTCTACGCAAACAGCAAACCA
6096	LYDLRGA	20419	TTGTATGATTTGCGGGGGGCG	34742	CTCTACGACCTCAGAGGAGCA
6097	LYDSQDT	20420	CTGTATGATTCGCAGGATACT	34743	CTCTACGACAGCCAAGACACA
6098	LYDTSLL	20421	TTGTATGATACTAGTCTGCTT	34744	CTCTACGACACAAGCCTCCTC
6099	LYEHSSP	20422	CTGTATGAGCATTCTAGTCCT	34745	CTCTACGAACACAGCAGCCCA
6100	LYEYPSG	20423	CTTTATGAGTATCCTAGTGGG	34746	CTCTACGAATACCCAAGCGGA
6101	LYGSLVP	20424	TTGTATGGTAGTTTGGTGCCG	34747	CTCTACGGAAGCCTCGTCCCA
6102	LYGTSAI	20425	TTGTATGGTACGTCTGCGATT	34748	CTCTACGGAACAAGCGCAATC
6103	LYKSPET	20426	CTGTATAAGTCGCCTGAGACT	34749	CTCTACAAAAGCCCAGAAACA
6104	LYLGSKD	20427	CTTTATCTGGGTAGTAAGGAT	34750	CTCTACCTCGGAAGCAAAGAC
6105	LYLQNDK	20428	TTGTATCTGCAGAATGATAAG	34751	CTCTACCTCCAAAACGACAAA
6106	LYLTSLD	20429	CTGTATCTTACGTCTCTTGAT	34752	CTCTACCTCACAAGCCTCGAC
6107	LYNDFSF	20430	CTGTATAATGATTTTAGTTTT	34753	CTCTACAACGACTTCAGCTTC
6108	LYNSSDS	20431	TTGTATAATTCTTCTGATTCG	34754	CTCTACAACAGCAGCGACAGC
6109	LYPHAPS	20432	CTTTATCCTCATGCTCCTTCT	34755	CTCTACCCACACGCACCAAGC

6110	LYPLQTA	20433	CTTTATCCTCTTCAGACTGCT	34756	CTCTACCCACTCCAAACAGCA
6111	LYQGSNS	20434	TTGTATCAGGGTAGTAATTCT	34757	CTCTACCAAGGAAGCAACAGC
6112	LYQGYSA	20435	CTTTATCAGGGTTATAGTGCT	34758	CTCTACCAAGGATACAGCGCA
6113	LYSAASK	20436	CTGTATTCTGCTGCGAGTAAG	34759	CTCTACAGCGCAGCAAGCAAA
6114	LYSEVGL	20437	CTGTATAGTGAGGTTGGTTTG	34760	CTCTACAGCGAAGTCGGACTC
6115	LYSGTIP	20438	CTGTATTCGGGGACTATTCCT	34761	CTCTACAGCGGAACAATCCCA
6116	LYSNPNV	20439	CTGTATTCTAATCCTAATGTG	34762	CTCTACAGCAACCCAAACGTC
6117	LYSPLSN	20440	TTGTATTCTCCTCTGTCTAAT	34763	CTCTACAGCCCACTCAGCAAC
6118	LYTATAK	20441	CTGTATACTGCGACGGCGAAG	34764	CTCTACACAGCAACAGCAAAA
6119	LYTDSAF	20442	TTGTATACGGATTCTGCTTTT	34765	CTCTACACAGACAGCGCATTC
6120	LYTGLGT	20443	TTGTATACTGGGCTTGGGACT	34766	CTCTACACAGGACTCGGAACA
6121	LYTKNEG	20444	TTGTATACGAAGAATGAGGGT	34767	CTCTACACAAAAAACGAAGGA
6122	LYTKSVP	20445	CTGTATACTAAGTCGGTGCCT	34768	CTCTACACAAAAAGCGTCCCA
6123	LYTPNGA	20446	CTTTATACTCCGAATGGTGCT	34769	CTCTACACACCAAACGGAGCA
6124	LYTSLPQ	20447	CTTTATACTAGTCTGCCTCAG	34770	CTCTACACAAGCCTCCCACAA
6125	LYTSSGS	20448	CTGTATACTTCTAGTGGGTCG	34771	CTCTACACAAGCAGCGGAAGC
6126	LYTVTSG	20449	TTGTATACGGTTACTTCGGGG	34772	CTCTACACAGTCACAAGCGGA
6127	LYVSEKP	20450	CTGTATGTGTCTGAGAAGCCT	34773	CTCTACGTCAGCGAAAAACCA
6128	LYYPSTE	20451	TTGTATTATCCGAGTACGGAG	34774	CTCTACTACCCAAGCACAGAA
6129	MAALNDF	20452	ATGGCGGCGTTGAATGATTTT	34775	ATGGCAGCACTCAACGACTTC
6130	MAAQDYA	20453	ATGGCGGCGCAGGATTATGCG	34776	ATGGCAGCACAAGACTACGCA
6131	MAARTSN	20454	ATGGCGGCGAGGACTAGTAAT	34777	ATGGCAGCAAGAACAAGCAAC
6132	MAASKTF	20455	ATGGCTGCTAGTAAGACGTTT	34778	ATGGCAGCAAGCAAAACATTC
6133	MAEFVHR	20456	ATGGCGGAGTTTGTTCATCGT	34779	ATGGCAGAATTCGTCCACAGA
6134	MAGKASH	20457	ATGGCTGGGAAGGCTTCTCAT	34780	ATGGCAGGAAAAGCAAGCCAC
6135	MAGNLVT	20458	ATGGCGGGGAATCTTGTTACT	34781	ATGGCAGGAAACCTCGTCACA
6136	MAKLTVS	20459	ATGGCTAAGCTTACTGTGTCT	34782	ATGGCAAAACTCACAGTCAGC
6137	MALQGSL	20460	ATGGCGTTGCAGGGTTCTCTG	34783	ATGGCACTCCAAGGAAGCCTC
6138	MALRLVN	20461	ATGGCGCTTCGGCTTGTTAAT	34784	ATGGCACTCAGACTCGTCAAC
6139	MANMSSP	20462	ATGGCTAATATGTCGTCGCCG	34785	ATGGCAAACATGAGCAGCCCA
6140	MAPVRVP	20463	ATGGCTCCGGTGCGGGTTCCT	34786	ATGGCACCAGTCAGAGTCCCA
6141	MARALPP	20464	ATGGCTCGGGCTCTTCCGCCG	34787	ATGGCAAGAGCACTCCCACCA
6142	MARDVDR	20465	ATGGCTCGGGATGTGGATCGG	34788	ATGGCAAGAGACGTCGACAGA
6143	MARETTY	20466	ATGGCGCGTGAGACGACTTAT	34789	ATGGCAAGAGAAACAACATAC
6144	MASATPV	20467	ATGGCGAGTGCTACGCCGGTT	34790	ATGGCAAGCGCAACACCAGTC
6145	MASGQSL	20468	ATGGCGTCGGGGCAGTCGCTG	34791	ATGGCAAGCGGACAAAGCCTC
6146	MASHVPV	20469	ATGGCGTCGCATGTTCCTGTG	34792	ATGGCAAGCCACGTCCCAGTC
6147	MASPYSS	20470	ATGGCGTCTCCTTATTCGAGT	34793	ATGGCAAGCCCATACAGCAGC
6148	MASQIRP	20471	ATGGCTTCTCAGATTAGGCCT	34794	ATGGCAAGCCAAATCAGACCA
6149	MASSYND	20472	ATGGCGTCTTCGTATAATGAT	34795	ATGGCAAGCAGCTACAACGAC
6150	MASTESR	20473	ATGGCTTCTACTGAGTCGCGT	34796	ATGGCAAGCACAGAAAGCAGA
6151	MATAPLH	20474	ATGGCGACGGCGCCTCTTCAT	34797	ATGGCAACAGCACCACTCCAC
6152	MATDRRY	20475	ATGGCTACTGATCGGAGGTAT	34798	ATGGCAACAGACAGAAGATAC
6153	MATHVMG	20476	ATGGCTACTCATGTGATGGGG	34799	ATGGCAACACACGTCATGGGA
6154	MAVKVGE	20477	ATGGCTGTTAAGGTTGGTGAG	34800	ATGGCAGTCAAAGTCGGAGAA

6155	MAYQPTL	20478	ATGGCGTATCAGCCGACGCTG	34801	ATGGCATACCAACCAACACTC
6156	MAYQQIP	20479	ATGGCGTATCAGCAGATTCCT	34802	ATGGCATACCAACAAATCCCA
6157	MCDSDRP	20480	ATGTGTGATTCTGATCGTCCT	34803	ATGTGCGACAGCGACAGACCA
6158	MDDRAGF	20481	ATGGATGATAGGGCGGGGTTT	34804	ATGGACGACAGAGCAGGATTC
6159	MDEPEPS	20482	ATGGATGAGCCTGAGCCTTCT	34805	ATGGACGAACCAGAACCAAGC
6160	MDKILTS	20483	ATGGATAAGATTCTTACTTCT	34806	ATGGACAAAATCCTCACAAGC
6161	MDLTGPV	20484	ATGGATTTGACTGGGCCGGTG	34807	ATGGACCTCACAGGACCAGTC
6162	MDMGGSP	20485	ATGGATATGGGTGGTAGTCCT	34808	ATGGACATGGGAGGAAGCCCA
6163	MDNLRQS	20486	ATGGATAATTTGAGGCAGTCG	34809	ATGGACAACCTCAGACAAAGC
6164	MDRALHG	20487	ATGGATCGGGCGTTGCATGGG	34810	ATGGACAGAGCACTCCACGGA
6165	MDRMTLM	20488	ATGGATAGGATGACTTTGATG	34811	ATGGACAGAATGACACTCATG
6166	MDRNFVM	20489	ATGGATCGTAATTTTGTGATG	34812	ATGGACAGAAACTTCGTCATG
6167	MDRPSTS	20490	ATGGATCGGCCTTCGACTTCG	34813	ATGGACAGACCAAGCACAAGC
6168	MDSADYE	20491	ATGGATTCGGCTGATTATGAG	34814	ATGGACAGCGCAGACTACGAA
6169	MDSLPPP	20492	ATGGATTCGCTTCCGCCGCCG	34815	ATGGACAGCCTCCCACCACCA
6170	MDSRTLL	20493	ATGGATAGTAGGACGCTTCTT	34816	ATGGACAGCAGAACACTCCTC
6171	MDSTSPP	20494	ATGGATAGTACTTCGCCGCCG	34817	ATGGACAGCACAAGCCCACCA
6172	MDVSHGS	20495	ATGGATGTTTCGCATGGGAGT	34818	ATGGACGTCAGCCACGGAAGC
6173	MEFGTTP	20496	ATGGAGTTTGGTACGACGCCT	34819	ATGGAATTCGGAACAACACCA
6174	MEFVSTF	20497	ATGGAGTTTGTTTCGACGTTT	34820	ATGGAATTCGTCAGCACATTC
6175	MEGSGRN	20498	ATGGAGGGTTCTGGTCGTAAT	34821	ATGGAAGGAAGCGGAAGAAAC
6176	MEIESLN	20499	ATGGAGATTGAGTCGCTGAAT	34822	ATGGAAATCGAAAGCCTCAAC
6177	MEITRAP	20500	ATGGAGATTACGCGTGCGCCT	34823	ATGGAAATCACAAGAGCACCA
6178	MEKATPS	20501	ATGGAGAAGGCTACGCCGTCT	34824	ATGGAAAAAGCAACACCAAGC
6179	MEKLKQN	20502	ATGGAGAAGCTGAAGCAGAAT	34825	ATGGAAAAACTCAAACAAAAC
6180	MELIEGP	20503	ATGGAGTTGATTGAGGGTCCT	34826	ATGGAACTCATCGAAGGACCA
6181	MENTTRS	20504	ATGGAGAATACGACGCGGAGT	34827	ATGGAAAACACAACAAGAAGC
6182	MEPKRSY	20505	ATGGAGCCGAAGCGTTCTTAT	34828	ATGGAACCAAAAAGAAGCTAC
6183	MEPPINP	20506	ATGGAGCCTCCGATTAATCCG	34829	ATGGAACCACCAATCAACCCA
6184	MERTLCN	20507	ATGGAGAGGACTCTTTGTAAT	34830	ATGGAAAGAACACTCTGCAAC
6185	MESLGLA	20508	ATGGAGAGTCTTGGTCTGGCG	34831	ATGGAAAGCCTCGGACTCGCA
6186	MESNHSR	20509	ATGGAGTCGAATCATTCTCGT	34832	ATGGAAAGCAACCACAGCAGA
6187	MESRPSY	20510	ATGGAGAGTCGTCCTAGTTAT	34833	ATGGAAAGCAGACCAAGCTAC
6188	METKSIS	20511	ATGGAGACGAAGTCTATTTCT	34834	ATGGAAACAAAAAGCATCAGC
6189	METNWPA	20512	ATGGAGACTAATTGGCCTGCG	34835	ATGGAAACAAACTGGCCAGCA
6190	METSHRM	20513	ATGGAGACGTCGCATCGTATG	34836	ATGGAAACAAGCCACAGAATG
6191	MFGNAEY	20514	ATGTTTGGGAATGCTGAGTAT	34837	ATGTTCGGAAACGCAGAATAC
6192	MFGTSQD	20515	ATGTTTGGGACGTCGCAGGAT	34838	ATGTTCGGAACAAGCCAAGAC
6193	MFLKVSP	20516	ATGTTTCTGAAGGTGTCGCCT	34839	ATGTTCCTCAAAGTCAGCCCA
6194	MFRVVSD	20517	ATGTTTCGGGTGGTTTCGGAT	34840	ATGTTCAGAGTCGTCAGCGAC
6195	MFSSTKP	20518	ATGTTTTCGTCTACTAAGCCT	34841	ATGTTCAGCAGCACAAAACCA
6196	MFTDSRS	20519	ATGTTTACTGATTCTCGTTCT	34842	ATGTTCACAGACAGCAGAAGC
6197	MFVNELK	20520	ATGTTTGTGAATGAGCTGAAG	34843	ATGTTCGTCAACGAACTCAAA
6198	MGATHPR	20521	ATGGGGGCTACGCATCCTCGG	34844	ATGGGAGCAACACACCCAAGA
6199	MGDRSRN	20522	ATGGGGGATCGTAGTCGTAAT	34845	ATGGGAGACAGAAGCAGAAAC

6200	MGDYTTK	20523	ATGGGTGATTATACTACTAAG	34846	ATGGGAGACTACACAACAAAA
6201	MGERLFS	20524	ATGGGTGAGAGGCTTTTTTCT	34847	ATGGGAGAAAGACTCTTCAGC
6202	MGGHGRT	20525	ATGGGTGGTCATGGTCGTACT	34848	ATGGGAGGACACGGAAGAACA
6203	MGGNSPF	20526	ATGGGTGGTAATTCGCCGTTT	34849	ATGGGAGGAAACAGCCCATTC
6204	MGGTRGT	20527	ATGGGGGGTACGAGGGGGACT	34850	ATGGGAGGAACAAGAGGAACA
6205	MGGTYCR	20528	ATGGGTGGTACGTATTGTCGT	34851	ATGGGAGGAACATACTGCAGA
6206	MGHSDTP	20529	ATGGGGCATTCGGATACGCCG	34852	ATGGGACACAGCGACACACCA
6207	MGHTPRE	20530	ATGGGTCATACTCCTAGGGAG	34853	ATGGGACACACACCAAGAGAA
6208	MGKTAER	20531	ATGGGTAAGACTGCTGAGCGT	34854	ATGGGAAAAACAGCAGAAAGA
6209	MGLGSSN	20532	ATGGGTCTTGGGTCGTCTAAT	34855	ATGGGACTCGGAAGCAGCAAC
6210	MGLRPEG	20533	ATGGGGTTGCGGCCGGAGGGT	34856	ATGGGACTCAGACCAGAAGGA
6211	MGMHGTS	20534	ATGGGGATGCATGGGACGAGT	34857	ATGGGAATGCACGGAACAAGC
6212	MGNHAGS	20535	ATGGGTAATCATGCGGGTTCG	34858	ATGGGAAACCACGCAGGAAGC
6213	MGNSLKQ	20536	ATGGGGAATTCGCTTAAGCAG	34859	ATGGGAAACAGCCTCAAACAA
6214	MGPDGSI	20537	ATGGGGCCGGATGGTTCGATT	34860	ATGGGACCAGACGGAAGCATC
6215	MGPITPQ	20538	ATGGGTCCGATTACGCCTCAG	34861	ATGGGACCAATCACACCACAA
6216	MGQNMAL	20539	ATGGGGCAGAATATGGCGTTG	34862	ATGGGACAAAACATGGCACTC
6217	MGRDEPG	20540	ATGGGGCGTGATGAGCCTGGT	34863	ATGGGAAGAGACGAACCAGGA
6218	MGSGYTM	20541	ATGGGTAGTGGTTATACTATG	34864	ATGGGAAGCGGATACACAATG
6219	MGSTIAL	20542	ATGGGTTCTACGATTGCTTTG	34865	ATGGGAAGCACAATCGCACTC
6220	MGSVHNL	20543	ATGGGTTCTGTTCATAATCTG	34866	ATGGGAAGCGTCCACAACCTC
6221	MGSVIGT	20544	ATGGGGAGTGTTATTGGTACT	34867	ATGGGAAGCGTCATCGGAACA
6222	MGTTHTS	20545	ATGGGTACGACGCATACTTCT	34868	ATGGGAACAACACACACAAGC
6223	MGTTPTL	20546	ATGGGTACTACTCCTACGCTT	34869	ATGGGAACAACACCAACACTC
6224	MGVRNAA	20547	ATGGGTGTGCGGAATGCGGCG	34870	ATGGGAGTCAGAAACGCAGCA
6225	MGYLTGE	20548	ATGGGTTATCTTACGGGTGAG	34871	ATGGGATACCTCACAGGAGAA
6226	MHDADKP	20549	ATGCATGATGCTGATAAGCCG	34872	ATGCACGACGCAGACAAACCA
6227	MHDFPEL	20550	ATGCATGATTTTCCTGAGCTT	34873	ATGCACGACTTCCCAGAACTC
6228	MHDSPQA	20551	ATGCATGATAGTCCGCAGGCT	34874	ATGCACGACAGCCCACAAGCA
6229	MHESLYP	20552	ATGCATGAGTCTCTGTATCCG	34875	ATGCACGAAAGCCTCTACCCA
6230	MHFSAEP	20553	ATGCATTTTTCGGCTGAGCCG	34876	ATGCACTTCAGCGCAGAACCA
6231	MHHATAP	20554	ATGCATCATGCGACGGCGCCG	34877	ATGCACCACGCAACAGCACCA
6232	MHPAPLR	20555	ATGCATCCTGCGCCTCTGCGG	34878	ATGCACCCAGCACCACTCAGA
6233	MHPGGGS	20556	ATGCATCCTGGTGGTGGGTCT	34879	ATGCACCCAGGAGGAGGAAGC
6234	MHQRDGA	20557	ATGCATCAGCGGGATGGTGCT	34880	ATGCACCAAAGAGACGGAGCA
6235	MHQTSMG	20558	ATGCATCAGACTTCGATGGGG	34881	ATGCACCAAACAAGCATGGGA
6236	MHSKGAN	20559	ATGCATTCTAAGGGTGCGAAT	34882	ATGCACAGCAAAGGAGCAAAC
6237	MHSPQTH	20560	ATGCATAGTCCGCAGACTCAT	34883	ATGCACAGCCCACAAACACAC
6238	MHSSPLD	20561	ATGCATTCTTCTCCTCTGGAT	34884	ATGCACAGCAGCCCACTCGAC
6239	MHSTVPA	20562	ATGCATTCTACTGTTCCTGCG	34885	ATGCACAGCACAGTCCCAGCA
6240	MIDRVRT	20563	ATGATTGATCGTGTTCGTACT	34886	ATGATCGACAGAGTCAGAACA
6241	MIEIKEL	20564	ATGATTGAGATTAAGGAGCTT	34887	ATGATCGAAATCAAAGAACTC
6242	MIEVLPS	20565	ATGATTGAGGTGCTGCCGTCG	34888	ATGATCGAAGTCCTCCCAAGC
6243	MIGDAPA	20566	ATGATTGGTGATGCTCCGGCT	34889	ATGATCGGAGACGCACCAGCA
6244	MIGKSTD	20567	ATGATTGGTAAGAGTACGGAT	34890	ATGATCGGAAAAAGCACAGAC

6245	MIKKDYA	20568	ATGATTAAGAAGGATTATGCG	34891	ATGATCAAAAAAGACTACGCA
6246	MIKTNSV	20569	ATGATTAAGACGAATAGTGTT	34892	ATGATCAAAACAAACAGCGTC
6247	MINANTN	20570	ATGATTAATGCTAATACGAAT	34893	ATGATCAACGCAAACACAAAC
6248	MIPVRPD	20571	ATGATTCCTGTTAGGCCGGAT	34894	ATGATCCCAGTCAGACCAGAC
6249	MISEPLT	20572	ATGATTTCTGAGCCGTTGACT	34895	ATGATCAGCGAACCACTCACA
6250	MISGRTT	20573	ATGATTAGTGGTCGGACGACT	34896	ATGATCAGCGGAAGAACAACA
6251	MISHQPP	20574	ATGATTTCGCATCAGCCTCCG	34897	ATGATCAGCCACCAACCACCA
6252	MISIQQT	20575	ATGATTTCTATTCAGCAGACG	34898	ATGATCAGCATCCAACAAACA
6253	MISSMLG	20576	ATGATTAGTTCTATGTTGGGG	34899	ATGATCAGCAGCATGCTCGGA
6254	MIVTTPE	20577	ATGATTGTTACTACTCCTGAG	34900	ATGATCGTCACAACACCAGAA
6255	MKAAVRE	20578	ATGAAGGCGGCGGTTAGGGAG	34901	ATGAAAGCAGCAGTCAGAGAA
6256	MKADPEW	20579	ATGAAGGCGGATCCGGAGTGG	34902	ATGAAAGCAGACCCAGAATGG
6257	MKDNNVT	20580	ATGAAGGATAATAATGTTACT	34903	ATGAAAGACAACAACGTCACA
6258	MKHAAQL	20581	ATGAAGCATGCTGCGCAGCTG	34904	ATGAAACACGCAGCACAACTC
6259	MKHPQYN	20582	ATGAAGCATCCTCAGTATAAT	34905	ATGAAACACCCACAATACAAC
6260	MKMNRNE	20583	ATGAAGATGAATCGGAATGAG	34906	ATGAAAATGAACAGAAACGAA
6261	MKPGLPM	20584	ATGAAGCCGGGTTTGCCTATG	34907	ATGAAACCAGGACTCCCAATG
6262	MKPLAAS	20585	ATGAAGCCGCTTGCTGCGTCT	34908	ATGAAACCACTCGCAGCAAGC
6263	MKPTSQV	20586	ATGAAGCCTACGAGTCAGGTT	34909	ATGAAACCAACAAGCCAAGTC
6264	MKSGLTM	20587	ATGAAGAGTGGGCTGACGATG	34910	ATGAAAAGCGGACTCACAATG
6265	MKSIIPS	20588	ATGAAGAGTATTATTCCGTCG	34911	ATGAAAAGCATCATCCCAAGC
6266	MKSPYGL	20589	ATGAAGAGTCCTTATGGGCTG	34912	ATGAAAAGCCCATACGGACTC
6267	MKSQSDP	20590	ATGAAGTCGCAGTCGGATCCT	34913	ATGAAAAGCCAAAGCGACCCA
6268	MKSSESR	20591	ATGAAGTCTTCTGAGTCGCGT	34914	ATGAAAAGCAGCGAAAGCAGA
6269	MKTELPA	20592	ATGAAGACTGAGCTTCCTGCG	34915	ATGAAAACAGAACTCCCAGCA
6270	MKTPPQS	20593	ATGAAGACGCCTCCTCAGAGT	34916	ATGAAAACACCACCACAAAGC
6271	MKWDGKA	20594	ATGAAGTGGGATGGTAAGGCG	34917	ATGAAATGGGACGGAAAAGCA
6272	MKYSDIG	20595	ATGAAGTATTCGGATATTGGG	34918	ATGAAATACAGCGACATCGGA
6273	MLDDINE	20596	ATGCTTGATGATATTAATGAG	34919	ATGCTCGACGACATCAACGAA
6274	MLDTTKR	20597	ATGCTGGATACTACTAAGCGG	34920	ATGCTCGACACAACAAAAAGA
6275	MLEMNQT	20598	ATGCTTGAGATGAATCAGACT	34921	ATGCTCGAAATGAACCAAACA
6276	MLGHLTA	20599	ATGCTGGGGCATCTGACGGCT	34922	ATGCTCGGACACCTCACAGCA
6277	MLGLSHT	20600	ATGCTTGGTCTTAGTCATACG	34923	ATGCTCGGACTCAGCCACACA
6278	MLHPTAT	20601	ATGCTGCATCCGACTGCGACG	34924	ATGCTCCACCCAACAGCAACA
6279	MLHSSGA	20602	ATGCTTCATAGTAGTGGGGCG	34925	ATGCTCCACAGCAGCGGAGCA
6280	MLKYTEH	20603	ATGCTTAAGTATACGGAGCAT	34926	ATGCTCAAATACACAGAACAC
6281	MLLPTTK	20604	ATGCTGTTGCCTACTACTAAG	34927	ATGCTCCTCCCAACAACAAAA
6282	MLPDSNA	20605	ATGTTGCCGGATTCTAATGCT	34928	ATGCTCCCAGACAGCAACGCA
6283	MLPFDTD	20606	ATGCTGCCGTTTGATACTGAT	34929	ATGCTCCCATTCGACACAGAC
6284	MLPGDSA	20607	ATGTTGCCGGGGGATTCGGCT	34930	ATGCTCCCAGGAGACAGCGCA
6285	MLPGTPH	20608	ATGCTTCCTGGGACTCCTCAT	34931	ATGCTCCCAGGAACACCACAC
6286	MLQGQLS	20609	ATGTTGCAGGGGCAGTTGAGT	34932	ATGCTCCAAGGACAACTCAGC
6287	MLQNGQR	20610	ATGTTGCAGAATGGGCAGCGT	34933	ATGCTCCAAAACGGACAAAGA
6288	MLRIAGD	20611	ATGTTGCGGATTGCGGGTGAT	34934	ATGCTCAGAATCGCAGGAGAC
6289	MLRQGLQ	20612	ATGTTGCGGCAGGGTCTTCAG	34935	ATGCTCAGACAAGGACTCCAA

6290	MLRTSQD	20613	ATGCTTAGGACGTCGCAGGAT	34936	ATGCTCAGAACAAGCCAAGAC
6291	MLSGEMH	20614	ATGCTTTCTGGTGAGATGCAT	34937	ATGCTCAGCGGAGAAATGCAC
6292	MLSNEVI	20615	ATGCTTTCTAATGAGGTTATT	34938	ATGCTCAGCAACGAAGTCATC
6293	MLSRDDQ	20616	ATGCTTAGTCGTGATGATCAG	34939	ATGCTCAGCAGAGACGACCAA
6294	MLSRLAQ	20617	ATGCTGTCTAGGCTTGCGCAG	34940	ATGCTCAGCAGACTCGCACAA
6295	MMDRIEG	20618	ATGATGGATCGGATTGAGGGG	34941	ATGATGGACAGAATCGAAGGA
6296	MMELQLP	20619	ATGATGGAGTTGCAGCTTCCT	34942	ATGATGGAACTCCAACTCCCA
6297	MMGNSKG	20620	ATGATGGGGAATTCTAAGGGG	34943	ATGATGGGAAACAGCAAAGGA
6298	MMHAGAQ	20621	ATGATGCATGCGGGTGCTCAG	34944	ATGATGCACGCAGGAGCACAA
6299	MMHQEDS	20622	ATGATGCATCAGGAGGATAGT	34945	ATGATGCACCAAGAAGACAGC
6300	MMNMRGG	20623	ATGATGAATATGAGGGGTGGG	34946	ATGATGAACATGAGAGGAGGA
6301	MMPQEIV	20624	ATGATGCCGCAGGAGATTGTG	34947	ATGATGCCACAAGAAATCGTC
6302	MMSDNAK	20625	ATGATGTCGGATAATGCGAAG	34948	ATGATGAGCGACAACGCAAAA
6303	MMTDSQR	20626	ATGATGACTGATTCTCAGCGT	34949	ATGATGACAGACAGCCAAAGA
6304	MMTGASD	20627	ATGATGACGGGGGCGTCGGAT	34950	ATGATGACAGGAGCAAGCGAC
6305	MMTKTGT	20628	ATGATGACGAAGACTGGTACT	34951	ATGATGACAAAAACAGGAACA
6306	MMTSAGP	20629	ATGATGACGTCTGCTGGGCCT	34952	ATGATGACAAGCGCAGGACCA
6307	MNAFKQE	20630	ATGAATGCGTTTAAGCAGGAG	34953	ATGAACGCATTCAAACAAGAA
6308	MNAKCCS	20631	ATGAATGCGAAGTGTTGTAGT	34954	ATGAACGCAAAATGCTGCAGC
6309	MNARLID	20632	ATGAATGCGCGGTTGATTGAT	34955	ATGAACGCAAGACTCATCGAC
6310	MNASANS	20633	ATGAATGCTTCGGCGAATAGT	34956	ATGAACGCAAGCGCAAACAGC
6311	MNASTMI	20634	ATGAATGCGTCTACGATGATT	34957	ATGAACGCAAGCACAATGATC
6312	MNGSLPM	20635	ATGAATGGTAGTCTTCCTATG	34958	ATGAACGGAAGCCTCCCAATG
6313	MNGSRQM	20636	ATGAATGGGAGTCGTCAGATG	34959	ATGAACGGAAGCAGACAAATG
6314	MNHGANY	20637	ATGAATCATGGTGCGAATTAT	34960	ATGAACCACGGAGCAAACTAC
6315	MNKASFA	20638	ATGAATAAGGCTTCGTTTGCT	34961	ATGAACAAAGCAAGCTTCGCA
6316	MNKGTVA	20639	ATGAATAAGGGTACGGTTGCG	34962	ATGAACAAAGGAACAGTCGCA
6317	MNKLKVE	20640	ATGAATAAGCTTAAGGTTGAG	34963	ATGAACAAACTCAAAGTCGAA
6318	MNLHNPA	20641	ATGAATTTGCATAATCCTGCT	34964	ATGAACCTCCACAACCCAGCA
6319	MNLKLSP	20642	ATGAATCTTAAGCTTAGTCCG	34965	ATGAACCTCAAACTCAGCCCA
6320	MNLRMAP	20643	ATGAATTTGCGGATGGCTCCG	34966	ATGAACCTCAGAATGGCACCA
6321	MNLSTKP	20644	ATGAATCTGTCTACGAAGCCT	34967	ATGAACCTCAGCACAAAACCA
6322	MNNLSGR	20645	ATGAATAATCTTTCTGGGCGG	34968	ATGAACAACCTCAGCGGAAGA
6323	MNPISKC	20646	ATGAATCCGATTTCGAAGTGT	34969	ATGAACCCAATCAGCAAATGC
6324	MNPLPYP	20647	ATGAATCCTCTTCCGTATCCT	34970	ATGAACCCACTCCCATACCCA
6325	MNPSVEL	20648	ATGAATCCTTCTGTTGAGCTT	34971	ATGAACCCAAGCGTCGAACTC
6326	MNQTKPY	20649	ATGAATCAGACGAAGCCTTAT	34972	ATGAACCAAACAAAACCATAC
6327	MNQVRSL	20650	ATGAATCAGGTGAGGAGTCTT	34973	ATGAACCAAGTCAGAAGCCTC
6328	MNRIVMS	20651	ATGAATCGGATTGTTATGTCT	34974	ATGAACAGAATCGTCATGAGC
6329	MNSGCED	20652	ATGAATAGTGGTTGTGAGGAT	34975	ATGAACAGCGGATGCGAAGAC
6330	MNSGMPF	20653	ATGAATTCTGGTATGCCGTTT	34976	ATGAACAGCGGAATGCCATTC
6331	MNSKGEP	20654	ATGAATTCTAAGGGTGAGCCG	34977	ATGAACAGCAAAGGAGAACCA
6332	MNSKMYP	20655	ATGAATAGTAAGATGTATCCT	34978	ATGAACAGCAAAATGTACCCA
6333	MNSLPRS	20656	ATGAATTCTCTTCCTCGTTCG	34979	ATGAACAGCCTCCCAAGAAGC
6334	MNSRNGY	20657	ATGAATTCTCGTAATGGGTAT	34980	ATGAACAGCAGAAACGGATAC

6335	MNSTLAA	20658	ATGAATTCTACGTTGGCTGCT	34981	ATGAACAGCACACTCGCAGCA
6336	MNSTTTP	20659	ATGAATTCTACGACTACGCCT	34982	ATGAACAGCACAACAACACCA
6337	MNTKTFP	20660	ATGAATACTAAGACGTTTCCG	34983	ATGAACACAAAAACATTCCCA
6338	MNTSVVY	20661	ATGAATACTTCGGTGGTGTAT	34984	ATGAACACAAGCGTCGTCTAC
6339	MNVVGQS	20662	ATGAATGTTGTTGGGCAGTCT	34985	ATGAACGTCGTCGGACAAAGC
6340	MPAHVLP	20663	ATGCCGGCTCATGTTCTGCCT	34986	ATGCCAGCACACGTCCTCCCA
6341	MPASSVS	20664	ATGCCGGCGTCTTCGGTTTCG	34987	ATGCCAGCAAGCAGCGTCAGC
6342	MPATFTD	20665	ATGCCTGCTACGTTTACGGAT	34988	ATGCCAGCAACATTCACAGAC
6343	MPDAKIS	20666	ATGCCTGATGCTAAGATTTCG	34989	ATGCCAGACGCAAAAATCAGC
6344	MPDHPLR	20667	ATGCCTGATCATCCTCTTCGG	34990	ATGCCAGACCACCCACTCAGA
6345	MPESMNT	20668	ATGCCGGAGAGTATGAATACG	34991	ATGCCAGAAAGCATGAACACA
6346	MPFNDNV	20669	ATGCCTTTTAATGATAATGTT	34992	ATGCCATTCAACGACAACGTC
6347	MPHGSFA	20670	ATGCCGCATGGGAGTTTTGCT	34993	ATGCCACACGGAAGCTTCGCA
6348	MPHLEMN	20671	ATGCCGCATTTGGAGATGAAT	34994	ATGCCACACCTCGAAATGAAC
6349	MPHLITS	20672	ATGCCTCATCTTATTACGAGT	34995	ATGCCACACCTCATCACAAGC
6350	MPHMGLT	20673	ATGCCTCATATGGGTCTGACG	34996	ATGCCACACATGGGACTCACA
6351	MPISPLA	20674	ATGCCGATTTCGCCGTTGGCG	34997	ATGCCAATCAGCCCACTCGCA
6352	MPIVRIS	20675	ATGCCGATTGTTCGTATTAGT	34998	ATGCCAATCGTCAGAATCAGC
6353	MPKQELI	20676	ATGCCTAAGCAGGAGTTGATT	34999	ATGCCAAAACAAGAACTCATC
6354	MPLDSVA	20677	ATGCCTTTGGATAGTGTGGCG	35000	ATGCCACTCGACAGCGTCGCA
6355	MPLGGAY	20678	ATGCCGCTTGGTGGTGCGTAT	35001	ATGCCACTCGGAGGAGCATAC
6356	MPLRNTM	20679	ATGCCTTTGCGGAATACTATG	35002	ATGCCACTCAGAAACACAATG
6357	MPLSNSS	20680	ATGCCGCTTAGTAATAGTTCG	35003	ATGCCACTCAGCAACAGCAGC
6358	MPMGDPI	20681	ATGCCGATGGGGGATCCGATT	35004	ATGCCAATGGGAGACCCAATC
6359	MPMMLRL	20682	ATGCCTATGATGCTGCGTCTT	35005	ATGCCAATGATGCTCAGACTC
6360	MPMNRTP	20683	ATGCCTATGAATCGGACTCCT	35006	ATGCCAATGAACAGAACACCA
6361	MPMRANG	20684	ATGCCGATGCGTGCTAATGGG	35007	ATGCCAATGAGAGCAAACGGA
6362	MPNVPPT	20685	ATGCCGAATGTTCCTCCTACG	35008	ATGCCAAACGTCCCACCAACA
6363	MPPALLT	20686	ATGCCGCCTGCTCTTCTGACG	35009	ATGCCACCAGCACTCCTCACA
6364	MPPEVPV	20687	ATGCCGCCTGAGGTTCCTGTT	35010	ATGCCACCAGAAGTCCCAGTC
6365	MPPPNLN	20688	ATGCCTCCGCCGAATCTTAAT	35011	ATGCCACCACCAAACCTCAAC
6366	MPPQNAM	20689	ATGCCTCCGCAGAATGCGATG	35012	ATGCCACCACAAAACGCAATG
6367	MPPSNRP	20690	ATGCCTCCTTCGAATCGGCCT	35013	ATGCCACCAAGCAACAGACCA
6368	MPPSTYA	20691	ATGCCTCCTTCTACGTATGCG	35014	ATGCCACCAAGCACATACGCA
6369	MPQLHET	20692	ATGCCTCAGTTGCATGAGACT	35015	ATGCCACAACTCCACGAAACA
6370	MPQSRDE	20693	ATGCCGCAGTCGCGTGATGAG	35016	ATGCCACAAAGCAGAGACGAA
6371	MPRDAYG	20694	ATGCCTAGGGATGCGTATGGT	35017	ATGCCAAGAGACGCATACGGA
6372	MPRGEIP	20695	ATGCCGCGTGGGGAGATTCCG	35018	ATGCCAAGAGGAGAAATCCCA
6373	MPRNGPP	20696	ATGCCGAGGAATGGTCCGCCT	35019	ATGCCAAGAAACGGACCACCA
6374	MPRVASN	20697	ATGCCTCGTGTGGCGTCTAAT	35020	ATGCCAAGAGTCGCAAGCAAC
6375	MPSASEV	20698	ATGCCTAGTGCTTCTGAGGTT	35021	ATGCCAAGCGCAAGCGAAGTC
6376	MPSGRVH	20699	ATGCCTTCGGGTAGGGTTCAT	35022	ATGCCAAGCGGAAGAGTCCAC
6377	MPSGRVP	20700	ATGCCGTCGGGTCGTGTTCCT	35023	ATGCCAAGCGGAAGAGTCCCA
6378	MPSISLP	20701	ATGCCGTCGATTTCTCTGCCT	35024	ATGCCAAGCATCAGCCTCCCA
6379	MPSNSIS	20702	ATGCCGTCTAATAGTATTTCT	35025	ATGCCAAGCAACAGCATCAGC

6380	MPSPEVY	20703	ATGCCGTCTCCGGAGGTGTAT	35026	ATGCCAAGCCCAGAAGTCTAC
6381	MPTDPKM	20704	ATGCCTACGGATCCTAAGATG	35027	ATGCCAACAGACCCAAAAATG
6382	MPTGTDL	20705	ATGCCGACGGGTACTGATCTT	35028	ATGCCAACAGGAACAGACCTC
6383	MPTPRTG	20706	ATGCCTACGCCTCGGACTGGT	35029	ATGCCAACACCAAGAACAGGA
6384	MPTSGPP	20707	ATGCCTACGTCTGGGCCTCCG	35030	ATGCCAACAAGCGGACCACCA
6385	MPTYDKR	20708	ATGCCTACTTATGATAAGCGT	35031	ATGCCAACATACGACAAAAGA
6386	MPVPERP	20709	ATGCCTGTGCCGGAGAGGCCT	35032	ATGCCAGTCCCAGAAAGACCA
6387	MPVSGHV	20710	ATGCCGGTGAGTGGTCATGTT	35033	ATGCCAGTCAGCGGACACGTC
6388	MPVSRLE	20711	ATGCCTGTGTCGCGTCTGGAG	35034	ATGCCAGTCAGCAGACTCGAA
6389	MPVSSTR	20712	ATGCCTGTTAGTAGTACTCGT	35035	ATGCCAGTCAGCAGCACAAGA
6390	MPWKDAA	20713	ATGCCGTGGAAGGATGCGGCT	35036	ATGCCATGGAAAGACGCAGCA
6391	MQAASSP	20714	ATGCAGGCGGCTTCTTCTCCT	35037	ATGCAAGCAGCAAGCAGCCCA
6392	MQAGSMR	20715	ATGCAGGCTGGTAGTATGCGT	35038	ATGCAAGCAGGAAGCATGAGA
6393	MQASHSP	20716	ATGCAGGCTAGTCATTCTCCG	35039	ATGCAAGCAAGCCACAGCCCA
6394	MQDGYTN	20717	ATGCAGGATGGGTATACGAAT	35040	ATGCAAGACGGATACACAAAC
6395	MQGKLLA	20718	ATGCAGGGGAAGTTGTTGGCT	35041	ATGCAAGGAAAACTCCTCGCA
6396	MQHGAHP	20719	ATGCAGCATGGTGCTCATCCT	35042	ATGCAACACGGAGCACACCCA
6397	MQLEHSP	20720	ATGCAGCTTGAGCATTCTCCT	35043	ATGCAACTCGAACACAGCCCA
6398	MQLGNVS	20721	ATGCAGCTTGGTAATGTTTCG	35044	ATGCAACTCGGAAACGTCAGC
6399	MQLGPVM	20722	ATGCAGCTTGGTCCTGTGATG	35045	ATGCAACTCGGACCAGTCATG
6400	MQNMPPP	20723	ATGCAGAATATGCCTCCGCCG	35046	ATGCAAAACATGCCACCACCA
6401	MQPNTSF	20724	ATGCAGCCGAATACGTCGTTT	35047	ATGCAACCAAACACAAGCTTC
6402	MQRRLDI	20725	ATGCAGCGTAGGCTTGATATT	35048	ATGCAAAGAAGACTCGACATC
6403	MQRTTHV	20726	ATGCAGAGGACGACTCATGTT	35049	ATGCAAAGAACAACACACGTC
6404	MQSRVPL	20727	ATGCAGTCGCGTGTTCCTTTG	35050	ATGCAAAGCAGAGTCCCACTC
6405	MQSSPDG	20728	ATGCAGTCTTCGCCTGATGGG	35051	ATGCAAAGCAGCCCAGACGGA
6406	MQTATQG	20729	ATGCAGACGGCGACGCAGGGT	35052	ATGCAAACAGCAACACAAGGA
6407	MQTQSLP	20730	ATGCAGACTCAGTCTCTTCCT	35053	ATGCAAACACAAAGCCTCCCA
6408	MQVSERP	20731	ATGCAGGTGTCTGAGAGGCCT	35054	ATGCAAGTCAGCGAAAGACCA
6409	MQVSGPP	20732	ATGCAGGTTTCTGGGCCGCCT	35055	ATGCAAGTCAGCGGACCACCA
6410	MQVTEGL	20733	ATGCAGGTGACTGAGGGGCTT	35056	ATGCAAGTCACAGAAGGACTC
6411	MRAGAAG	20734	ATGCGGGCTGGGGCGGCGGGT	35057	ATGAGAGCAGGAGCAGCAGGA
6412	MRASAGM	20735	ATGCGGGCTTCTGCGGGGATG	35058	ATGAGAGCAAGCGCAGGAATG
6413	MRDDAAV	20736	ATGCGGGATGATGCGGCTGTT	35059	ATGAGAGACGACGCAGCAGTC
6414	MRDGPPN	20737	ATGCGTGATGGTCCTCCGAAT	35060	ATGAGAGACGGACCACCAAAC
6415	MRERSSA	20738	ATGCGGGAGCGGTCGAGTGCT	35061	ATGAGAGAAAGAAGCAGCGCA
6416	MRGDSAP	20739	ATGAGGGGTGATTCGGCGCCT	35062	ATGAGAGGAGACAGCGCACCA
6417	MRGFDEL	20740	ATGAGGGGTTTTGATGAGTTG	35063	ATGAGAGGATTCGACGAACTC
6418	MRGTPVG	20741	ATGCGGGGTACGCCGGTTGGT	35064	ATGAGAGGAACACCAGTCGGA
6419	MRHGNPA	20742	ATGCGGCATGGGAATCCTGCG	35065	ATGAGACACGGAAACCCAGCA
6420	MRHVNTP	20743	ATGCGGCATGTTAATACGCCG	35066	ATGAGACACGTCAACACACCA
6421	MRIGDRH	20744	ATGCGGATTGGGGATAGGCAT	35067	ATGAGAATCGGAGACAGACAC
6422	MRLSTPE	20745	ATGCGTTTGAGTACGCCGGAG	35068	ATGAGACTCAGCACACCAGAA
6423	MRLVSAE	20746	ATGAGGTTGGTGTCGGCGGAG	35069	ATGAGACTCGTCAGCGCAGAA
6424	MRMAVSA	20747	ATGCGGATGGCGGTGAGTGCT	35070	ATGAGAATGGCAGTCAGCGCA

6425	MRMGGVP	20748	ATGAGGATGGGGGGTGTGCCT	35071	ATGAGAATGGGAGGAGTCCCA
6426	MRNAAKR	20749	ATGAGGAATGCGGCTAAGAGG	35072	ATGAGAAACGCAGCAAAAAGA
6427	MRNSVYP	20750	ATGAGGAATTCGGTGTATCCG	35073	ATGAGAAACAGCGTCTACCCA
6428	MRNTTFE	20751	ATGCGGAATACGACGTTTGAG	35074	ATGAGAAACACAACATTCGAA
6429	MRPANES	20752	ATGCGTCCGGCTAATGAGTCG	35075	ATGAGACCAGCAAACGAAAGC
6430	MRPAVGV	20753	ATGCGGCCGGCGGTGGGGGTT	35076	ATGAGACCAGCAGTCGGAGTC
6431	MRPGLEG	20754	ATGAGGCCGGGTTTGGAGGGT	35077	ATGAGACCAGGACTCGAAGGA
6432	MRPTHAC	20755	ATGAGGCCGACGCATGCGTGT	35078	ATGAGACCAACACACGCATGC
6433	MRPTNAT	20756	ATGCGGCCTACTAATGCTACT	35079	ATGAGACCAACAAACGCAACA
6434	MRQIGYH	20757	ATGCGGCAGATTGGTTATCAT	35080	ATGAGACAAATCGGATACCAC
6435	MRQVGRE	20758	ATGCGTCAGGTTGGGCGTGAG	35081	ATGAGACAAGTCGGAAGAGAA
6436	MRSFSYE	20759	ATGAGGTCGTTTTCTTATGAG	35082	ATGAGAAGCTTCAGCTACGAA
6437	MRSNDVV	20760	ATGAGGAGTAATGATGTGGTT	35083	ATGAGAAGCAACGACGTCGTC
6438	MRSPPLY	20761	ATGCGGAGTCCGCCGTTGTAT	35084	ATGAGAAGCCCACCACTCTAC
6439	MRSQSFS	20762	ATGCGGTCTCAGAGTTTTAGT	35085	ATGAGAAGCCAAAGCTTCAGC
6440	MRSRVDT	20763	ATGCGGTCTCGTGTGGATACT	35086	ATGAGAAGCAGAGTCGACACA
6441	MRSVIAQ	20764	ATGAGGTCTGTGATTGCGCAG	35087	ATGAGAAGCGTCATCGCACAA
6442	MRTESTL	20765	ATGCGTACGGAGTCGACTTTG	35088	ATGAGAACAGAAAGCACACTC
6443	MRTNSST	20766	ATGCGTACGAATAGTAGTACT	35089	ATGAGAACAAACAGCAGCACA
6444	MRTSNTA	20767	ATGCGTACTTCTAATACTGCT	35090	ATGAGAACAAGCAACACAGCA
6445	MRVNTDP	20768	ATGCGTGTTAATACTGATCCT	35091	ATGAGAGTCAACACAGACCCA
6446	MRVSTAA	20769	ATGCGTGTGTCGACTGCGGCG	35092	ATGAGAGTCAGCACAGCAGCA
6447	MRYAPGT	20770	ATGCGTTATGCTCCGGGTACG	35093	ATGAGATACGCACCAGGAACA
6448	MSADRFS	20771	ATGAGTGCTGATAGGTTTTCG	35094	ATGAGCGCAGACAGATTCAGC
6449	MSAKTYL	20772	ATGAGTGCTAAGACTTATCTT	35095	ATGAGCGCAAAAACATACCTC
6450	MSASIGS	20773	ATGAGTGCTTCGATTGGTTCT	35096	ATGAGCGCAAGCATCGGAAGC
6451	MSAVLPH	20774	ATGTCTGCTGTGTTGCCGCAT	35097	ATGAGCGCAGTCCTCCCACAC
6452	MSDQLRF	20775	ATGTCTGATCAGCTGCGGTTT	35098	ATGAGCGACCAACTCAGATTC
6453	MSDSHSR	20776	ATGTCGGATTCGCATTCGCGT	35099	ATGAGCGACAGCCACAGCAGA
6454	MSDWNGI	20777	ATGTCGGATTGGAATGGTATT	35100	ATGAGCGACTGGAACGGAATC
6455	MSEMSTH	20778	ATGTCTGAGATGAGTACTCAT	35101	ATGAGCGAAATGAGCACACAC
6456	MSGGSSY	20779	ATGAGTGGTGGGTCGTCTTAT	35102	ATGAGCGGAGGAAGCAGCTAC
6457	MSGNHAT	20780	ATGTCTGGGAATCATGCTACT	35103	ATGAGCGGAAACCACGCAACA
6458	MSGPQLS	20781	ATGTCGGGTCCGCAGTTGAGT	35104	ATGAGCGGACCACAACTCAGC
6459	MSGRGQI	20782	ATGAGTGGGCGTGGTCAGATT	35105	ATGAGCGGAAGAGGACAAATC
6460	MSHHSTT	20783	ATGTCTCATCATAGTACTACG	35106	ATGAGCCACCACAGCACAACA
6461	MSHPYKP	20784	ATGTCTCATCCGTATAAGCCG	35107	ATGAGCCACCCATACAAACCA
6462	MSHYLKA	20785	ATGTCTCATTATCTGAAGGCT	35108	ATGAGCCACTACCTCAAAGCA
6463	MSIDEAE	20786	ATGTCGATTGATGAGGCTGAG	35109	ATGAGCATCGACGAAGCAGAA
6464	MSIGTSE	20787	ATGTCTATTGGTACGTCGGAG	35110	ATGAGCATCGGAACAAGCGAA
6465	MSIIGGV	20788	ATGTCTATTATTGGTGGTGTT	35111	ATGAGCATCATCGGAGGAGTC
6466	MSISHTT	20789	ATGTCTATTTCTCATACTACG	35112	ATGAGCATCAGCCACACAACA
6467	MSITHHS	20790	ATGTCGATTACTCATCATTCT	35113	ATGAGCATCACACACCACAGC
6468	MSKIWPS	20791	ATGTCGAAGATTTGGCCGTCT	35114	ATGAGCAAAATCTGGCCAAGC
6469	MSKNLSA	20792	ATGTCTAAGAATTTGTCGGCT	35115	ATGAGCAAAAACCTCAGCGCA

6470	MSKRTDS	20793	ATGAGTAAGAGGACTGATTCG	35116	ATGAGCAAAAGAACAGACAGC
6471	MSKTIAQ	20794	ATGAGTAAGACTATTGCGCAG	35117	ATGAGCAAAACAATCGCACAA
6472	MSKVPFN	20795	ATGTCGAAGGTGCCTTTTAAT	35118	ATGAGCAAAGTCCCATTCAAC
6473	MSLANKS	20796	ATGTCGTTGGCGAATAAGAGT	35119	ATGAGCCTCGCAAACAAAAGC
6474	MSLKLSG	20797	ATGTCTCTGAAGCTGTCTGGT	35120	ATGAGCCTCAAACTCAGCGGA
6475	MSLPSTQ	20798	ATGTCTTTGCCGTCGACTCAG	35121	ATGAGCCTCCCAAGCACACAA
6476	MSLTVTA	20799	ATGTCTTTGACGGTTACGGCT	35122	ATGAGCCTCACAGTCACAGCA
6477	MSMHGGS	20800	ATGTCTATGCATGGGGGTTCT	35123	ATGAGCATGCACGGAGGAAGC
6478	MSNGWQD	20801	ATGTCGAATGGGTGGCAGGAT	35124	ATGAGCAACGGATGGCAAGAC
6479	MSNIGLG	20802	ATGAGTAATATTGGTCTGGGT	35125	ATGAGCAACATCGGACTCGGA
6480	MSNNHGL	20803	ATGTCTAATAATCATGGTCTT	35126	ATGAGCAACAACCACGGACTC
6481	MSNSEFG	20804	ATGTCTAATTCGGAGTTTGGT	35127	ATGAGCAACAGCGAATTCGGA
6482	MSPAMQT	20805	ATGAGTCCTGCTATGCAGACG	35128	ATGAGCCCAGCAATGCAAACA
6483	MSPDQRY	20806	ATGAGTCCTGATCAGAGGTAT	35129	ATGAGCCCAGACCAAAGATAC
6484	MSPGVNA	20807	ATGTCTCCTGGTGTTAATGCT	35130	ATGAGCCCAGGAGTCAACGCA
6485	MSPHFNT	20808	ATGTCTCCGCATTTTAATACG	35131	ATGAGCCCACACTTCAACACA
6486	MSPMVTA	20809	ATGAGTCCGATGGTGACTGCG	35132	ATGAGCCCAATGGTCACAGCA
6487	MSPSDFG	20810	ATGTCTCCGTCTGATTTTGGT	35133	ATGAGCCCAAGCGACTTCGGA
6488	MSPSSPM	20811	ATGAGTCCTTCTAGTCCTATG	35134	ATGAGCCCAAGCAGCCCAATG
6489	MSQQSSG	20812	ATGTCTCAGCAGTCGAGTGGT	35135	ATGAGCCAACAAAGCAGCGGA
6490	MSQRRDP	20813	ATGTCTCAGCGTAGGGATCCT	35136	ATGAGCCAAAGAAGAGACCCA
6491	MSRDVSH	20814	ATGAGTCGGGATGTGTCGCAT	35137	ATGAGCAGAGACGTCAGCCAC
6492	MSRESGG	20815	ATGTCTCGTGAGTCGGGTGGG	35138	ATGAGCAGAGAAAGCGGAGGA
6493	MSRLDSP	20816	ATGTCGAGGTTGGATTCTCCG	35139	ATGAGCAGACTCGACAGCCCA
6494	MSRLGAT	20817	ATGAGTCGGCTTGGTGCGACG	35140	ATGAGCAGACTCGGAGCAACA
6495	MSRNLCC	20818	ATGTCTCGTAATTTGTGTTGT	35141	ATGAGCAGAAACCTCTGCTGC
6496	MSSASSP	20819	ATGAGTTCGGCGTCTAGTCCT	35142	ATGAGCAGCGCAAGCAGCCCA
6497	MSSEPVK	20820	ATGTCTAGTGAGCCGGTTAAG	35143	ATGAGCAGCGAACCAGTCAAA
6498	MSSHGVA	20821	ATGTCGTCTCATGGTGTGGCT	35144	ATGAGCAGCCACGGAGTCGCA
6499	MSSLNSL	20822	ATGTCGAGTCTTAATTCTCTT	35145	ATGAGCAGCCTCAACAGCCTC
6500	MSSLNVH	20823	ATGTCGTCGCTTAATGTTCAT	35146	ATGAGCAGCCTCAACGTCCAC
6501	MSSLRQA	20824	ATGTCTAGTCTGCGGCAGGCG	35147	ATGAGCAGCCTCAGACAAGCA
6502	MSSPQLS	20825	ATGTCGTCGCCTCAGTTGAGT	35148	ATGAGCAGCCCACAACTCAGC
6503	MSSQTSK	20826	ATGAGTTCTCAGACTTCTAAG	35149	ATGAGCAGCCAAACAAGCAAA
6504	MSSRWAA	20827	ATGTCGAGTCGTTGGGCGGCG	35150	ATGAGCAGCAGATGGGCAGCA
6505	MSSSVHT	20828	ATGAGTTCTTCTGTGCATACT	35151	ATGAGCAGCAGCGTCCACACA
6506	MSSTRTD	20829	ATGTCGAGTACTCGTACTGAT	35152	ATGAGCAGCACAAGAACAGAC
6507	MSSTSYS	20830	ATGTCGAGTACTTCGTATAGT	35153	ATGAGCAGCACAAGCTACAGC
6508	MSTEDHA	20831	ATGTCTACTGAGGATCATGCG	35154	ATGAGCACAGAAGACCACGCA
6509	MSTERNA	20832	ATGTCGACTGAGCGTAATGCG	35155	ATGAGCACAGAAAGAAACGCA
6510	MSTFPPP	20833	ATGAGTACTTTTCCGCCTCCT	35156	ATGAGCACATTCCCACCACCA
6511	MSTGRLI	20834	ATGAGTACTGGGAGGCTTATT	35157	ATGAGCACAGGAAGACTCATC
6512	MSTHVVS	20835	ATGTCTACGCATGTGGTGAGT	35158	ATGAGCACACACGTCGTCAGC
6513	MSTLPHA	20836	ATGAGTACTCTGCCTCATGCT	35159	ATGAGCACACTCCCACACGCA
6514	MSTMQRS	20837	ATGTCTACGATGCAGAGGAGT	35160	ATGAGCACAATGCAAAGAAGC

6515	MSTNFKG	20838	ATGTCTACTAATTTTAAGGGT	35161	ATGAGCACAAACTTCAAAGGA
6516	MSTNTHL	20839	ATGTCGACTAATACGCATTTG	35162	ATGAGCACAAACACACACCTC
6517	MSTRIAN	20840	ATGTCGACGAGGATTGCGAAT	35163	ATGAGCACAAGAATCGCAAAC
6518	MSTRPMP	20841	ATGTCTACGAGGCCTATGCCG	35164	ATGAGCACAAGACCAATGCCA
6519	MSTRSPS	20842	ATGAGTACGCGGAGTCCGTCG	35165	ATGAGCACAAGAAGCCCAAGC
6520	MSVPHGD	20843	ATGTCTGTGCCTCATGGTGAT	35166	ATGAGCGTCCCACACGGAGAC
6521	MSYPYQN	20844	ATGTCTTATCCTTATCAGAAT	35167	ATGAGCTACCCATACCAAAAC
6522	MSYQKPS	20845	ATGTCTTATCAGAAGCCTTCG	35168	ATGAGCTACCAAAAACCAAGC
6523	MSYTSDS	20846	ATGTCTTATACTTCTGATTCT	35169	ATGAGCTACACAAGCGACAGC
6524	MTANTAL	20847	ATGACGGCTAATACTGCTCTT	35170	ATGACAGCAAACACAGCACTC
6525	MTDITGR	20848	ATGACGGATATTACGGGTAGG	35171	ATGACAGACATCACAGGAAGA
6526	MTDSQPG	20849	ATGACGGATTCGCAGCCGGGT	35172	ATGACAGACAGCCAACCAGGA
6527	MTDTRRL	20850	ATGACTGATACTCGGCGGCTG	35173	ATGACAGACACAAGAAGACTC
6528	MTDVGVR	20851	ATGACGGATGTGGGTGTGCGT	35174	ATGACAGACGTCGGAGTCAGA
6529	MTDYSKG	20852	ATGACGGATTATTCGAAGGGG	35175	ATGACAGACTACAGCAAAGGA
6530	MTEPMVD	20853	ATGACTGAGCCGATGGTGGAT	35176	ATGACAGAACCAATGGTCGAC
6531	MTESLTA	20854	ATGACGGAGTCTTTGACGGCG	35177	ATGACAGAAAGCCTCACAGCA
6532	MTEVTIF	20855	ATGACGGAGGTTACGACGTTT	35178	ATGACAGAAGTCACAACATTC
6533	MTFPKLN	20856	ATGACTTTTCCGAAGCTGAAT	35179	ATGACATTCCCAAAACTCAAC
6534	MTGMTSA	20857	ATGACTGGTATGACTAGTGCG	35180	ATGACAGGAATGACAAGCGCA
6535	MTGNHRI	20858	ATGACTGGTAATCATCGGATT	35181	ATGACAGGAAACCACAGAATC
6536	MTGTSQP	20859	ATGACTGGTACGTCGCAGCCT	35182	ATGACAGGAACAAGCCAACCA
6537	MTHPPSD	20860	ATGACTCATCCTCCTTCGGAT	35183	ATGACACACCCACCAAGCGAC
6538	MTHTGTL	20861	ATGACTCATACGGGTACTTTG	35184	ATGACACACACAGGAACACTC
6539	MTKPHIV	20862	ATGACGAAGCCTCATATTGTG	35185	ATGACAAAACCACACATCGTC
6540	MTLGSVV	20863	ATGACTCTTGGTTCTGTTGTT	35186	ATGACACTCGGAAGCGTCGTC
6541	MTLHQQF	20864	ATGACTTTGCATCAGCAGTTT	35187	ATGACACTCCACCAACAATTC
6542	MTLSTGA	20865	ATGACGCTGTCGACTGGTGCT	35188	ATGACACTCAGCACAGGAGCA
6543	MTLVASP	20866	ATGACGCTTGTGGCTAGTCCG	35189	ATGACACTCGTCGCAAGCCCA
6544	MTMEAAK	20867	ATGACTATGGAGGCGGCTAAG	35190	ATGACAATGGAAGCAGCAAAA
6545	MTMGEFK	20868	ATGACGATGGGTGAGTTTAAG	35191	ATGACAATGGGAGAATTCAAA
6546	MTMTHRG	20869	ATGACGATGACGCATCGTGGG	35192	ATGACAATGACACACAGAGGA
6547	MTNAVVD	20870	ATGACTAATGCTGTTGTTGAT	35193	ATGACAAACGCAGTCGTCGAC
6548	MTNGHGM	20871	ATGACGAATGGTCATGGTATG	35194	ATGACAAACGGACACGGAATG
6549	MTNLQSL	20872	ATGACTAATCTTCAGTCTTTG	35195	ATGACAAACCTCCAAAGCCTC
6550	MTNRATA	20873	ATGACTAATCGTGCTACGGCG	35196	ATGACAAACAGAGCAACAGCA
6551	MTPHNSR	20874	ATGACGCCGCATAATAGTAGG	35197	ATGACACCACACAACAGCAGA
6552	MTPPHGA	20875	ATGACGCCGCCTCATGGGGCG	35198	ATGACACCACCACACGGAGCA
6553	MTPTSYN	20876	ATGACTCCTACGTCGTATAAT	35199	ATGACACCAACAAGCTACAAC
6554	MTQTDVT	20877	ATGACGCAGACTGATGTTACG	35200	ATGACACAAACAGACGTCACA
6555	MTRSEWS	20878	ATGACGCGTTCTGAGTGGTCT	35201	ATGACAAGAAGCGAATGGAGC
6556	MTSLAAL	20879	ATGACTAGTTTGGCGGCTCTT	35202	ATGACAAGCCTCGCAGCACTC
6557	MTSNTRM	20880	ATGACGAGTAATACGAGGATG	35203	ATGACAAGCAACACAAGAATG
6558	MTSVRMS	20881	ATGACTTCGGTTCGGATGTCG	35204	ATGACAAGCGTCAGAATGAGC
6559	MTTGIDS	20882	ATGACGACGGGGATTGATAGT	35205	ATGACAACAGGAATCGACAGC

6560	MTTSPFA	20883	ATGACGACGAGTCCTTTTGCT	35206	ATGACAACAAGCCCATTCGCA
6561	MTTSSDL	20884	ATGACGACTTCGAGTGATTTG	35207	ATGACAACAAGCAGCGACCTC
6562	MTVGDSA	20885	ATGACGGTGGGGGATAGTGCT	35208	ATGACAGTCGGAGACAGCGCA
6563	MTVGIPA	20886	ATGACTGTTGGTATTCCTGCG	35209	ATGACAGTCGGAATCCCAGCA
6564	MTVSNKY	20887	ATGACTGTTAGTAATAAGTAT	35210	ATGACAGTCAGCAACAAATAC
6565	MTVSPGT	20888	ATGACTGTTTCTCCTGGTACT	35211	ATGACAGTCAGCCCAGGAACA
6566	MVASDNS	20889	ATGGTTGCGTCTGATAATAGT	35212	ATGGTCGCAAGCGACAACAGC
6567	MVDRVLD	20890	ATGGTGGATCGTGTGCTTGAT	35213	ATGGTCGACAGAGTCCTCGAC
6568	MVELTWE	20891	ATGGTTGAGCTGACGTGGGAG	35214	ATGGTCGAACTCACATGGGAA
6569	MVGFGAA	20892	ATGGTTGGTTTTGGTGCGGCG	35215	ATGGTCGGATTCGGAGCAGCA
6570	MVGQVKN	20893	ATGGTTGGGCAGGTGAAGAAT	35216	ATGGTCGGACAAGTCAAAAAC
6571	MVGRPIV	20894	ATGGTGGGTAGGCCGATTGTT	35217	ATGGTCGGAAGACCAATCGTC
6572	MVGRTGG	20895	ATGGTTGGTAGGACGGGTGGG	35218	ATGGTCGGAAGAACAGGAGGA
6573	MVGRVPS	20896	ATGGTTGGTCGTGTGCCTAGT	35219	ATGGTCGGAAGAGTCCCAAGC
6574	MVHSSAH	20897	ATGGTGCATTCGTCGGCGCAT	35220	ATGGTCCACAGCAGCGCACAC
6575	MVHSSES	20898	ATGGTGCATTCTTCTGAGTCG	35221	ATGGTCCACAGCAGCGAAAGC
6576	MVIHPDH	20899	ATGGTGATTCATCCGGATCAT	35222	ATGGTCATCCACCCAGACCAC
6577	MVLKLAA	20900	ATGGTGTTGAAGCTGGCTGCT	35223	ATGGTCCTCAAACTCGCAGCA
6578	MVNVIMP	20901	ATGGTTAATGTGATTATGCCG	35224	ATGGTCAACGTCATCATGCCA
6579	MVNYLDV	20902	ATGGTGAATTATCTGGATGTT	35225	ATGGTCAACTACCTCGACGTC
6580	MVPGNSG	20903	ATGGTGCCTGGTAATAGTGGT	35226	ATGGTCCCAGGAAACAGCGGA
6581	MVPRENL	20904	ATGGTTCCTCGTGAGAATCTT	35227	ATGGTCCCAAGAGAAAACCTC
6582	MVPSQHS	20905	ATGGTGCCGAGTCAGCATTCT	35228	ATGGTCCCAAGCCAACACAGC
6583	MVPSSEM	20906	ATGGTGCCGAGTAGTGAGATG	35229	ATGGTCCCAAGCAGCGAAATG
6584	MVQRTTT	20907	ATGGTTCAGCGGACGACGACG	35230	ATGGTCCAAAGAACAACAACA
6585	MVRALPC	20908	ATGGTTCGGGCGCTGCCGTGT	35231	ATGGTCAGAGCACTCCCATGC
6586	MVSNRQT	20909	ATGGTGTCGAATCGTCAGACG	35232	ATGGTCAGCAACAGACAAACA
6587	MVSPSPT	20910	ATGGTGTCTCCTAGTCCGACT	35233	ATGGTCAGCCCAAGCCCAACA
6588	MVSVDRD	20911	ATGGTGTCGGTTGATAGGGAT	35234	ATGGTCAGCGTCGACAGAGAC
6589	MVTLTPG	20912	ATGGTTACTCTGACTCCGGGT	35235	ATGGTCACACTCACACCAGGA
6590	MVTNVTK	20913	ATGGTTACTAATGTTACTAAG	35236	ATGGTCACAAACGTCACAAAA
6591	MVTRPES	20914	ATGGTTACGCGTCCGGAGAGT	35237	ATGGTCACAAGACCAGAAAGC
6592	MVTSSTS	20915	ATGGTGACGTCTTCGACTTCT	35238	ATGGTCACAAGCAGCACAAGC
6593	MVTYGQQ	20916	ATGGTTACGTATGGGCAGCAG	35239	ATGGTCACATACGGACAACAA
6594	MVVHHNN	20917	ATGGTTGTGCATCATAATAAT	35240	ATGGTCGTCCACCACAACAAC
6595	MVVKMVS	20918	ATGGTGGTGAAGATGGTGTCG	35241	ATGGTCGTCAAAATGGTCAGC
6596	MWNKEHD	20919	ATGTGGAATAAGGAGCATGAT	35242	ATGTGGAACAAAGAACACGAC
6597	MYDNDVW	20920	ATGTATGATAATGATGTGTGG	35243	ATGTACGACAACGACGTCTGG
6598	MYDRSGL	20921	ATGTATGATAGGAGTGGGCTG	35244	ATGTACGACAGAAGCGGACTC
6599	MYESRGV	20922	ATGTATGAGTCTCGGGGGGTT	35245	ATGTACGAAAGCAGAGGAGTC
6600	MYPGMMM	20923	ATGTATCCGGGGATGATGATG	35246	ATGTACCCAGGAATGATGATG
6601	MYPSGIV	20924	ATGTATCCTAGTGGGATTGTT	35247	ATGTACCCAAGCGGAATCGTC
6602	MYPTHTG	20925	ATGTATCCGACTCATACGGGG	35248	ATGTACCCAACACACACAGGA
6603	MYPVRLD	20926	ATGTATCCTGTGAGGCTTGAT	35249	ATGTACCCAGTCAGACTCGAC
6604	MYQEHTE	20927	ATGTATCAGGAGCATACGGAG	35250	ATGTACCAAGAACACACAGAA

6605	MYQQAHS	20928	ATGTATCAGCAGGCTCATAGT	35251	ATGTACCAACAAGCACACAGC
6606	MYRDELT	20929	ATGTATAGGGATGAGCTTACT	35252	ATGTACAGAGACGAACTCACA
6607	MYSMSNV	20930	ATGTATTCGATGTCTAATGTT	35253	ATGTACAGCATGAGCAACGTC
6608	MYSTQSS	20931	ATGTATTCGACGCAGTCTTCG	35254	ATGTACAGCACACAAAGCAGC
6609	MYTSMAG	20932	ATGTATACGTCGATGGCGGGT	35255	ATGTACACAAGCATGGCAGGA
6610	MYVAASP	20933	ATGTATGTTGCTGCTTCTCCT	35256	ATGTACGTCGCAGCAAGCCCA
6611	NAAPSTI	20934	AATGCGGCTCCGTCGACTATT	35257	AACGCAGCACCAAGCACAATC
6612	NAARLTS	20935	AATGCTGCTCGGTTGACGTCT	35258	AACGCAGCAAGACTCACAAGC
6613	NAASPGF	20936	AATGCGGCTAGTCCTGGTTTT	35259	AACGCAGCAAGCCCAGGATTC
6614	NAASQSP	20937	AATGCGGCGTCTCAGTCGCCT	35260	AACGCAGCAAGCCAAAGCCCA
6615	NADALGS	20938	AATGCGGATGCGCTGGGTTCG	35261	AACGCAGACGCACTCGGAAGC
6616	NADPRDR	20939	AATGCGGATCCTCGTGATCGG	35262	AACGCAGACCCAAGAGACAGA
6617	NADRRSE	20940	AATGCGGATCGTCGTTCTGAG	35263	AACGCAGACAGAAGAAGCGAA
6618	NAEAFLD	20941	AATGCTGAGGCGTTTTTGGAT	35264	AACGCAGAAGCATTCCTCGAC
6619	NAEDRTV	20942	AATGCGGAGGATAGGACTGTG	35265	AACGCAGAAGACAGAACAGTC
6620	NAFSTST	20943	AATGCTTTTAGTACGTCGACG	35266	AACGCATTCAGCACAAGCACA
6621	NAGGTWD	20944	AATGCTGGTGGTACGTGGGAT	35267	AACGCAGGAGGAACATGGGAC
6622	NAGTRQA	20945	AATGCTGGGACGCGGCAGGCT	35268	AACGCAGGAACAAGACAAGCA
6623	NAHLSLN	20946	AATGCTCATCTTAGTTTGAAT	35269	AACGCACACCTCAGCCTCAAC
6624	NAHSTLV	20947	AATGCTCATAGTACGCTGGTT	35270	AACGCACACAGCACACTCGTC
6625	NAHTDRQ	20948	AATGCGCATACGGATCGTCAG	35271	AACGCACACACAGACAGACAA
6626	NAHTQIQ	20949	AATGCTCATACTCAGATTCAG	35272	AACGCACACACACAAATCCAA
6627	NAKALAM	20950	AATGCGAAGGCTCTGGCGATG	35273	AACGCAAAAGCACTCGCAATG
6628	NAKSTIG	20951	AATGCTAAGAGTACGATTGGG	35274	AACGCAAAAAGCACAATCGGA
6629	NALARSG	20952	AATGCGCTTGCTCGTTCTGGG	35275	AACGCACTCGCAAGAAGCGGA
6630	NALDDNV	20953	AATGCGTTGGATGATAATGTG	35276	AACGCACTCGACGACAACGTC
6631	NALDRSM	20954	AATGCGCTGGATCGGTCTATG	35277	AACGCACTCGACAGAAGCATG
6632	NALEASG	20955	AATGCTCTTGAGGCGTCTGGT	35278	AACGCACTCGAAGCAAGCGGA
6633	NALNPNF	20956	AATGCGCTTAATCCGAATTTT	35279	AACGCACTCAACCCAAACTTC
6634	NALRSYS	20957	AATGCTCTGCGTTCTTATTCG	35280	AACGCACTCAGAAGCTACAGC
6635	NALSHVT	20958	AATGCTTTGTCGCATGTTACG	35281	AACGCACTCAGCCACGTCACA
6636	NALVSES	20959	AATGCTCTTGTGTCTGAGTCT	35282	AACGCACTCGTCAGCGAAAGC
6637	NANGSRV	20960	AATGCTAATGGGTCTCGGGTT	35283	AACGCAAACGGAAGCAGAGTC
6638	NANHQNV	20961	AATGCGAATCATCAGAATGTG	35284	AACGCAAACCACCAAAACGTC
6639	NANLNSA	20962	AATGCTAATTTGAATAGTGCG	35285	AACGCAAACCTCAACAGCGCA
6640	NANTGRL	20963	AATGCTAATACGGGGAGGCTG	35286	AACGCAAACACAGGAAGACTC
6641	NANVPNR	20964	AATGCTAATGTGCCTAATCGG	35287	AACGCAAACGTCCCAAACAGA
6642	NAPRSAV	20965	AATGCGCCGCGTTCGGCTGTT	35288	AACGCACCAAGAAGCGCAGTC
6643	NAPSESR	20966	AATGCGCCGAGTGAGTCGCGT	35289	AACGCACCAAGCGAAAGCAGA
6644	NAQIRPM	20967	AATGCTCAGATTCGTCCTATG	35290	AACGCACAAATCAGACCAATG
6645	NARLSTS	20968	AATGCTCGTCTTTCTACGAGT	35291	AACGCAAGACTCAGCACAAGC
6646	NARMLAS	20969	AATGCGCGGATGCTGGCTAGT	35292	AACGCAAGAATGCTCGCAAGC
6647	NARPHDP	20970	AATGCGCGGCCTCATGATCCG	35293	AACGCAAGACCACACGACCCA
6648	NARPSDM	20971	AATGCGAGGCCTAGTGATATG	35294	AACGCAAGACCAAGCGACATG
6649	NARSIDY	20972	AATGCTAGGAGTATTGATTAT	35295	AACGCAAGAAGCATCGACTAC

6650	NARSSSY	20973	AATGCGAGGAGTTCTAGTTAT	35296	AACGCAAGAAGCAGCAGCTAC
6651	NARVEAP	20974	AATGCGCGGGTTGAGGCTCCT	35297	AACGCAAGAGTCGAAGCACCA
6652	NARYTHS	20975	AATGCTCGGTATACTCATTCT	35298	AACGCAAGATACACACACAGC
6653	NASGLPR	20976	AATGCTTCTGGGCTGCCGCGT	35299	AACGCAAGCGGACTCCCAAGA
6654	NASIHSH	20977	AATGCGTCTATTCATAGTCAT	35300	AACGCAAGCATCCACAGCCAC
6655	NASLPLS	20978	AATGCTAGTCTTCCGTTGAGT	35301	AACGCAAGCCTCCCACTCAGC
6656	NASNSEK	20979	AATGCTTCTAATTCGGAGAAG	35302	AACGCAAGCAACAGCGAAAAA
6657	NASPIRL	20980	AATGCGTCGCCTATTAGGCTG	35303	AACGCAAGCCCAATCAGACTC
6658	NASSRSL	20981	AATGCTTCGTCTAGGTCGCTT	35304	AACGCAAGCAGCAGAAGCCTC
6659	NASTVPE	20982	AATGCGTCTACGGTGCCTGAG	35305	AACGCAAGCACAGTCCCAGAA
6660	NATADGF	20983	AATGCTACGGCTGATGGGTTT	35306	AACGCAACAGCAGACGGATTC
6661	NATHPNF	20984	AATGCGACGCATCCTAATTTT	35307	AACGCAACACACCCAAACTTC
6662	NATHTST	20985	AATGCGACGCATACGTCGACT	35308	AACGCAACACACACAAGCACA
6663	NATPVAV	20986	AATGCGACTCCGGTTGCGGTT	35309	AACGCAACACCAGTCGCAGTC
6664	NATSGSH	20987	AATGCGACGTCTGGTTCTCAT	35310	AACGCAACAAGCGGAAGCCAC
6665	NATSTLC	20988	AATGCGACTAGTACGCTTTGT	35311	AACGCAACAAGCACACTCTGC
6666	NATSYTM	20989	AATGCTACGAGTTATACTATG	35312	AACGCAACAAGCTACACAATG
6667	NATVSPR	20990	AATGCTACGGTGTCTCCGAGG	35313	AACGCAACAGTCAGCCCAAGA
6668	NAVPGRS	20991	AATGCTGTGCCTGGTCGGAGT	35314	AACGCAGTCCCAGGAAGAAGC
6669	NAVPIPP	20992	AATGCGGTTCCTATTCCTCCG	35315	AACGCAGTCCCAATCCCACCA
6670	NAVQSLM	20993	AATGCTGTTCAGAGTCTTATG	35316	AACGCAGTCCAAAGCCTCATG
6671	NAVSVNS	20994	AATGCGGTGTCGGTGAATTCT	35317	AACGCAGTCAGCGTCAACAGC
6672	NAWKTPV	20995	AATGCTTGGAAGACTCCTGTG	35318	AACGCATGGAAAACACCAGTC
6673	NAYTTGP	20996	AATGCTTATACTACGGGTCCG	35319	AACGCATACACAACAGGACCA
6674	NCDAVAW	20997	AATTGTGATGCTGTTGCGTGG	35320	AACTGCGACGCAGTCGCATGG
6675	NDDIQRK	20998	AATGATGATATTCAGCGTAAG	35321	AACGACGACATCCAAAGAAAA
6676	NDGHRNF	20999	AATGATGGGCATCGGAATTTT	35322	AACGACGGACACAGAAACTTC
6677	NDILLLS	21000	AATGATATTCTGCTGCTGAGT	35323	AACGACATCCTCCTCCTCAGC
6678	NDITEVP	21001	AATGATATTACTGAGGTGCCT	35324	AACGACATCACAGAAGTCCCA
6679	NDKFRLS	21002	AATGATAAGTTTAGGTTGTCT	35325	AACGACAAATTCAGACTCAGC
6680	NDKMLQR	21003	AATGATAAGATGTTGCAGCGT	35326	AACGACAAAATGCTCCAAAGA
6681	NDPKVPQ	21004	AATGATCCGAAGGTGCCTCAG	35327	AACGACCCAAAAGTCCCACAA
6682	NDPMTSQ	21005	AATGATCCGATGACGTCTCAG	35328	AACGACCCAATGACAAGCCAA
6683	NDRMKNS	21006	AATGATCGGATGAAGAATTCT	35329	AACGACAGAATGAAAAACAGC
6684	NDRSKYP	21007	AATGATCGGTCTAAGTATCCT	35330	AACGACAGAAGCAAATACCCA
6685	NDSSLGA	21008	AATGATTCTAGTCTTGGTGCG	35331	AACGACAGCAGCCTCGGAGCA
6686	NDSSSTM	21009	AATGATAGTAGTAGTACGATG	35332	AACGACAGCAGCAGCACAATG
6687	NDTFSSL	21010	AATGATACGTTTTCGTCTCTG	35333	AACGACACATTCAGCAGCCTC
6688	NDTGALM	21011	AATGATACTGGGGCTTTGATG	35334	AACGACACAGGAGCACTCATG
6689	NDTYRTS	21012	AATGATACTTATCGTACTTCT	35335	AACGACACATACAGAACAAGC
6690	NDVPNTP	21013	AATGATGTGCCGAATACTCCT	35336	AACGACGTCCCAAACACACCA
6691	NDVTTHK	21014	AATGATGTTACGACGCATAAG	35337	AACGACGTCACAACACACAAA
6692	NDWLIAG	21015	AATGATTGGTTGATTGCGGGG	35338	AACGACTGGCTCATCGCAGGA
6693	NEALSQL	21016	AATGAGGCTCTTTCGCAGTTG	35339	AACGAAGCACTCAGCCAACTC
6694	NEAVASM	21017	AATGAGGCTGTTGCGTCTATG	35340	AACGAAGCAGTCGCAAGCATG

6695	NECDDLM	21018	AATGAGTGTGATGATCTGATG	35341	AACGAATGCGACGACCTCATG
6696	NEGFLLG	21019	AATGAGGGTTTTCTGCTTGGG	35342	AACGAAGGATTCCTCCTCGGA
6697	NEHHKTE	21020	AATGAGCATCATAAGACTGAG	35343	AACGAACACCACAAAACAGAA
6698	NEIFTPM	21021	AATGAGATTTTTACGCCGATG	35344	AACGAAATCTTCACACCAATG
6699	NELASRA	21022	AATGAGCTGGCTTCGAGGGCG	35345	AACGAACTCGCAAGCAGAGCA
6700	NELGGHH	21023	AATGAGTTGGGGGGGCATCAT	35346	AACGAACTCGGAGGACACCAC
6701	NELVSKT	21024	AATGAGTTGGTGTCTAAGACG	35347	AACGAACTCGTCAGCAAAACA
6702	NEMSGQR	21025	AATGAGATGTCTGGGCAGCGG	35348	AACGAAATGAGCGGACAAAGA
6703	NEPLGMR	21026	AATGAGCCGCTTGGGATGCGT	35349	AACGAACCACTCGGAATGAGA
6704	NEQHATH	21027	AATGAGCAGCATGCGACTCAT	35350	AACGAACAACACGCAACACAC
6705	NERGSSW	21028	AATGAGCGGGGTTCGAGTTGG	35351	AACGAAAGAGGAAGCAGCTGG
6706	NERHHQV	21029	AATGAGCGTCATCATCAGGTT	35352	AACGAAAGACACCACCAAGTC
6707	NERNVQL	21030	AATGAGCGGAATGTGCAGCTG	35353	AACGAAAGAAACGTCCAACTC
6708	NERRVVL	21031	AATGAGCGTAGGGTTGTGCTG	35354	AACGAAAGAAGAGTCGTCCTC
6709	NESHKNV	21032	AATGAGTCGCATAAGAATGTG	35355	AACGAAAGCCACAAAAACGTC
6710	NESLRTA	21033	AATGAGTCGCTGAGGACTGCG	35356	AACGAAAGCCTCAGAACAGCA
6711	NESLTSA	21034	AATGAGAGTTTGACGTCTGCT	35357	AACGAAAGCCTCACAAGCGCA
6712	NESVRSY	21035	AATGAGAGTGTTCGTAGTTAT	35358	AACGAAAGCGTCAGAAGCTAC
6713	NEYVLGL	21036	AATGAGTATGTGCTTGGGCTT	35359	AACGAATACGTCCTCGGACTC
6714	NFAARSY	21037	AATTTTGCGGCGAGGAGTTAT	35360	AACTTCGCAGCAAGAAGCTAC
6715	NFDRHGA	21038	AATTTTGATCGTCATGGTGCG	35361	AACTTCGACAGACACGGAGCA
6716	NFDRPRT	21039	AATTTTGATCGGCCTAGGACT	35362	AACTTCGACAGACCAAGAACA
6717	NFNTRVA	21040	AATTTTAATACTAGGGTGGCT	35363	AACTTCAACACAAGAGTCGCA
6718	NFRVSSG	21041	AATTTTCGTGTGTCTAGTGGT	35364	AACTTCAGAGTCAGCAGCGGA
6719	NFSPTSP	21042	AATTTTAGTCCTACTAGTCCT	35365	AACTTCAGCCCAACAAGCCCA
6720	NFTKAGA	21043	AATTTTACTAAGGCTGGGGCT	35366	AACTTCACAAAAGCAGGAGCA
6721	NFTKSAG	21044	AATTTTACTAAGAGTGCGGGG	35367	AACTTCACAAAAAGCGCAGGA
6722	NFTLKPI	21045	AATTTTACGCTGAAGCCGATT	35368	AACTTCACACTCAAACCAATC
6723	NFVGVPT	21046	AATTTTGTGGGGGTGCCGACG	35369	AACTTCGTCGGAGTCCCAACA
6724	NFVVPSD	21047	AATTTTGTTGTGCCTAGTGAT	35370	AACTTCGTCGTCCCAAGCGAC
6725	NGAAEVA	21048	AATGGTGCTGCGGAGGTTGCG	35371	AACGGAGCAGCAGAAGTCGCA
6726	NGADRAS	21049	AATGGTGCGGATCGTGCGTCG	35372	AACGGAGCAGACAGAGCAAGC
6727	NGAGLTI	21050	AATGGTGCGGGTCTGACTATT	35373	AACGGAGCAGGACTCACAATC
6728	NGALRLP	21051	AATGGGGCTCTGCGTCTGCCT	35374	AACGGAGCACTCAGACTCCCA
6729	NGDACPS	21052	AATGGTGATGCTTGTCCGAGT	35375	AACGGAGACGCATGCCCAAGC
6730	NGEAQAR	21053	AATGGGGAGGCTCAGGCTCGT	35376	AACGGAGAAGCACAAGCAAGA
6731	NGEPFSI	21054	AATGGTGAGCCGTTTAGTATT	35377	AACGGAGAACCATTCAGCATC
6732	NGGAYTL	21055	AATGGTGGTGCGTATACGCTG	35378	AACGGAGGAGCATACACACTC
6733	NGGISRT	21056	AATGGGGGGATTAGTAGGACG	35379	AACGGAGGAATCAGCAGAACA
6734	NGGNLLL	21057	AATGGTGGGAATTTGCTTTTG	35380	AACGGAGGAAACCTCCTCCTC
6735	NGHFVDA	21058	AATGGTCATTTTGTTGATGCT	35381	AACGGACACTTCGTCGACGCA
6736	NGHNHML	21059	AATGGGCATAATCATATGTTG	35382	AACGGACACAACCACATGCTC
6737	NGHSVSE	21060	AATGGTCATAGTGTGTCTGAG	35383	AACGGACACAGCGTCAGCGAA
6738	NGKNGST	21061	AATGGTAAGAATGGTTCGACG	35384	AACGGAAAAAACGGAAGCACA
6739	NGLQTGV	21062	AATGGGCTTCAGACGGGGGTT	35385	AACGGACTCCAAACAGGAGTC

6740	NGMGAVV	21063	AATGGGATGGGGGCTGTGGTG	35386	AACGGAATGGGAGCAGTCGTC
6741	NGMQPLN	21064	AATGGTATGCAGCCTTTGAAT	35387	AACGGAATGCAACCACTCAAC
6742	NGMYPYP	21065	AATGGGATGTATCCGTATCCT	35388	AACGGAATGTACCCATACCCA
6743	NGNEVLS	21066	AATGGGAATGAGGTTTTGTCT	35389	AACGGAAACGAAGTCCTCAGC
6744	NGPHRMV	21067	AATGGTCCTCATCGTATGGTT	35390	AACGGACCACACAGAATGGTC
6745	NGPPAVG	21068	AATGGGCCGCCGGCTGTTGGG	35391	AACGGACCACCAGCAGTCGGA
6746	NGPPKGI	21069	AATGGTCCTCCGAAGGGTATT	35392	AACGGACCACCAAAAGGAATC
6747	NGPSAQQ	21070	AATGGGCCTAGTGCGCAGCAG	35393	AACGGACCAAGCGCACAACAA
6748	NGQAEPA	21071	AATGGGCAGGCTGAGCCTGCT	35394	AACGGACAAGCAGAACCAGCA
6749	NGSHIDR	21072	AATGGGTCTCATATTGATCGG	35395	AACGGAAGCCACATCGACAGA
6750	NGSWVPA	21073	AATGGGTCGTGGGTGCCGGCT	35396	AACGGAAGCTGGGTCCCAGCA
6751	NGSYQPP	21074	AATGGTTCTTATCAGCCTCCG	35397	AACGGAAGCTACCAACCACCA
6752	NGTQLLS	21075	AATGGTACTCAGCTTCTGAGT	35398	AACGGAACACAACTCCTCAGC
6753	NGTTALF	21076	AATGGGACTACTGCGCTTTTT	35399	AACGGAACAACAGCACTCTTC
6754	NGTYSVE	21077	AATGGGACGTATAGTGTGGAG	35400	AACGGAACATACAGCGTCGAA
6755	NGVLLHA	21078	AATGGTGTGCTGCTTCATGCG	35401	AACGGAGTCCTCCTCCACGCA
6756	NGVPSLG	21079	AATGGTGTGCCGAGTTTGGGT	35402	AACGGAGTCCCAAGCCTCGGA
6757	NGYAVSA	21080	AATGGGTATGCGGTTTCTGCG	35403	AACGGATACGCAGTCAGCGCA
6758	NGYTRDE	21081	AATGGTTATACTCGGGATGAG	35404	AACGGATACACAAGAGACGAA
6759	NHASNTT	21082	AATCATGCGAGTAATACGACG	35405	AACCACGCAAGCAACACAACA
6760	NHHNAYS	21083	AATCATCATAATGCGTATTCT	35406	AACCACCACAACGCATACAGC
6761	NHITYEN	21084	AATCATATTACGTATGAGAAT	35407	AACCACATCACATACGAAAAC
6762	NHKCADE	21085	AATCATAAGTGTGCTGATGAG	35408	AACCACAAATGCGCAGACGAA
6763	NHKGLNL	21086	AATCATAAGGGTTTGAATTTG	35409	AACCACAAAGGACTCAACCTC
6764	NHMPSVY	21087	AATCATATGCCTTCGGTGTAT	35410	AACCACATGCCAAGCGTCTAC
6765	NHNGLQM	21088	AATCATAATGGTCTTCAGATG	35411	AACCACAACGGACTCCAAATG
6766	NHNRPAN	21089	AATCATAATAGGCCGGCTAAT	35412	AACCACAACAGACCAGCAAAC
6767	NHPSAST	21090	AATCATCCTTCTGCTAGTACT	35413	AACCACCCAAGCGCAAGCACA
6768	NHPVPSS	21091	AATCATCCTGTTCCGTCGTCT	35414	AACCACCCAGTCCCAAGCAGC
6769	NHPYPKM	21092	AATCATCCGTATCCTAAGATG	35415	AACCACCCATACCCAAAAATG
6770	NHQLVSE	21093	AATCATCAGTTGGTTTCGGAG	35416	AACCACCAACTCGTCAGCGAA
6771	NHRASPY	21094	AATCATCGGGCGAGTCCTTAT	35417	AACCACAGAGCAAGCCCATAC
6772	NHRTGNA	21095	AATCATCGGACTGGTAATGCT	35418	AACCACAGAACAGGAAACGCA
6773	NHRTSGS	21096	AATCATAGGACGAGTGGTTCG	35419	AACCACAGAACAAGCGGAAGC
6774	NHSAEMS	21097	AATCATTCTGCGGAGATGAGT	35420	AACCACAGCGCAGAAATGAGC
6775	NHSETLM	21098	AATCATAGTGAGACTTTGATG	35421	AACCACAGCGAAACACTCATG
6776	NHSGTIV	21099	AATCATTCGGGTACGATTGTT	35422	AACCACAGCGGAACAATCGTC
6777	NHSPVPL	21100	AATCATTCTCCGGTGCCTCTG	35423	AACCACAGCCCAGTCCCACTC
6778	NHSSDGA	21101	AATCATAGTTCGGATGGTGCT	35424	AACCACAGCAGCGACGGAGCA
6779	NHTGSTL	21102	AATCATACTGGTTCTACTCTG	35425	AACCACACAGGAAGCACACTC
6780	NHTPSIP	21103	AATCATACTCCGTCGATTCCT	35426	AACCACACACCAAGCATCCCA
6781	NHVAKSW	21104	AATCATGTTGCGAAGAGTTGG	35427	AACCACGTCGCAAAAAGCTGG
6782	NHYNVNE	21105	AATCATTATAATGTGAATGAG	35428	AACCACTACAACGTCAACGAA
6783	NIANALN	21106	AATATTGCTAATGCTTTGAAT	35429	AACATCGCAAACGCACTCAAC
6784	NIFDDAD	21107	AATATTTTTGATGATGCTGAT	35430	AACATCTTCGACGACGCAGAC

6785	NIGATPS	21108	AATATTGGTGCGACTCCGAGT	35431	AACATCGGAGCAACACCAAGC
6786	NIGGMMS	21109	AATATTGGGGGTATGATGTCG	35432	AACATCGGAGGAATGATGAGC
6787	NIGMTTG	21110	AATATTGGGATGACTACGGGG	35433	AACATCGGAATGACAACAGGA
6788	NIKHGPH	21111	AATATTAAGCATGGGCCGCAT	35434	AACATCAAACACGGACCACAC
6789	NIKLGHD	21112	AATATTAAGCTGGGGCATGAT	35435	AACATCAAACTCGGACACGAC
6790	NILQYTS	21113	AATATTCTGCAGTATACTTCT	35436	AACATCCTCCAATACACAAGC
6791	NILRTDE	21114	AATATTTTGCGTACGGATGAG	35437	AACATCCTCAGAACAGACGAA
6792	NIPDRFI	21115	AATATTCCGGATCGTTTTATT	35438	AACATCCCAGACAGATTCATC
6793	NIPLGAA	21116	AATATTCCGCTGGGTGCGGCG	35439	AACATCCCACTCGGAGCAGCA
6794	NIPPRPL	21117	AATATTCCTCCGCGGCCTCTT	35440	AACATCCCACCAAGACCACTC
6795	NIQVRSG	21118	AATATTCAGGTTAGGAGTGGG	35441	AACATCCAAGTCAGAAGCGGA
6796	NIRDLVH	21119	AATATTCGTGATCTTGTTCAT	35442	AACATCAGAGACCTCGTCCAC
6797	NIRTNNI	21120	AATATTCGTACGAATAATATT	35443	AACATCAGAACAAACAACATC
6798	NISLPLL	21121	AATATTTCGTTGCCGTTGTTG	35444	AACATCAGCCTCCCACTCCTC
6799	NISYTIE	21122	AATATTAGTTATACGATTGAG	35445	AACATCAGCTACACAATCGAA
6800	NITLAHL	21123	AATATTACGCTGGCTCATCTG	35446	AACATCACACTCGCACACCTC
6801	NITSNES	21124	AATATTACTTCTAATGAGAGT	35447	AACATCACAAGCAACGAAAGC
6802	NITTRGT	21125	AATATTACTACTCGTGGGACG	35448	AACATCACAACAAGAGGAACA
6803	NIVERSR	21126	AATATTGTGGAGCGTTCGAGG	35449	AACATCGTCGAAAGAAGCAGA
6804	NKALTHM	21127	AATAAGGCGCTTACTCATATG	35450	AACAAAGCACTCACACACATG
6805	NKEHVQG	21128	AATAAGGAGCATGTTCAGGGG	35451	AACAAAGAACACGTCCAAGGA
6806	NKEPTDS	21129	AATAAGGAGCCGACTGATTCT	35452	AACAAAGAACCAACAGACAGC
6807	NKEVHNS	21130	AATAAGGAGGTGCATAATTCG	35453	AACAAAGAAGTCCACAACAGC
6808	NKGVYSG	21131	AATAAGGGTGTGTATTCGGGT	35454	AACAAAGGAGTCTACAGCGGA
6809	NKHFQAH	21132	AATAAGCATTTTCAGGCGCAT	35455	AACAAACACTTCCAAGCACAC
6810	NKIDPYT	21133	AATAAGATTGATCCTTATACT	35456	AACAAAATCGACCCATACACA
6811	NKMTTYA	21134	AATAAGATGACTACTTATGCT	35457	AACAAAATGACAACATACGCA
6812	NKQFTPE	21135	AATAAGCAGTTTACGCCTGAG	35458	AACAAACAATTCACACCAGAA
6813	NKSINTD	21136	AATAAGAGTATTAATACTGAT	35459	AACAAAAGCATCAACACAGAC
6814	NKSLTTG	21137	AATAAGTCTTTGACGACGGGT	35460	AACAAAAGCCTCACAACAGGA
6815	NKSMNVP	21138	AATAAGAGTATGAATGTTCCG	35461	AACAAAAGCATGAACGTCCCA
6816	NKTDNVS	21139	AATAAGACTGATAATGTTTCT	35462	AACAAAACAGACAACGTCAGC
6817	NKTQSRH	21140	AATAAGACGCAGAGTAGGCAT	35463	AACAAAACACAAAGCAGACAC
6818	NKVLHAP	21141	AATAAGGTGTTGCATGCTCCG	35464	AACAAAGTCCTCCACGCACCA
6819	NKVSGPM	21142	AATAAGGTGTCTGGTCCGATG	35465	AACAAAGTCAGCGGACCAATG
6820	NKYQDLR	21143	AATAAGTATCAGGATTTGCGT	35466	AACAAATACCAAGACCTCAGA
6821	NLAHTKF	21144	AATTTGGCTCATACTAAGTTT	35467	AACCTCGCACACACAAAATTC
6822	NLALDAR	21145	AATCTTGCGCTGGATGCTCGT	35468	AACCTCGCACTCGACGCAAGA
6823	NLAPIQR	21146	AATCTTGCTCCTATTCAGCGG	35469	AACCTCGCACCAATCCAAAGA
6824	NLDRPVT	21147	AATTTGGATCGTCCGGTGACG	35470	AACCTCGACAGACCAGTCACA
6825	NLETIPR	21148	AATCTTGAGACTATTCCTAGG	35471	AACCTCGAAACAATCCCAAGA
6826	NLGGSVE	21149	AATTTGGGTGGTTCGGTGGAG	35472	AACCTCGGAGGAAGCGTCGAA
6827	NLGKKEL	21150	AATCTGGGTAAGAAGGAGCTT	35473	AACCTCGGAAAAAAAGAACTC
6828	NLGPTLP	21151	AATTTGGGGCCTACGCTGCCG	35474	AACCTCGGACCAACACTCCCA
6829	NLGPYPL	21152	AATTTGGGTCCTTATCCTCTT	35475	AACCTCGGACCATACCCACTC

6830	NLHLISA	21153	AATTTGCATCTTATTAGTGCG	35476	AACCTCCACCTCATCAGCGCA
6831	NLHLPSS	21154	AATCTGCATTTGCCGTCGAGT	35477	AACCTCCACCTCCCAAGCAGC
6832	NLHRTPD	21155	AATTTGCATCGGACGCCTGAT	35478	AACCTCCACAGAACACCAGAC
6833	NLHSTTA	21156	AATTTGCATTCGACTACGGCG	35479	AACCTCCACAGCACAACAGCA
6834	NLIAMGS	21157	AATCTGATTGCTATGGGTTCT	35480	AACCTCATCGCAATGGGAAGC
6835	NLIPTKA	21158	AATTTGATTCCGACGAAGGCG	35481	AACCTCATCCCAACAAAAGCA
6836	NLKLMSG	21159	AATCTGAAGCTTATGTCTGGT	35482	AACCTCAAACTCATGAGCGGA
6837	NLKVLVT	21160	AATTTGAAGGTGCTGGTTACG	35483	AACCTCAAAGTCCTCGTCACA
6838	NLKVTRD	21161	AATTTGAAGGTGACGAGGGAT	35484	AACCTCAAAGTCACAAGAGAC
6839	NLLDVHL	21162	AATCTGCTTGATGTGCATTTG	35485	AACCTCCTCGACGTCCACCTC
6840	NLLGHAV	21163	AATCTGTTGGGTCATGCTGTG	35486	AACCTCCTCGGACACGCAGTC
6841	NLLTNAV	21164	AATCTTCTGACTAATGCTGTT	35487	AACCTCCTCACAAACGCAGTC
6842	NLNATSV	21165	AATCTGAATGCGACGTCGGTG	35488	AACCTCAACGCAACAAGCGTC
6843	NLPPSSP	21166	AATTTGCCGCCGAGTTCGCCT	35489	AACCTCCCACCAAGCAGCCCA
6844	NLPRPSL	21167	AATTTGCCGCGGCCTTCTTTG	35490	AACCTCCCAAGACCAAGCCTC
6845	NLPRRTD	21168	AATTTGCCTAGGCGGACTGAT	35491	AACCTCCCAAGAAGAACAGAC
6846	NLPYSLV	21169	AATTTGCCTTATTCGTTGGTT	35492	AACCTCCCATACAGCCTCGTC
6847	NLPYTQA	21170	AATCTTCCTTATACGCAGGCT	35493	AACCTCCCATACACACAAGCA
6848	NLQLTNG	21171	AATCTGCAGCTTACGAATGGT	35494	AACCTCCAACTCACAAACGGA
6849	NLRDGGT	21172	AATTTGAGGGATGGTGGGACT	35495	AACCTCAGAGACGGAGGAACA
6850	NLRGNPA	21173	AATTTGCGTGGGAATCCGGCT	35496	AACCTCAGAGGAAACCCAGCA
6851	NLRMQIP	21174	AATCTGCGGATGCAGATTCCT	35497	AACCTCAGAATGCAAATCCCA
6852	NLRPMSS	21175	AATTTGCGTCCTATGTCGTCG	35498	AACCTCAGACCAATGAGCAGC
6853	NLSDDRE	21176	AATCTTTCTGATGATAGGGAG	35499	AACCTCAGCGACGACAGAGAA
6854	NLSDSRS	21177	AATCTGTCGGATAGTAGGAGT	35500	AACCTCAGCGACAGCAGAAGC
6855	NLSHGVL	21178	AATTTGAGTCATGGTGTGTTG	35501	AACCTCAGCCACGGAGTCCTC
6856	NLSHRPM	21179	AATCTTTCGCATAGGCCTATG	35502	AACCTCAGCCACAGACCAATG
6857	NLSMGSP	21180	AATTTGTCTATGGGTTCGCCG	35503	AACCTCAGCATGGGAAGCCCA
6858	NLSNSVK	21181	AATCTGAGTAATTCGGTGAAG	35504	AACCTCAGCAACAGCGTCAAA
6859	NLSPYPM	21182	AATCTTTCTCCTTATCCTATG	35505	AACCTCAGCCCATACCCAATG
6860	NLSPYTM	21183	AATCTTTCTCCTTATACTATG	35506	AACCTCAGCCCATACACAATG
6861	NLSRDST	21184	AATCTGAGTCGGGATTCTACT	35507	AACCTCAGCAGAGACAGCACA
6862	NLSSGQV	21185	AATCTTTCTTCGGGTCAGGTT	35508	AACCTCAGCAGCGGACAAGTC
6863	NLSYTQQ	21186	AATTTGTCGTATACGCAGCAG	35509	AACCTCAGCTACACACAACAA
6864	NLTAGPP	21187	AATTTGACTGCGGGTCCTCCT	35510	AACCTCACAGCAGGACCACCA
6865	NLTGGSS	21188	AATTTGACGGGTGGTAGTTCT	35511	AACCTCACAGGAGGAAGCAGC
6866	NLTHTVM	21189	AATCTTACTCATACTGTTATG	35512	AACCTCACACACACAGTCATG
6867	NLTNSSM	21190	AATCTGACTAATTCGAGTATG	35513	AACCTCACAAACAGCAGCATG
6868	NLTRMIH	21191	AATCTGACGCGTATGATTCAT	35514	AACCTCACAAGAATGATCCAC
6869	NLTVKVQ	21192	AATCTGACGGTTAAGGTTCAG	35515	AACCTCACAGTCAAAGTCCAA
6870	NLVQFVH	21193	AATTTGGTTCAGTTTGTTCAT	35516	AACCTCGTCCAATTCGTCCAC
6871	NLVQNKP	21194	AATTTGGTTCAGAATAAGCCG	35517	AACCTCGTCCAAAACAAACCA
6872	NLYAYDP	21195	AATCTTTATGCGTATGATCCG	35518	AACCTCTACGCATACGACCCA
6873	NLYTPYP	21196	AATTTGTATACTCCTTATCCT	35519	AACCTCTACACACCATACCCA
6874	NMAHSPP	21197	AATATGGCGCATTCTCCGCCG	35520	AACATGGCACACAGCCCACCA

6875	NMAHVQY	21198	AATATGGCGCATGTGCAGTAT	35521	AACATGGCACACGTCCAATAC
6876	NMAIVEQ	21199	AATATGGCTATTGTTGAGCAG	35522	AACATGGCAATCGTCGAACAA
6877	NMATIRV	21200	AATATGGCTACGATTAGGGTT	35523	AACATGGCAACAATCAGAGTC
6878	NMHIRST	21201	AATATGCATATTCGTTCTACT	35524	AACATGCACATCAGAAGCACA
6879	NMHTRTS	21202	AATATGCATACTCGGACTTCT	35525	AACATGCACACAAGAACAAGC
6880	NMIALQT	21203	AATATGATTGCTCTGCAGACG	35526	AACATGATCGCACTCCAAACA
6881	NMKASSV	21204	AATATGAAGGCTTCGTCTGTT	35527	AACATGAAAGCAAGCAGCGTC
6882	NMLTDRV	21205	AATATGCTGACGGATCGTGTG	35528	AACATGCTCACAGACAGAGTC
6883	NMPNTSH	21206	AATATGCCGAATACTTCTCAT	35529	AACATGCCAAACACAAGCCAC
6884	NMPRHGL	21207	AATATGCCTAGGCATGGGCTT	35530	AACATGCCAAGACACGGACTC
6885	NMPVGST	21208	AATATGCCGGTTGGTTCGACG	35531	AACATGCCAGTCGGAAGCACA
6886	NMQGTNP	21209	AATATGCAGGGGACTAATCCT	35532	AACATGCAAGGAACAAACCCA
6887	NMRDTAS	21210	AATATGCGGGATACGGCGAGT	35533	AACATGAGAGACACAGCAAGC
6888	NMRLDQG	21211	AATATGCGGCTGGATCAGGGT	35534	AACATGAGACTCGACCAAGGA
6889	NMRPHTG	21212	AATATGCGGCCTCATACTGGT	35535	AACATGAGACCACACACAGGA
6890	NMRVTPQ	21213	AATATGCGGGTTACTCCGCAG	35536	AACATGAGAGTCACACCACAA
6891	NMSANIN	21214	AATATGTCTGCTAATATTAAT	35537	AACATGAGCGCAAACATCAAC
6892	NMSKSPG	21215	AATATGTCGAAGAGTCCTGGT	35538	AACATGAGCAAAAGCCCAGGA
6893	NMSNVHT	21216	AATATGAGTAATGTGCATACG	35539	AACATGAGCAACGTCCACACA
6894	NMSRGAM	21217	AATATGTCGCGGGGTGCGATG	35540	AACATGAGCAGAGGAGCAATG
6895	NMYPVPP	21218	AATATGTATCCGGTGCCTCCT	35541	AACATGTACCCAGTCCCACCA
6896	NNAKAMT	21219	AATAATGCTAAGGCGATGACT	35542	AACAACGCAAAAGCAATGACA
6897	NNASSSD	21220	AATAATGCTTCGAGTTCTGAT	35543	AACAACGCAAGCAGCAGCGAC
6898	NNDRLVH	21221	AATAATGATCGGCTGGTGCAT	35544	AACAACGACAGACTCGTCCAC
6899	NNELRSS	21222	AATAATGAGTTGAGGTCGTCT	35545	AACAACGAACTCAGAAGCAGC
6900	NNFGNTY	21223	AATAATTTTGGTAATACTTAT	35546	AACAACTTCGGAAACACATAC
6901	NNGKGPV	21224	AATAATGGGAAGGGTCCTGTG	35547	AACAACGGAAAAGGACCAGTC
6902	NNGLPSR	21225	AATAATGGGTTGCCTTCTCGG	35548	AACAACGGACTCCCAAGCAGA
6903	NNGRAQL	21226	AATAATGGGCGTGCTCAGCTT	35549	AACAACGGAAGAGCACAACTC
6904	NNGRLPN	21227	AATAATGGGAGGTTGCCGAAT	35550	AACAACGGAAGACTCCCAAAC
6905	NNHKIQS	21228	AATAATCATAAGATTCAGTCT	35551	AACAACCACAAAATCCAAAGC
6906	NNLRLNL	21229	AATAATCTGAGGTTGAATCTT	35552	AACAACCTCAGACTCAACCTC
6907	NNLRTSL	21230	AATAATCTTAGGACGTCTTTG	35553	AACAACCTCAGAACAAGCCTC
6908	NNMNTMP	21231	AATAATATGAATACTATGCCG	35554	AACAACATGAACACAATGCCA
6909	NNNEHYV	21232	AATAATAATGAGCATTATGTT	35555	AACAACAACGAACACTACGTC
6910	NNNLETM	21233	AATAATAATCTTGAGACGATG	35556	AACAACAACCTCGAAACAATG
6911	NNNPKYG	21234	AATAATAATCCTAAGTATGGG	35557	AACAACAACCCAAAATACGGA
6912	NNNTTPL	21235	AATAATAATACGACTCCGTTG	35558	AACAACAACACAACACCACTC
6913	NNPAPPS	21236	AATAATCCGGCTCCTCCGTCG	35559	AACAACCCAGCACCACCAAGC
6914	NNPDAYS	21237	AATAATCCGGATGCGTATAGT	35560	AACAACCCAGACGCATACAGC
6915	NNRPARE	21238	AATAATCGTCCGGCGCGGGAG	35561	AACAACAGACCAGCAAGAGAA
6916	NNSMALM	21239	AATAATAGTATGGCTCTGATG	35562	AACAACAGCATGGCACTCATG
6917	NNSRISS	21240	AATAATTCGCGGATTAGTTCT	35563	AACAACAGCAGAATCAGCAGC
6918	NNSRVGT	21241	AATAATTCGCGGGTTGGGACG	35564	AACAACAGCAGAGTCGGAACA
6919	NNSSYSE	21242	AATAATTCTAGTTATTCTGAG	35565	AACAACAGCAGCTACAGCGAA

6920	NNVNPIA	21243	AATAATGTGAATCCTATTGCG	35566	AACAACGTCAACCCAATCGCA
6921	NNVSTII	21244	AATAATGTTTCTACGATTATT	35567	AACAACGTCAGCACAATCATC
6922	NNWHNTP	21245	AATAATTGGCATAATACGCCG	35568	AACAACTGGCACAACACACCA
6923	NNYNPPT	21246	AATAATTATAATCCTCCTACT	35569	AACAACTACAACCCACCAACA
6924	NPAASTH	21247	AATCCGGCTGCTTCGACTCAT	35570	AACCCAGCAGCAAGCACACAC
6925	NPALPGH	21248	AATCCGGCTCTTCCTGGTCAT	35571	AACCCAGCACTCCCAGGACAC
6926	NPEGWGL	21249	AATCCGGAGGGTTGGGGGCTT	35572	AACCCAGAAGGATGGGGACTC
6927	NPETLIR	21250	AATCCTGAGACGCTGATTAGG	35573	AACCCAGAAACACTCATCAGA
6928	NPEVSPS	21251	AATCCTGAGGTTTCTCCGTCT	35574	AACCCAGAAGTCAGCCCAAGC
6929	NPGANMS	21252	AATCCTGGTGCGAATATGTCG	35575	AACCCAGGAGCAAACATGAGC
6930	NPGSQMV	21253	AATCCGGGTTCTCAGATGGTT	35576	AACCCAGGAAGCCAAATGGTC
6931	NPGTTTT	21254	AATCCGGGTACTACTACGACT	35577	AACCCAGGAACAACAACAACA
6932	NPGVKSA	21255	AATCCTGGTGTGAAGAGTGCT	35578	AACCCAGGAGTCAAAAGCGCA
6933	NPGVTHL	21256	AATCCTGGTGTGACTCATCTT	35579	AACCCAGGAGTCACACACCTC
6934	NPHISVS	21257	AATCCTCATATTTCGGTTTCT	35580	AACCCACACATCAGCGTCAGC
6935	NPHMQNI	21258	AATCCTCATATGCAGAATATT	35581	AACCCACACATGCAAAACATC
6936	NPHNDTG	21259	AATCCGCATAATGATACGGGT	35582	AACCCACACAACGACACAGGA
6937	NPILKTQ	21260	AATCCGATTCTGAAGACTCAG	35583	AACCCAATCCTCAAAACACAA
6938	NPISSGP	21261	AATCCTATTAGTTCGGGGCCT	35584	AACCCAATCAGCAGCGGACCA
6939	NPKLMKE	21262	AATCCGAAGTTGATGAAGGAG	35585	AACCCAAAACTCATGAAAGAA
6940	NPLSNDG	21263	AATCCGCTTTCGAATGATGGT	35586	AACCCACTCAGCAACGACGGA
6941	NPLTTHD	21264	AATCCTCTTACGACTCATGAT	35587	AACCCACTCACAACACACGAC
6942	NPMMHGS	21265	AATCCTATGATGCATGGGTCG	35588	AACCCAATGATGCACGGAAGC
6943	NPMTPDP	21266	AATCCGATGACGCCTGATCCT	35589	AACCCAATGACACCAGACCCA
6944	NPNQVAE	21267	AATCCGAATCAGGTTGCGGAG	35590	AACCCAAACCAAGTCGCAGAA
6945	NPNTRNC	21268	AATCCTAATACGCGTAATTGT	35591	AACCCAAACACAAGAAACTGC
6946	NPPALLP	21269	AATCCGCCTGCGCTGTTGCCT	35592	AACCCACCAGCACTCCTCCCA
6947	NPPPPSP	21270	AATCCGCCTCCTCCGAGTCCT	35593	AACCCACCACCACCAAGCCCA
6948	NPPRYGS	21271	AATCCGCCGAGGTATGGTAGT	35594	AACCCACCAAGATACGGAAGC
6949	NPPSLSS	21272	AATCCTCCTAGTCTGTCTTCG	35595	AACCCACCAAGCCTCAGCAGC
6950	NPPSRGN	21273	AATCCTCCTTCGCGGGGTAAT	35596	AACCCACCAAGCAGAGGAAAC
6951	NPPYALA	21274	AATCCTCCTTATGCGCTGGCT	35597	AACCCACCATACGCACTCGCA
6952	NPQMPSP	21275	AATCCGCAGATGCCTAGTCCG	35598	AACCCACAAATGCCAAGCCCA
6953	NPQRLGQ	21276	AATCCGCAGAGGCTTGGGCAG	35599	AACCCACAAAGACTCGGACAA
6954	NPQSVTH	21277	AATCCTCAGAGTGTGACGCAT	35600	AACCCACAAAGCGTCACACAC
6955	NPRAQMS	21278	AATCCTAGGGCGCAGATGAGT	35601	AACCCAAGAGCACAAATGAGC
6956	NPRASSW	21279	AATCCGCGTGCTTCGTCTTGG	35602	AACCCAAGAGCAAGCAGCTGG
6957	NPRNPTL	21280	AATCCTCGGAATCCGACTCTG	35603	AACCCAAGAAACCCAACACTC
6958	NPRPGQV	21281	AATCCGAGGCCTGGGCAGGTG	35604	AACCCAAGACCAGGACAAGTC
6959	NPSGKVA	21282	AATCCGAGTGGTAAGGTTGCG	35605	AACCCAAGCGGAAAAGTCGCA
6960	NPSLQTT	21283	AATCCGTCGCTTCAGACTACG	35606	AACCCAAGCCTCCAAACAACA
6961	NPSLRIG	21284	AATCCGTCTTTGCGGATTGGT	35607	AACCCAAGCCTCAGAATCGGA
6962	NPSNHAL	21285	AATCCTTCGAATCATGCGCTT	35608	AACCCAAGCAACCACGCACTC
6963	NPSQFDF	21286	AATCCTTCTCAGTTTGATTTT	35609	AACCCAAGCCAATTCGACTTC
6964	NPSRLPQ	21287	AATCCTTCGCGGCTGCCGCAG	35610	AACCCAAGCAGACTCCCACAA

6965	NPSRQAP	21288	AATCCTAGTAGGCAGGCGCCG	35611	AACCCAAGCAGACAAGCACCA
6966	NPSSSGC	21289	AATCCTTCGTCTTCGGGTTGT	35612	AACCCAAGCAGCAGCGGATGC
6967	NPSVVTA	21290	AATCCGTCTGTGGTTACTGCT	35613	AACCCAAGCGTCGTCACAGCA
6968	NPTASNA	21291	AATCCTACTGCGTCGAATGCT	35614	AACCCAACAGCAAGCAACGCA
6969	NPTFHGS	21292	AATCCTACGTTTCATGGGTCT	35615	AACCCAACATTCCACGGAAGC
6970	NPTQPIK	21293	AATCCTACTCAGCCGATTAAG	35616	AACCCAACACAACCAATCAAA
6971	NPTSLPS	21294	AATCCGACGTCGTTGCCGTCT	35617	AACCCAACAAGCCTCCCAAGC
6972	NPTTRYM	21295	AATCCGACGACTCGTTATATG	35618	AACCCAACAACAAGATACATG
6973	NPTVTGS	21296	AATCCGACTGTTACGGGGTCG	35619	AACCCAACAGTCACAGGAAGC
6974	NPYNTEA	21297	AATCCTTATAATACTGAGGCG	35620	AACCCATACAACACAGAAGCA
6975	NPYVLRA	21298	AATCCGTATGTGCTTCGTGCT	35621	AACCCATACGTCCTCAGAGCA
6976	NQDKATH	21299	AATCAGGATAAGGCTACTCAT	35622	AACCAAGACAAAGCAACACAC
6977	NQDPYMY	21300	AATCAGGATCCTTATATGTAT	35623	AACCAAGACCCATACATGTAC
6978	NQEGSPI	21301	AATCAGGAGGGTTCTCCTATT	35624	AACCAAGAAGGAAGCCCAATC
6979	NQENKIG	21302	AATCAGGAGAATAAGATTGGG	35625	AACCAAGAAAACAAAATCGGA
6980	NQGQNPV	21303	AATCAGGGTCAGAATCCTGTG	35626	AACCAAGGACAAAACCCAGTC
6981	NQIAVSR	21304	AATCAGATTGCTGTGTCGAGG	35627	AACCAAATCGCAGTCAGCAGA
6982	NQLHPVR	21305	AATCAGCTGCATCCTGTGCGT	35628	AACCAACTCCACCCAGTCAGA
6983	NQLVAHA	21306	AATCAGCTTGTGGCTCATGCT	35629	AACCAACTCGTCGCACACGCA
6984	NQNYQIV	21307	AATCAGAATTATCAGATTGTG	35630	AACCAAAACTACCAAATCGTC
6985	NQQGSMA	21308	AATCAGCAGGGTTCGATGGCT	35631	AACCAACAAGGAAGCATGGCA
6986	NQRDTMT	21309	AATCAGCGGGATACTATGACT	35632	AACCAAAGAGACACAATGACA
6987	NQRPVNF	21310	AATCAGCGTCCGGTTAATTTT	35633	AACCAAAGACCAGTCAACTTC
6988	NQRSTSM	21311	AATCAGAGGTCGACTAGTATG	35634	AACCAAAGAAGCACAAGCATG
6989	NQSIHQT	21312	AATCAGAGTATTCATCAGACT	35635	AACCAAAGCATCCACCAAACA
6990	NQTACEV	21313	AATCAGACGGCGTGTGAGGTT	35636	AACCAAACAGCATGCGAAGTC
6991	NQTLMAS	21314	AATCAGACGTTGATGGCTAGT	35637	AACCAAACACTCATGGCAAGC
6992	NQTNGRA	21315	AATCAGACTAATGGGCGGGCT	35638	AACCAAACAAACGGAAGAGCA
6993	NQTRVVP	21316	AATCAGACTCGGGTGGTTCCG	35639	AACCAAACAAGAGTCGTCCCA
6994	NQYPRDP	21317	AATCAGTATCCGAGGGATCCT	35640	AACCAATACCCAAGAGACCCA
6995	NRAESLL	21318	AATCGTGCTGAGTCGCTGCTG	35641	AACAGAGCAGAAAGCCTCCTC
6996	NRAPPLS	21319	AATCGGGCTCCTCCTCTGTCG	35642	AACAGAGCACCACCACTCAGC
6997	NRDIAGR	21320	AATCGGGATATTGCGGGTAGG	35643	AACAGAGACATCGCAGGAAGA
6998	NRDILSS	21321	AATCGGGATATTTTGAGTTCG	35644	AACAGAGACATCCTCAGCAGC
6999	NRDVPES	21322	AATCGTGATGTTCCGGAGTCG	35645	AACAGAGACGTCCCAGAAAGC
7000	NRDYSTA	21323	AATCGTGATTATAGTACGGCT	35646	AACAGAGACTACAGCACAGCA
7001	NRDYSVD	21324	AATCGTGATTATAGTGTTGAT	35647	AACAGAGACTACAGCGTCGAC
7002	NRDYTSP	21325	AATCGTGATTATACTTCTCCT	35648	AACAGAGACTACACAAGCCCA
7003	NREPGLN	21326	AATCGTGAGCCGGGGCTTAAT	35649	AACAGAGAACCAGGACTCAAC
7004	NRERAMT	21327	AATCGGGAGCGGGCGATGACT	35650	AACAGAGAAAGAGCAATGACA
7005	NRESYSL	21328	AATAGGGAGAGTTATTCTCTG	35651	AACAGAGAAAGCTACAGCCTC
7006	NRFPHVD	21329	AATCGTTTTCCTCATGTTGAT	35652	AACAGATTCCCACACGTCGAC
7007	NRGHLDS	21330	AATCGTGGTCATTTGGATTCT	35653	AACAGAGGACACCTCGACAGC
7008	NRGLVAA	21331	AATCGGGGTCTGGTTGCTGCG	35654	AACAGAGGACTCGTCGCAGCA
7009	NRGNFDR	21332	AATCGTGGTAATTTTGATCGT	35655	AACAGAGGAAACTTCGACAGA

7010	NRGPSNT	21333	AATCGTGGTCCTTCTAATACG	35656	AACAGAGGACCAAGCAACACA
7011	NRGQTAQ	21334	AATAGGGGGCAGACTGCGCAG	35657	AACAGAGGACAAACAGCACAA
7012	NRGTLLS	21335	AATCGTGGGACGCTTCTGTCT	35658	AACAGAGGAACACTCCTCAGC
7013	NRIAAEA	21336	AATCGGATTGCTGCGGAGGCT	35659	AACAGAATCGCAGCAGAAGCA
7014	NRIMPIS	21337	AATCGGATTATGCCGATTTCT	35660	AACAGAATCATGCCAATCAGC
7015	NRISAQH	21338	AATAGGATTTCGGCGCAGCAT	35661	AACAGAATCAGCGCACAACAC
7016	NRISSFP	21339	AATAGGATTTCGTCGTTTCCG	35662	AACAGAATCAGCAGCTTCCCA
7017	NRKALSE	21340	AATCGTAAGGCTCTTTCTGAG	35663	AACAGAAAAGCACTCAGCGAA
7018	NRKPTMD	21341	AATCGTAAGCCTACGATGGAT	35664	AACAGAAAACCAACAATGGAC
7019	NRLLGYG	21342	AATCGTTTGCTTGGGTATGGT	35665	AACAGACTCCTCGGATACGGA
7020	NRMPSAA	21343	AATCGTATGCCTTCGGCGGCT	35666	AACAGAATGCCAAGCGCAGCA
7021	NRMSGSD	21344	AATAGGATGTCGGGGTCGGAT	35667	AACAGAATGAGCGGAAGCGAC
7022	NRNLDNG	21345	AATCGTAATTTGGATAATGGT	35668	AACAGAAACCTCGACAACGGA
7023	NRPMELL	21346	AATCGTCCTATGGAGCTGCTG	35669	AACAGACCAATGGAACTCCTC
7024	NRPQHAV	21347	AATCGGCCGCAGCATGCGGTT	35670	AACAGACCACAACACGCAGTC
7025	NRQDVPS	21348	AATCGTCAGGATGTGCCGAGT	35671	AACAGACAAGACGTCCCAAGC
7026	NRQGNEL	21349	AATCGGCAGGGTAATGAGCTT	35672	AACAGACAAGGAAACGAACTC
7027	NRQPLMT	21350	AATAGGCAGCCTTTGATGACT	35673	AACAGACAACCACTCATGACA
7028	NRQPPRE	21351	AATCGTCAGCCTCCGCGGGAG	35674	AACAGACAACCACCAAGAGAA
7029	NRQSLPL	21352	AATAGGCAGTCGCTGCCGCTG	35675	AACAGACAAAGCCTCCCACTC
7030	NRQTIAL	21353	AATCGTCAGACTATTGCGTTG	35676	AACAGACAAACAATCGCACTC
7031	NRRTNED	21354	AATAGGAGGACTAATGAGGAT	35677	AACAGAAGAACAAACGAAGAC
7032	NRSAECW	21355	AATAGGTCTGCTGAGTGTTGG	35678	AACAGAAGCGCAGAATGCTGG
7033	NRSALTP	21356	AATCGTAGTGCGCTGACGCCT	35679	AACAGAAGCGCACTCACACCA
7034	NRSARDP	21357	AATAGGTCGGCGCGTGATCCG	35680	AACAGAAGCGCAAGAGACCCA
7035	NRSEMVE	21358	AATCGTTCGGAGATGGTGGAG	35681	AACAGAAGCGAAATGGTCGAA
7036	NRSGLVS	21359	AATCGTTCGGGTTTGGTTTCG	35682	AACAGAAGCGGACTCGTCAGC
7037	NRSITHD	21360	AATAGGTCGATTACGCATGAT	35683	AACAGAAGCATCACACACGAC
7038	NRSLATV	21361	AATAGGAGTTTGGCGACGGTG	35684	AACAGAAGCCTCGCAACAGTC
7039	NRSVLSD	21362	AATCGTTCTGTGCTTTCGGAT	35685	AACAGAAGCGTCCTCAGCGAC
7040	NRSYDSP	21363	AATCGGAGTTATGATTCTCCG	35686	AACAGAAGCTACGACAGCCCA
7041	NRTLDMS	21364	AATAGGACGTTGGATATGAGT	35687	AACAGAACACTCGACATGAGC
7042	NRTLPTS	21365	AATCGTACGCTGCCGACTTCT	35688	AACAGAACACTCCCAACAAGC
7043	NRTLYPA	21366	AATCGTACTCTTTATCCTGCG	35689	AACAGAACACTCTACCCAGCA
7044	NRTQQSS	21367	AATCGTACGCAGCAGAGTAGT	35690	AACAGAACACAACAAAGCAGC
7045	NRTQSIS	21368	AATCGTACTCAGTCTATTAGT	35691	AACAGAACACAAAGCATCAGC
7046	NRTTLMS	21369	AATCGTACTACGCTTATGAGT	35692	AACAGAACAACACTCATGAGC
7047	NRVGETR	21370	AATCGGGTGGGTGAGACGCGT	35693	AACAGAGTCGGAGAAACAAGA
7048	NRVGIAP	21371	AATAGGGTTGGGATTGCTCCT	35694	AACAGAGTCGGAATCGCACCA
7049	NRVVFEG	21372	AATCGTGTTGTGTTTGAGGGG	35695	AACAGAGTCGTCTTCGAAGGA
7050	NRYDASD	21373	AATCGTTATGATGCGTCTGAT	35696	AACAGATACGACGCAAGCGAC
7051	NSAARIH	21374	AATTCGGCGGCTCGGATTCAT	35697	AACAGCGCAGCAAGAATCCAC
7052	NSADSSP	21375	AATTCTGCGGATTCTAGTCCG	35698	AACAGCGCAGACAGCAGCCCA
7053	NSAMHGT	21376	AATAGTGCGATGCATGGTACT	35699	AACAGCGCAATGCACGGAACA
7054	NSASEFV	21377	AATAGTGCGTCTGAGTTTGTG	35700	AACAGCGCAAGCGAATTCGTC

7055	NSASEMT	21378	AATAGTGCTTCGGAGATGACG	35701	AACAGCGCAAGCGAAATGACA
7056	NSASTFQ	21379	AATTCTGCTTCGACGTTTCAG	35702	AACAGCGCAAGCACATTCCAA
7057	NSASTFT	21380	AATTCTGCTAGTACTTTTACG	35703	AACAGCGCAAGCACATTCACA
7058	NSAVMTR	21381	AATTCTGCTGTGATGACTCGT	35704	AACAGCGCAGTCATGACAAGA
7059	NSAYPVH	21382	AATTCTGCTTATCCGGTGCAT	35705	AACAGCGCATACCCAGTCCAC
7060	NSDFSLA	21383	AATAGTGATTTTTCGCTTGCT	35706	AACAGCGACTTCAGCCTCGCA
7061	NSDLHKP	21384	AATAGTGATCTTCATAAGCCG	35707	AACAGCGACCTCCACAAACCA
7062	NSDSRTP	21385	AATTCTGATTCTCGTACGCCT	35708	AACAGCGACAGCAGAACACCA
7063	NSDSSIR	21386	AATTCGGATTCTTCTATTCGT	35709	AACAGCGACAGCAGCATCAGA
7064	NSGLELL	21387	AATTCGGGTCTGGAGCTGCTT	35710	AACAGCGGACTCGAACTCCTC
7065	NSGNSTP	21388	AATTCTGGGAATTCGACTCCT	35711	AACAGCGGAAACAGCACACCA
7066	NSGRAHI	21389	AATAGTGGTCGGGCTCATATT	35712	AACAGCGGAAGAGCACACATC
7067	NSHAHHD	21390	AATTCGCATGCGCATCATGAT	35713	AACAGCCACGCACACCACGAC
7068	NSHNLTL	21391	AATTCTCATAATTTGACGCTT	35714	AACAGCCACAACCTCACACTC
7069	NSHPQTR	21392	AATTCGCATCCGCAGACGAGG	35715	AACAGCCACCCACAAACAAGA
7070	NSHSSPA	21393	AATTCTCATAGTTCTCCGGCT	35716	AACAGCCACAGCAGCCCAGCA
7071	NSHSVST	21394	AATTCGCATTCTGTGAGTACG	35717	AACAGCCACAGCGTCAGCACA
7072	NSIPERF	21395	AATTCGATTCCGGAGCGGTTT	35718	AACAGCATCCCAGAAAGATTC
7073	NSIRLSG	21396	AATAGTATTAGGTTGTCGGGG	35719	AACAGCATCAGACTCAGCGGA
7074	NSKMPRA	21397	AATAGTAAGATGCCTCGTGCG	35720	AACAGCAAAATGCCAAGAGCA
7075	NSKYTPM	21398	AATTCGAAGTATACGCCTATG	35721	AACAGCAAATACACACCAATG
7076	NSLAARN	21399	AATTCGTTGGCTGCGAGGAAT	35722	AACAGCCTCGCAGCAAGAAAC
7077	NSLARKE	21400	AATTCTCTGGCTCGGAAGGAG	35723	AACAGCCTCGCAAGAAAAGAA
7078	NSLNDRA	21401	AATTCGCTGAATGATCGGGCT	35724	AACAGCCTCAACGACAGAGCA
7079	NSLNPGL	21402	AATTCTTTGAATCCTGGTTTG	35725	AACAGCCTCAACCCAGGACTC
7080	NSLPDSV	21403	AATAGTCTTCCGGATTCTGTG	35726	AACAGCCTCCCAGACAGCGTC
7081	NSLPMAS	21404	AATAGTCTTCCGATGGCTTCG	35727	AACAGCCTCCCAATGGCAAGC
7082	NSMQYSA	21405	AATTCGATGCAGTATAGTGCG	35728	AACAGCATGCAATACAGCGCA
7083	NSNAASG	21406	AATTCGAATGCGGCGAGTGGG	35729	AACAGCAACGCAGCAAGCGGA
7084	NSNHERY	21407	AATTCTAATCATGAGCGGTAT	35730	AACAGCAACCACGAAAGATAC
7085	NSNTPGM	21408	AATTCGAATACTCCTGGGATG	35731	AACAGCAACACACCAGGAATG
7086	NSNVSPG	21409	AATTCGAATGTTAGTCCTGGT	35732	AACAGCAACGTCAGCCCAGGA
7087	NSPIFVG	21410	AATTCGCCGATTTTTGTGGGG	35733	AACAGCCCAATCTTCGTCGGA
7088	NSPNERT	21411	AATTCTCCTAATGAGCGTACG	35734	AACAGCCCAAACGAAAGAACA
7089	NSPNQLG	21412	AATAGTCCTAATCAGCTGGGT	35735	AACAGCCCAAACCAACTCGGA
7090	NSPRHVA	21413	AATTCGCCTAGGCATGTGGCG	35736	AACAGCCCAAGACACGTCGCA
7091	NSPSHSP	21414	AATAGTCCGTCGCATTCGCCG	35737	AACAGCCCAAGCCACAGCCCA
7092	NSPTVQL	21415	AATAGTCCGACGGTTCAGCTG	35738	AACAGCCCAACAGTCCAACTC
7093	NSPVVSR	21416	AATAGTCCTGTTGTTAGTCGG	35739	AACAGCCCAGTCGTCAGCAGA
7094	NSQHSTT	21417	AATTCGCAGCATTCTACGACT	35740	AACAGCCAACACAGCACAACA
7095	NSQLQSS	21418	AATAGTCAGTTGCAGTCGTCG	35741	AACAGCCAACTCCAAAGCAGC
7096	NSQRYLS	21419	AATAGTCAGCGTTATTTGAGT	35742	AACAGCCAAAGATACCTCAGC
7097	NSQSATP	21420	AATAGTCAGTCTGCTACTCCG	35743	AACAGCCAAAGCGCAACACCA
7098	NSRAVLV	21421	AATAGTCGTGCTGTGCTGGTT	35744	AACAGCAGAGCAGTCCTCGTC
7099	NSRDLLT	21422	AATTCTCGTGATTTGCTGACT	35745	AACAGCAGAGACCTCCTCACA

7100	NSRGASL	21423	AATAGTCGTGGTGCTTCGTTG	35746	AACAGCAGAGGAGCAAGCCTC
7101	NSRGLGH	21424	AATTCGCGGGGTTTGGGGCAT	35747	AACAGCAGAGGACTCGGACAC
7102	NSRGMPD	21425	AATAGTAGGGGGATGCCTGAT	35748	AACAGCAGAGGAATGCCAGAC
7103	NSRGPVA	21426	AATTCGCGTGGGCCGGTTGCG	35749	AACAGCAGAGGACCAGTCGCA
7104	NSRLVTS	21427	AATAGTCGGCTGGTTACTTCG	35750	AACAGCAGACTCGTCACAAGC
7105	NSRSNES	21428	AATTCGCGTTCTAATGAGAGT	35751	AACAGCAGAAGCAACGAAAGC
7106	NSRSTPN	21429	AATAGTCGGTCGACTCCGAAT	35752	AACAGCAGAAGCACACCAAAC
7107	NSRTAHE	21430	AATTCTAGGACTGCGCATGAG	35753	AACAGCAGAACAGCACACGAA
7108	NSRTVQI	21431	AATTCTCGGACTGTGCAGATT	35754	AACAGCAGAACAGTCCAAATC
7109	NSRVVGF	21432	AATTCTCGTGTTGTGGGTTTT	35755	AACAGCAGAGTCGTCGGATTC
7110	NSSEWPD	21433	AATTCTAGTGAGTGGCCTGAT	35756	AACAGCAGCGAATGGCCAGAC
7111	NSSGKTP	21434	AATTCGAGTGGTAAGACTCCG	35757	AACAGCAGCGGAAAAACACCA
7112	NSSIRNA	21435	AATAGTAGTATTCGTAATGCT	35758	AACAGCAGCATCAGAAACGCA
7113	NSSLKLN	21436	AATAGTTCGCTTAAGCTGAAT	35759	AACAGCAGCCTCAAACTCAAC
7114	NSSMRIN	21437	AATTCTTCGATGCGTATTAAT	35760	AACAGCAGCATGAGAATCAAC
7115	NSSMSSG	21438	AATAGTTCGATGTCTTCGGGT	35761	AACAGCAGCATGAGCAGCGGA
7116	NSSPSLA	21439	AATAGTTCTCCGTCGCTGGCT	35762	AACAGCAGCCCAAGCCTCGCA
7117	NSSQVHL	21440	AATAGTTCTCAGGTTCATTTG	35763	AACAGCAGCCAAGTCCACCTC
7118	NSSSTPI	21441	AATAGTTCGTCGACTCCTATT	35764	AACAGCAGCAGCACACCAATC
7119	NSTKLLD	21442	AATTCTACTAAGCTGCTGGAT	35765	AACAGCACAAAACTCCTCGAC
7120	NSTLEGR	21443	AATTCGACGCTGGAGGGTAGG	35766	AACAGCACACTCGAAGGAAGA
7121	NSTLTVH	21444	AATTCTACTTTGACTGTGCAT	35767	AACAGCACACTCACAGTCCAC
7122	NSTNFRT	21445	AATTCGACGAATTTTCGTACT	35768	AACAGCACAAACTTCAGAACA
7123	NSTPQPQ	21446	AATAGTACTCCTCAGCCTCAG	35769	AACAGCACACCACAACCACAA
7124	NSTSTYG	21447	AATTCTACGTCGACTTATGGT	35770	AACAGCACAAGCACATACGGA
7125	NSVKGVV	21448	AATTCTGTGAAGGGTGTGGTG	35771	AACAGCGTCAAAGGAGTCGTC
7126	NSVRHNS	21449	AATTCGGTTCGTCATAATTCG	35772	AACAGCGTCAGACACAACAGC
7127	NSVSGVT	21450	AATTCGGTGTCTGGTGTTACG	35773	AACAGCGTCAGCGGAGTCACA
7128	NSVSQMY	21451	AATTCGGTTTCGCAGATGTAT	35774	AACAGCGTCAGCCAAATGTAC
7129	NSVYDRS	21452	AATAGTGTGTATGATCGTTCT	35775	AACAGCGTCTACGACAGAAGC
7130	NSYQVSR	21453	AATTCGTATCAGGTGAGTCGT	35776	AACAGCTACCAAGTCAGCAGA
7131	NTAGKPS	21454	AATACGGCGGGGAAGCCTAGT	35777	AACACAGCAGGAAAACCAAGC
7132	NTARERS	21455	AATACGGCGAGGGAGCGTTCG	35778	AACACAGCAAGAGAAAGAAGC
7133	NTARTSL	21456	AATACTGCGAGGACGTCTTTG	35779	AACACAGCAAGAACAAGCCTC
7134	NTDGDRL	21457	AATACGGATGGGGATAGGCTG	35780	AACACAGACGGAGACAGACTC
7135	NTEDVHM	21458	AATACTGAGGATGTTCATATG	35781	AACACAGAAGACGTCCACATG
7136	NTEHNRS	21459	AATACGGAGCATAATAGGAGT	35782	AACACAGAACACAACAGAAGC
7137	NTETPLA	21460	AATACTGAGACTCCGTTGGCT	35783	AACACAGAAACACCACTCGCA
7138	NTFSNSS	21461	AATACGTTTAGTAATTCGTCT	35784	AACACATTCAGCAACAGCAGC
7139	NTGPGMA	21462	AATACGGGTCCTGGTATGGCT	35785	AACACAGGACCAGGAATGGCA
7140	NTHGAAQ	21463	AATACGCATGGTGCGGCTCAG	35786	AACACACACGGAGCAGCACAA
7141	NTHPTPF	21464	AATACTCATCCGACTCCGTTT	35787	AACACACACCCAACACCATTC
7142	NTHTKMS	21465	AATACGCATACTAAGATGTCG	35788	AACACACACACAAAAATGAGC
7143	NTHVEDW	21466	AATACTCATGTTGAGGATTGG	35789	AACACACACGTCGAAGACTGG
7144	NTIPNVK	21467	AATACGATTCCTAATGTGAAG	35790	AACACAATCCCAAACGTCAAA

7145	NTIRDSI	21468	AATACTATTCGTGATTCTATT	35791	AACACAATCAGAGACAGCATC
7146	NTISGSR	21469	AATACTATTTCGGGGAGTCGT	35792	AACACAATCAGCGGAAGCAGA
7147	NTKLTNN	21470	AATACGAAGCTGACGAATAAT	35793	AACACAAAACTCACAAACAAC
7148	NTKNNNL	21471	AATACTAAGAATAATAATCTT	35794	AACACAAAAAACAACAACCTC
7149	NTKSDPA	21472	AATACTAAGTCGGATCCTGCT	35795	AACACAAAAAGCGACCCAGCA
7150	NTKSPFS	21473	AATACTAAGAGTCCTTTTTCT	35796	AACACAAAAAGCCCATTCAGC
7151	NTLGETL	21474	AATACTTTGGGGGAGACGTTG	35797	AACACACTCGGAGAAACACTC
7152	NTLKLSQ	21475	AATACTCTGAAGCTGAGTCAG	35798	AACACACTCAAACTCAGCCAA
7153	NTLQSYP	21476	AATACTTTGCAGTCTTATCCT	35799	AACACACTCCAAAGCTACCCA
7154	NTNIPRS	21477	AATACGAATATTCCGAGGTCT	35800	AACACAAACATCCCAAGAAGC
7155	NTNVESR	21478	AATACTAATGTTGAGAGTCGT	35801	AACACAAACGTCGAAAGCAGA
7156	NTNVSVS	21479	AATACGAATGTTTCGGTTAGT	35802	AACACAAACGTCAGCGTCAGC
7157	NTPRVLS	21480	AATACTCCTCGGGTGCTGTCG	35803	AACACACCAAGAGTCCTCAGC
7158	NTPSTRQ	21481	AATACTCCGTCTACTCGGCAG	35804	AACACACCAAGCACAAGACAA
7159	NTRGGSS	21482	AATACGCGTGGGGGTTCTTCT	35805	AACACAAGAGGAGGAAGCAGC
7160	NTRHDVS	21483	AATACTCGTCATGATGTTTCT	35806	AACACAAGACACGACGTCAGC
7161	NTRNDPP	21484	AATACGCGGAATGATCCGCCG	35807	AACACAAGAAACGACCCACCA
7162	NTRQLVS	21485	AATACTCGTCAGTTGGTGTCG	35808	AACACAAGACAACTCGTCAGC
7163	NTRRTDG	21486	AATACGCGGCGTACTGATGGT	35809	AACACAAGAAGAACAGACGGA
7164	NTRTLSN	21487	AATACGCGGACGTTGTCGAAT	35810	AACACAAGAACACTCAGCAAC
7165	NTRTYSS	21488	AATACTCGGACGTATTCTAGT	35811	AACACAAGAACATACAGCAGC
7166	NTSDNAR	21489	AATACGTCTGATAATGCGCGT	35812	AACACAAGCGACAACGCAAGA
7167	NTSFSSS	21490	AATACGTCTTTTAGTAGTTCG	35813	AACACAAGCTTCAGCAGCAGC
7168	NTSKDLP	21491	AATACGAGTAAGGATCTGCCG	35814	AACACAAGCAAAGACCTCCCA
7169	NTSQFAS	21492	AATACGAGTCAGTTTGCTTCT	35815	AACACAAGCCAATTCGCAAGC
7170	NTSSSDK	21493	AATACGTCGAGTTCTGATAAG	35816	AACACAAGCAGCAGCGACAAA
7171	NTSVMMV	21494	AATACTTCTGTTATGATGGTG	35817	AACACAAGCGTCATGATGGTC
7172	NTSVRVV	21495	AATACTTCGGTGAGGGTGGTG	35818	AACACAAGCGTCAGAGTCGTC
7173	NTSWNGS	21496	AATACTTCTTGGAATGGGTCT	35819	AACACAAGCTGGAACGGAAGC
7174	NTTNSQL	21497	AATACGACGAATTCTCAGTTG	35820	AACACAACAAACAGCCAACTC
7175	NTTPITN	21498	AATACGACGCCGATTACGAAT	35821	AACACAACACCAATCACAAAC
7176	NTTVLPK	21499	AATACTACTGTTCTGCCTAAG	35822	AACACAACAGTCCTCCCAAAA
7177	NTVPIKA	21500	AATACTGTTCCTATTAAGGCT	35823	AACACAGTCCCAATCAAAGCA
7178	NTYRRDG	21501	AATACTTATAGGAGGGATGGT	35824	AACACATACAGAAGAGACGGA
7179	NVAARAH	21502	AATGTGGCGGCTCGTGCGCAT	35825	AACGTCGCAGCAAGAGCACAC
7180	NVAINFS	21503	AATGTTGCTATTAATTTTTCG	35826	AACGTCGCAATCAACTTCAGC
7181	NVARNFV	21504	AATGTTGCGCGTAATTTTGTG	35827	AACGTCGCAAGAAACTTCGTC
7182	NVAVGYQ	21505	AATGTTGCTGTTGGGTATCAG	35828	AACGTCGCAGTCGGATACCAA
7183	NVAVVLS	21506	AATGTTGCGGTGGTGTTGTCT	35829	AACGTCGCAGTCGTCCTCAGC
7184	NVAWVIE	21507	AATGTTGCGTGGGTGACGGAG	35830	AACGTCGCATGGGTCACAGAA
7185	NVDANVL	21508	AATGTGGATGCGAATGTTCTG	35831	AACGTCGACGCAAACGTCCTC
7186	NVDTSTD	21509	AATGTTGATACTTCGACGGAT	35832	AACGTCGACACAAGCACAGAC
7187	NVEQPSC	21510	AATGTTGAGCAGCCTTCGTGT	35833	AACGTCGAACAACCAAGCTGC
7188	NVESNPL	21511	AATGTGGAGTCGAATCCTTTG	35834	AACGTCGAAAGCAACCCACTC
7189	NVFAVCE	21512	AATGTTTTTGCGGTGTGTGAG	35835	AACGTCTTCGCAGTCTGCGAA

7190	NVFSATP	21513	AATGTTTTTAGTGCTACGCCT	35836	AACGTCTTCAGCGCAACACCA
7191	NVFVAVN	21514	AATGTGTTTGTTGCGGTTAAT	35837	AACGTCTTCGTCGCAGTCAAC
7192	NVGATEV	21515	AATGTGGGGGCGACGGAGGTG	35838	AACGTCGGAGCAACAGAAGTC
7193	NVHALES	21516	AATGTGCATGCTCTGGAGTCT	35839	AACGTCCACGCACTCGAAAGC
7194	NVHTPSQ	21517	AATGTGCATACGCCTTCGCAG	35840	AACGTCCACACACCAAGCCAA
7195	NVINTPQ	21518	AATGTTATTAATACGCCTCAG	35841	AACGTCATCAACACACCACAA
7196	NVKLNSF	21519	AATGTGAAGCTTAATTCGTTT	35842	AACGTCAAACTCAACAGCTTC
7197	NVLGAQQ	21520	AATGTGCTGGGGGCGCAGCAG	35843	AACGTCCTCGGAGCACAACAA
7198	NVLIKYS	21521	AATGTGCTGATTAAGTATAGT	35844	AACGTCCTCATCAAATACAGC
7199	NVLRPQV	21522	AATGTTTTGCGTCCGCAGGTG	35845	AACGTCCTCAGACCACAAGTC
7200	NVMMARM	21523	AATGTTATGATGGCTAGGATG	35846	AACGTCATGATGGCAAGAATG
7201	NVMVRLP	21524	AATGTGATGGTGCGGCTGCCT	35847	AACGTCATGGTCAGACTCCCA
7202	NVMVRMG	21525	AATGTTATGGTGAGGATGGGT	35848	AACGTCATGGTCAGAATGGGA
7203	NVNQPDT	21526	AATGTTAATCAGCCGGATACT	35849	AACGTCAACCAACCAGACACA
7204	NVNQYSG	21527	AATGTGAATCAGTATTCGGGT	35850	AACGTCAACCAATACAGCGGA
7205	NVPAASY	21528	AATGTGCCGGCGGCTTCTTAT	35851	AACGTCCCAGCAGCAAGCTAC
7206	NVPAATF	21529	AATGTTCCGGCGGCGACGTTT	35852	AACGTCCCAGCAGCAACATTC
7207	NVPESSD	21530	AATGTTCCTGAGTCGTCGGAT	35853	AACGTCCCAGAAAGCAGCGAC
7208	NVPSTKE	21531	AATGTTCCGTCGACGAAGGAG	35854	AACGTCCCAAGCACAAAAGAA
7209	NVQATGY	21532	AATGTTCAGGCGACGGGTTAT	35855	AACGTCCAAGCAACAGGATAC
7210	NVQFSSG	21533	AATGTGCAGTTTAGTTCTGGT	35856	AACGTCCAATTCAGCAGCGGA
7211	NVRLQAI	21534	AATGTGCGGCTTCAGGCGATT	35857	AACGTCAGACTCCAAGCAATC
7212	NVRLSID	21535	AATGTGCGGCTGTCTATTGAT	35858	AACGTCAGACTCAGCATCGAC
7213	NVRPQST	21536	AATGTGCGGCCGCAGTCGACG	35859	AACGTCAGACCACAAAGCACA
7214	NVRPVLS	21537	AATGTTCGGCCTGTGCTTTCT	35860	AACGTCAGACCAGTCCTCAGC
7215	NVRQQSA	21538	AATGTGAGGCAGCAGTCTGCT	35861	AACGTCAGACAACAAAGCGCA
7216	NVRSVTN	21539	AATGTGCGTTCGGTTACTAAT	35862	AACGTCAGAAGCGTCACAAAC
7217	NVRSYAA	21540	AATGTGCGGTCTTATGCTGCG	35863	AACGTCAGAAGCTACGCAGCA
7218	NVRTVAE	21541	AATGTGAGGACGGTTGCTGAG	35864	AACGTCAGAACAGTCGCAGAA
7219	NVSFPSL	21542	AATGTTTCGTTTCCTAGTCTG	35865	AACGTCAGCTTCCCAAGCCTC
7220	NVSNVPS	21543	AATGTTTCGAATGTTCCTTCT	35866	AACGTCAGCAACGTCCCAAGC
7221	NVSPLFL	21544	AATGTGAGTCCGCTTTTTCTG	35867	AACGTCAGCCCACTCTTCCTC
7222	NVSRTTL	21545	AATGTTTCTAGGACTACGCTG	35868	AACGTCAGCAGAACAACACTC
7223	NVSRTVS	21546	AATGTGAGTCGTACGGTTTCT	35869	AACGTCAGCAGAACAGTCAGC
7224	NVSSAPK	21547	AATGTTTCTTCGGCTCCGAAG	35870	AACGTCAGCAGCGCACCAAAA
7225	NVSTALS	21548	AATGTTTCGACTGCTCTGAGT	35871	AACGTCAGCACAGCACTCAGC
7226	NVTAIGL	21549	AATGTGACGGCTATTGGTCTG	35872	AACGTCACAGCAATCGGACTC
7227	NVTPPDN	21550	AATGTTACTCCTCCTGATAAT	35873	AACGTCACACCACCAGACAAC
7228	NVTTSEA	21551	AATGTTACGACGTCTGAGGCT	35874	AACGTCACAACAAGCGAAGCA
7229	NVVPPLT	21552	AATGTGGTGCCTCCTCTTACT	35875	AACGTCGTCCCACCACTCACA
7230	NVVSRSP	21553	AATGTGGTGAGTAGGTCTCCG	35876	AACGTCGTCAGCAGAAGCCCA
7231	NVVTKPM	21554	AATGTTGTTACTAAGCCGATG	35877	AACGTCGTCACAAAACCAATG
7232	NVVVPVG	21555	AATGTTGTGGTTCCTGTTGGT	35878	AACGTCGTCGTCCCAGTCGGA
7233	NWASDHV	21556	AATTGGGCTTCTGATCATGTG	35879	AACTGGGCAAGCGACCACGTC
7234	NWGQEKL	21557	AATTGGGGGCAGGAGAAGTTG	35880	AACTGGGGACAAGAAAAACTC

7235	NWPDPES	21558	AATTGGCCTGATCCTGAGTCT	35881	AACTGGCCAGACCCAGAAAGC
7236	NWTAATP	21559	AATTGGACTGCGGCGACTCCT	35882	AACTGGACAGCAGCAACACCA
7237	NYAGSDG	21560	AATTATGCTGGTTCTGATGGT	35883	AACTACGCAGGAAGCGACGGA
7238	NYAKVHT	21561	AATTATGCGAAGGTTCATACG	35884	AACTACGCAAAAGTCCACACA
7239	NYASQIV	21562	AATTATGCGTCGCAGATTGTT	35885	AACTACGCAAGCCAAATCGTC
7240	NYDREQM	21563	AATTATGATCGTGAGCAGATG	35886	AACTACGACAGAGAACAAATG
7241	NYEPTSD	21564	AATTATGAGCCTACTTCTGAT	35887	AACTACGAACCAACAAGCGAC
7242	NYGNSIP	21565	AATTATGGGAATAGTATTCCG	35888	AACTACGGAAACAGCATCCCA
7243	NYHTSLV	21566	AATTATCATACTTCTCTTGTG	35889	AACTACCACACAAGCCTCGTC
7244	NYNTPNP	21567	AATTATAATACTCCGAATCCT	35890	AACTACAACACACCAAACCCA
7245	NYPDTPN	21568	AATTATCCTGATACTCCTAAT	35891	AACTACCCAGACACACCAAAC
7246	NYPDVRS	21569	AATTATCCGGATGTTCGTAGT	35892	AACTACCCAGACGTCAGAAGC
7247	NYPPSRL	21570	AATTATCCTCCTAGTCGGCTG	35893	AACTACCCACCAAGCAGACTC
7248	NYRQTLS	21571	AATTATCGTCAGACGCTTTCG	35894	AACTACAGACAAACACTCAGC
7249	PAADRNL	21572	CCTGCGGCTGATCGGAATCTG	35895	CCAGCAGCAGACAGAAACCTC
7250	PAAEFAS	21573	CCTGCGGCTGAGTTTGCGTCG	35896	CCAGCAGCAGAATTCGCAAGC
7251	PAARERL	21574	CCTGCTGCTCGGGAGCGGCTG	35897	CCAGCAGCAAGAGAAAGACTC
7252	PADLGSM	21575	CCGGCGGATTTGGGGTCTATG	35898	CCAGCAGACCTCGGAAGCATG
7253	PADNGPW	21576	CCTGCTGATAATGGTCCGTGG	35899	CCAGCAGACAACGGACCATGG
7254	PADPPSV	21577	CCGGCTGATCCTCCTAGTGTG	35900	CCAGCAGACCCACCAAGCGTC
7255	PADRSPT	21578	CCTGCTGATAGGTCTCCGACT	35901	CCAGCAGACAGAAGCCCAACA
7256	PADYQKD	21579	CCGGCGGATTATCAGAAGGAT	35902	CCAGCAGACTACCAAAAAGAC
7257	PAEKVRT	21580	CCGGCTGAGAAGGTTCGTACT	35903	CCAGCAGAAAAAGTCAGAACA
7258	PAFSGRD	21581	CCTGCGTTTTCTGGGCGGGAT	35904	CCAGCATTCAGCGGAAGAGAC
7259	PAFSMSI	21582	CCTGCTTTTTCTATGTCTATT	35905	CCAGCATTCAGCATGAGCATC
7260	PAGLPDR	21583	CCGGCTGGGCTTCCTGATCGT	35906	CCAGCAGGACTCCCAGACAGA
7261	PAGSQPP	21584	CCTGCGGGGTCTCAGCCTCCG	35907	CCAGCAGGAAGCCAACCACCA
7262	PAGSTMP	21585	CCTGCTGGGAGTACGATGCCT	35908	CCAGCAGGAAGCACAATGCCA
7263	PAHALTM	21586	CCGGCTCATGCTCTGACTATG	35909	CCAGCACACGCACTCACAATG
7264	PAHFTTG	21587	CCGGCGCATTTTACTACTGGG	35910	CCAGCACACTTCACAACAGGA
7265	PAIGVHR	21588	CCTGCGATTGGGGTTCATAGG	35911	CCAGCAATCGGAGTCCACAGA
7266	PAIKSQL	21589	CCTGCTATTAAGTCTCAGCTT	35912	CCAGCAATCAAAAGCCAACTC
7267	PAILRTS	21590	CCTGCTATTCTGCGTACTTCT	35913	CCAGCAATCCTCAGAACAAGC
7268	PAISGTI	21591	CCGGCTATTTCGGGGACGATT	35914	CCAGCAATCAGCGGAACAATC
7269	PAKPIDF	21592	CCTGCTAAGCCGATTGATTTT	35915	CCAGCAAAACCAATCGACTTC
7270	PALAPIY	21593	CCTGCTTTGGCGCCGATTTAT	35916	CCAGCACTCGCACCAATCTAC
7271	PALMAPA	21594	CCTGCGCTGATGGCGCCGGCT	35917	CCAGCACTCATGGCACCAGCA
7272	PAMGQSD	21595	CCTGCGATGGGTCAGTCTGAT	35918	CCAGCAATGGGACAAAGCGAC
7273	PAMSDRS	21596	CCTGCGATGTCTGATCGGTCG	35919	CCAGCAATGAGCGACAGAAGC
7274	PAMSNTI	21597	CCGGCTATGAGTAATACTATT	35920	CCAGCAATGAGCAACACAATC
7275	PANDADR	21598	CCGGCGAATGATGCGGATCGT	35921	CCAGCAAACGACGCAGACAGA
7276	PANLTSP	21599	CCTGCTAATTTGACGTCTCCG	35922	CCAGCAAACCTCACAAGCCCA
7277	PANPPDS	21600	CCTGCGAATCCTCCTGATTCT	35923	CCAGCAAACCCACCAGACAGC
7278	PANPPKS	21601	CCGGCTAATCCTCCGAAGTCG	35924	CCAGCAAACCCACCAAAAAGC
7279	PANRVGT	21602	CCTGCGAATCGTGTGGGGACG	35925	CCAGCAAACAGAGTCGGAACA

7280	PANYLSV	21603	CCGGCGAATTATTTGTCTGTT	35926	CCAGCAAACTACCTCAGCGTC
7281	PAPMNFQ	21604	CCGGCGCCGATGAATTTTCAG	35927	CCAGCACCAATGAACTTCCAA
7282	PAPSHQS	21605	CCTGCTCCTAGTCATCAGTCG	35928	CCAGCACCAAGCCACCAAAGC
7283	PAPTSIA	21606	CCTGCTCCGACTAGTATTGCG	35929	CCAGCACCAACAAGCATCGCA
7284	PAQRTMA	21607	CCTGCTCAGAGGACGATGGCG	35930	CCAGCACAAAGAACAATGGCA
7285	PAQSTGP	21608	CCGGCGCAGTCGACTGGTCCT	35931	CCAGCACAAAGCACAGGACCA
7286	PARADPA	21609	CCTGCTCGGGCGGATCCGGCG	35932	CCAGCAAGAGCAGACCCAGCA
7287	PARAFDA	21610	CCGGCGCGTGCGTTTGATGCG	35933	CCAGCAAGAGCATTCGACGCA
7288	PARITGM	21611	CCTGCTCGGATTACTGGGATG	35934	CCAGCAAGAATCACAGGAATG
7289	PARLATN	21612	CCTGCTCGTCTTGCTACTAAT	35935	CCAGCAAGACTCGCAACAAAC
7290	PARRPDD	21613	CCTGCGCGGCGGCCTGATGAT	35936	CCAGCAAGAAGACCAGACGAC
7291	PARTLIH	21614	CCTGCGCGTACGCTTATTCAT	35937	CCAGCAAGAACACTCATCCAC
7292	PARTNPT	21615	CCGGCGAGGACTAATCCTACG	35938	CCAGCAAGAACAAACCCAACA
7293	PARTQVD	21616	CCGGCGCGTACGCAGGTGGAT	35939	CCAGCAAGAACACAAGTCGAC
7294	PASERSL	21617	CCGGCTTCGGAGCGGTCGCTT	35940	CCAGCAAGCGAAAGAAGCCTC
7295	PASFGIN	21618	CCTGCGAGTTTTGGGATTAAT	35941	CCAGCAAGCTTCGGAATCAAC
7296	PASHMNP	21619	CCTGCTTCGCATATGAATCCG	35942	CCAGCAAGCCACATGAACCCA
7297	PASPLHS	21620	CCTGCGAGTCCTTTGCATTCT	35943	CCAGCAAGCCCACTCCACAGC
7298	PASPVTS	21621	CCGGCGAGTCCTGTTACGTCT	35944	CCAGCAAGCCCAGTCACAAGC
7299	PASVMAG	21622	CCGGCTAGTGTTATGGCGGGG	35945	CCAGCAAGCGTCATGGCAGGA
7300	PATALSR	21623	CCGGCTACTGCGTTGAGTCGT	35946	CCAGCAACAGCACTCAGCAGA
7301	PATGLPY	21624	CCTGCGACGGGGCTGCCGTAT	35947	CCAGCAACAGGACTCCCATAC
7302	PATMIRH	21625	CCGGCGACGATGATTCGGCAT	35948	CCAGCAACAATGATCAGACAC
7303	PATNVRG	21626	CCTGCGACTAATGTGCGGGGT	35949	CCAGCAACAAACGTCAGAGGA
7304	PATPSVV	21627	CCGGCTACTCCGAGTGTTGTG	35950	CCAGCAACACCAAGCGTCGTC
7305	PATSSVS	21628	CCTGCGACGTCGTCGGTGTCG	35951	CCAGCAACAAGCAGCGTCAGC
7306	PAVEADG	21629	CCGGCTGTGGAGGCGGATGGT	35952	CCAGCAGTCGAAGCAGACGGA
7307	PAVKPSF	21630	CCTGCTGTTAAGCCGAGTTTT	35953	CCAGCAGTCAAACCAAGCTTC
7308	PAYPHAP	21631	CCTGCTTATCCTCATGCTCCG	35954	CCAGCATACCCACACGCACCA
7309	PDAEIRR	21632	CCTGATGCGGAGATTCGGCGT	35955	CCAGACGCAGAAATCAGAAGA
7310	PDDFRHH	21633	CCTGATGATTTTCGGCATCAT	35956	CCAGACGACTTCAGACACCAC
7311	PDELKVR	21634	CCTGATGAGCTTAAGGTTAGG	35957	CCAGACGAACTCAAAGTCAGA
7312	PDGDTAL	21635	CCGGATGGTGATACTGCGCTG	35958	CCAGACGGAGACACAGCACTC
7313	PDGSSRH	21636	CCGGATGGGTCTTCGAGGCAT	35959	CCAGACGGAAGCAGCAGACAC
7314	PDHASIS	21637	CCTGATCATGCGTCTATTAGT	35960	CCAGACCACGCAAGCATCAGC
7315	PDHGGIA	21638	CCTGATCATGGGGGTATTGCT	35961	CCAGACCACGGAGGAATCGCA
7316	PDHRSPN	21639	CCGGATCATCGTAGTCCTAAT	35962	CCAGACCACAGAAGCCCAAAC
7317	PDHSNDQ	21640	CCGGATCATTCTAATGATCAG	35963	CCAGACCACAGCAACGACCAA
7318	PDIAFAE	21641	CCGGATATTGCTTTTGCGGAG	35964	CCAGACATCGCATTCGCAGAA
7319	PDLEVVK	21642	CCGGATTTGGAGGTGGTTAAG	35965	CCAGACCTCGAAGTCGTCAAA
7320	PDLISDA	21643	CCGGATCTGATTTCTGATGCG	35966	CCAGACCTCATCAGCGACGCA
7321	PDLPGIR	21644	CCGGATCTTCCTGGGATTAGG	35967	CCAGACCTCCCAGGAATCAGA
7322	PDNLQVS	21645	CCTGATAATCTTCAGGTGAGT	35968	CCAGACAACCTCCAAGTCAGC
7323	PDNVRTF	21646	CCTGATAATGTTAGGACTTTT	35969	CCAGACAACGTCAGAACATTC
7324	PDNVYND	21647	CCTGATAATGTGTATAATGAT	35970	CCAGACAACGTCTACAACGAC

7325	PDPAYLH	21648	CCTGATCCGGCTTATTTGCAT	35971	CCAGACCCAGCATACCTCCAC
7326	PDPIDRP	21649	CCGGATCCGATTGATCGGCCT	35972	CCAGACCCAATCGACAGACCA
7327	PDPPTSP	21650	CCTGATCCTCCTACTTCGCCG	35973	CCAGACCCACCAACAAGCCCA
7328	PDQASGR	21651	CCTGATCAGGCTTCGGGGCGG	35974	CCAGACCAAGCAAGCGGAAGA
7329	PDQMVRI	21652	CCGGATCAGATGGTGCGGATT	35975	CCAGACCAAATGGTCAGAATC
7330	PDQRGNH	21653	CCGGATCAGAGGGGTAATCAT	35976	CCAGACCAAAGAGGAAACCAC
7331	PDQSLTG	21654	CCGGATCAGAGTTTGACTGGT	35977	CCAGACCAAAGCCTCACAGGA
7332	PDRLLDR	21655	CCGGATCGGCTGCTTGATAGG	35978	CCAGACAGACTCCTCGACAGA
7333	PDRLSEF	21656	CCGGATAGGCTTTCTGAGTTT	35979	CCAGACAGACTCAGCGAATTC
7334	PDRMQNR	21657	CCTGATAGGATGCAGAATCGT	35980	CCAGACAGAATGCAAAACAGA
7335	PDRQQQL	21658	CCTGATCGGCAGCAGCAGTTG	35981	CCAGACAGACAACAACAACTC
7336	PDRVPTV	21659	CCGGATCGTGTTCCGACGGTT	35982	CCAGACAGAGTCCCAACAGTC
7337	PDSAPLP	21660	CCGGATTCTGCTCCTCTTCCT	35983	CCAGACAGCGCACCACTCCCA
7338	PDSDPPH	21661	CCGGATTCGGATCCGCCGCAT	35984	CCAGACAGCGACCCACCACAC
7339	PDSMYRS	21662	CCTGATTCTATGTATCGGTCT	35985	CCAGACAGCATGTACAGAAGC
7340	PDSTLQF	21663	CCTGATTCTACTCTTCAGTTT	35986	CCAGACAGCACACTCCAATTC
7341	PDTDPPL	21664	CCGGATACTGATCCGCCTCTT	35987	CCAGACACAGACCCACCACTC
7342	PDTKWCH	21665	CCTGATACTAAGTGGTGTCAT	35988	CCAGACACAAAATGGTGCCAC
7343	PDTSHDL	21666	CCTGATACTTCGCATGATTTG	35989	CCAGACACAAGCCACGACCTC
7344	PDVKAGR	21667	CCGGATGTGAAGGCTGGTAGG	35990	CCAGACGTCAAAGCAGGAAGA
7345	PDYAKLS	21668	CCGGATTATGCGAAGTTGTCG	35991	CCAGACTACGCAAAACTCAGC
7346	PDYEKKQ	21669	CCGGATTATGAGAAGAAGCAG	35992	CCAGACTACGAAAAAAAACAA
7347	PDYSAVL	21670	CCTGATTATTCGGCGGTTCTG	35993	CCAGACTACAGCGCAGTCCTC
7348	PEAEDDI	21671	CCTGAGGCTGAGGATGATATT	35994	CCAGAAGCAGAAGACGACATC
7349	PEALRTG	21672	CCTGAGGCGTTGCGGACGGGG	35995	CCAGAAGCACTCAGAACAGGA
7350	PEEPRLS	21673	CCGGAGGAGCCTCGTCTTTCT	35996	CCAGAAGAACCAAGACTCAGC
7351	PEEVCRI	21674	CCTGAGGAGGTGTGTCGGATT	35997	CCAGAAGAAGTCTGCAGAATC
7352	PEFAIDA	21675	CCGGAGTTTGCGATTGATGCG	35998	CCAGAATTCGCAATCGACGCA
7353	PEFKTRN	21676	CCTGAGTTTAAGACTCGTAAT	35999	CCAGAATTCAAAACAAGAAAC
7354	PEGRLHA	21677	CCGGAGGGTAGGTTGCATGCG	36000	CCAGAAGGAAGACTCCACGCA
7355	PEKDTHR	21678	CCTGAGAAGGATACTCATCGT	36001	CCAGAAAAAGACACACACAGA
7356	PEKYSQN	21679	CCGGAGAAGTATTCGCAGAAT	36002	CCAGAAAAATACAGCCAAAAC
7357	PEMGRLG	21680	CCGGAGATGGGGAGGCTGGGT	36003	CCAGAAATGGGAAGACTCGGA
7358	PEMKPGQ	21681	CCTGAGATGAAGCCGGGTCAG	36004	CCAGAAATGAAACCAGGACAA
7359	PENSKVD	21682	CCTGAGAATTCGAAGGTGGAT	36005	CCAGAAAACAGCAAAGTCGAC
7360	PENSQRG	21683	CCGGAGAATTCTCAGCGTGGT	36006	CCAGAAAACAGCCAAAGAGGA
7361	PENTTYA	21684	CCGGAGAATACGACGTATGCT	36007	CCAGAAAACACAACATACGCA
7362	PEPSNTR	21685	CCTGAGCCGTCGAATACGCGT	36008	CCAGAACCAAGCAACACAAGA
7363	PEPTLNL	21686	CCTGAGCCTACGCTTAATCTG	36009	CCAGAACCAACACTCAACCTC
7364	PERGLHV	21687	CCGGAGCGGGGGTTGCATGTG	36010	CCAGAAAGAGGACTCCACGTC
7365	PERKAHT	21688	CCTGAGCGGAAGGCGCATACT	36011	CCAGAAAGAAAAGCACACACA
7366	PERPALS	21689	CCTGAGAGGCCGGCTTTGAGT	36012	CCAGAAAGACCAGCACTCAGC
7367	PERSQAG	21690	CCGGAGCGGTCTCAGGCGGGG	36013	CCAGAAAGAAGCCAAGCAGGA
7368	PERSTWV	21691	CCTGAGCGGTCGACTTGGGTT	36014	CCAGAAAGAAGCACATGGGTC
7369	PESKDAH	21692	CCTGAGTCTAAGGATGCGCAT	36015	CCAGAAAGCAAAGACGCACAC

7370	PESPRTL	21693	CCGGAGTCTCCTCGTACGCTG	36016	CCAGAAAGCCCAAGAACACTC
7371	PESVLRR	21694	CCTGAGTCTGTTCTGCGTCGG	36017	CCAGAAAGCGTCCTCAGAAGA
7372	PESWPSP	21695	CCGGAGTCTTGGCCGAGTCCG	36018	CCAGAAAGCTGGCCAAGCCCA
7373	PETSPRP	21696	CCTGAGACTTCTCCTCGTCCT	36019	CCAGAAACAAGCCCAAGACCA
7374	PFAEAGI	21697	CCGTTTGCTGAGGCTGGTATT	36020	CCATTCGCAGAAGCAGGAATC
7375	PFAGHAL	21698	CCTTTTGCTGGGCATGCGCTT	36021	CCATTCGCAGGACACGCACTC
7376	PFAQTLT	21699	CCTTTTGCGCAGACTCTTACG	36022	CCATTCGCACAAACACTCACA
7377	PFASSTS	21700	CCTTTTGCTTCGAGTACGTCT	36023	CCATTCGCAAGCAGCACAAGC
7378	PFDHLTD	21701	CCGTTTGATCATTTGACGGAT	36024	CCATTCGACCACCTCACAGAC
7379	PFGVSVD	21702	CCGTTTGGTGTTTCGGTGGAT	36025	CCATTCGGAGTCAGCGTCGAC
7380	PFPHDRP	21703	CCTTTTCCGCATGATAGGCCT	36026	CCATTCCCACACGACAGACCA
7381	PFQTGSG	21704	CCTTTTCAGACTGGTTCTGGG	36027	CCATTCCAAACAGGAAGCGGA
7382	PFRIQTD	21705	CCGTTTCGGATTCAGACTGAT	36028	CCATTCAGAATCCAAACAGAC
7383	PFRPVVD	21706	CCGTTTCGGCCTGTTGTTGAT	36029	CCATTCAGACCAGTCGTCGAC
7384	PFSDLRM	21707	CCGTTTAGTGATCTTAGGATG	36030	CCATTCAGCGACCTCAGAATG
7385	PFSGLTG	21708	CCGTTTTCGGGTCTGACTGGT	36031	CCATTCAGCGGACTCACAGGA
7386	PFSNIQM	21709	CCTTTTTCGAATATTCAGATG	36032	CCATTCAGCAACATCCAAATG
7387	PFSSAVI	21710	CCTTTTTCGTCGGCGGTTATT	36033	CCATTCAGCAGCGCAGTCATC
7388	PFSSPSP	21711	CCTTTTAGTAGTCCTTCTCCG	36034	CCATTCAGCAGCCCAAGCCCA
7389	PFSTPDM	21712	CCTTTTTCTACTCCTGATATG	36035	CCATTCAGCACACCAGACATG
7390	PFTAGFS	21713	CCGTTTACTGCTGGTTTTTCG	36036	CCATTCACAGCAGGATTCAGC
7391	PFTATDR	21714	CCTTTTACGGCTACTGATCGT	36037	CCATTCACAGCAACAGACAGA
7392	PFTDELM	21715	CCGTTTACTGATGAGTTGATG	36038	CCATTCACAGACGAACTCATG
7393	PFTGAPQ	21716	CCTTTTACGGGGGCGCCGCAG	36039	CCATTCACAGGAGCACCACAA
7394	PGARREL	21717	CCTGGTGCTAGGCGGGAGCTT	36040	CCAGGAGCAAGAAGAGAACTC
7395	PGAVPPS	21718	CCTGGGGCTGTGCCGCCTTCT	36041	CCAGGAGCAGTCCCACCAAGC
7396	PGCSSVV	21719	CCTGGTTGTTCGTCTGTTGTT	36042	CCAGGATGCAGCAGCGTCGTC
7397	PGDAKPR	21720	CCGGGTGATGCGAAGCCTCGT	36043	CCAGGAGACGCAAAACCAAGA
7398	PGDPTHD	21721	CCTGGTGATCCGACTCATGAT	36044	CCAGGAGACCCAACACACGAC
7399	PGEATKL	21722	CCTGGTGAGGCTACTAAGCTG	36045	CCAGGAGAAGCAACAAAACTC
7400	PGEKLWC	21723	CCTGGGGAGAAGCTTTGGTGT	36046	CCAGGAGAAAAACTCTGGTGC
7401	PGETQEV	21724	CCTGGGGAGACGCAGGAGGTG	36047	CCAGGAGAAACACAAGAAGTC
7402	PGFDPSG	21725	CCGGGTTTTGATCCGTCTGGG	36048	CCAGGATTCGACCCAAGCGGA
7403	PGGSDHS	21726	CCGGGTGGTTCGGATCATTCT	36049	CCAGGAGGAAGCGACCACAGC
7404	PGGSLGE	21727	CCTGGTGGGTCGCTGGGGGAG	36050	CCAGGAGGAAGCCTCGGAGAA
7405	PGHDVAR	21728	CCTGGGCATGATGTGGCTCGT	36051	CCAGGACACGACGTCGCAAGA
7406	PGHMPAS	21729	CCGGGGCATATGCCTGCTAGT	36052	CCAGGACACATGCCAGCAAGC
7407	PGIDARI	21730	CCTGGGATTGATGCTCGTATT	36053	CCAGGAATCGACGCAAGAATC
7408	PGIDRKS	21731	CCTGGGATTGATCGTAAGTCG	36054	CCAGGAATCGACAGAAAAAGC
7409	PGIQAPI	21732	CCGGGTATTCAGGCTCCGATT	36055	CCAGGAATCCAAGCACCAATC
7410	PGKIHAA	21733	CCGGGGAAGATTCATGCGGCT	36056	CCAGGAAAAATCCACGCAGCA
7411	PGKLLNP	21734	CCGGGGAAGCTTTTGAATCCG	36057	CCAGGAAAACTCCTCAACCCA
7412	PGKSLEA	21735	CCTGGGAAGTCTCTTGAGGCG	36058	CCAGGAAAAAGCCTCGAAGCA
7413	PGKYSPS	21736	CCTGGGAAGTATAGTCCTTCG	36059	CCAGGAAAATACAGCCCAAGC
7414	PGLADYG	21737	CCTGGTCTTGCTGATTATGGT	36060	CCAGGACTCGCAGACTACGGA

7415	PGLLDHV	21738	CCGGGGCTTCTGGATCATGTG	36061	CCAGGACTCCTCGACCACGTC
7416	PGLQSMK	21739	CCTGGGTTGCAGTCGATGAAG	36062	CCAGGACTCCAAAGCATGAAA
7417	PGLRSDS	21740	CCTGGGCTGCGGTCGGATTCT	36063	CCAGGACTCAGAAGCGACAGC
7418	PGLTANP	21741	CCTGGTCTGACTGCTAATCCG	36064	CCAGGACTCACAGCAAACCCA
7419	PGLTKAI	21742	CCTGGTCTGACGAAGGCTATT	36065	CCAGGACTCACAAAAGCAATC
7420	PGMRMGQ	21743	CCTGGGATGAGGATGGGTCAG	36066	CCAGGAATGAGAATGGGACAA
7421	PGNHVTR	21744	CCGGGTAATCATGTTACGCGG	36067	CCAGGAAACCACGTCACAAGA
7422	PGNYEYR	21745	CCGGGTAATTATGAGTATCGG	36068	CCAGGAAACTACGAATACAGA
7423	PGPGQPR	21746	CCGGGGCCGGGGCAGCCGCGT	36069	CCAGGACCAGGACAACCAAGA
7424	PGPMNSS	21747	CCGGGGCCTATGAATTCGAGT	36070	CCAGGACCAATGAACAGCAGC
7425	PGPRRDI	21748	CCTGGTCCGCGGAGGGATATT	36071	CCAGGACCAAGAAGAGACATC
7426	PGPTGAY	21749	CCTGGGCCTACGGGTGCGTAT	36072	CCAGGACCAACAGGAGCATAC
7427	PGQETSY	21750	CCTGGGCAGGAGACTTCGTAT	36073	CCAGGACAAGAAACAAGCTAC
7428	PGQQKNM	21751	CCGGGTCAGCAGAAGAATATG	36074	CCAGGACAACAAAAAAACATG
7429	PGQRGTP	21752	CCGGGTCAGCGGGGTACTCCT	36075	CCAGGACAAAGAGGAACACCA
7430	PGQTQHN	21753	CCGGGGCAGACGCAGCATAAT	36076	CCAGGACAAACACAACACAAC
7431	PGRDAEG	21754	CCTGGGAGGGATGCGGAGGGT	36077	CCAGGAAGAGACGCAGAAGGA
7432	PGREGVT	21755	CCGGGGAGGGAGGGGGTGACT	36078	CCAGGAAGAGAAGGAGTCACA
7433	PGRPQPS	21756	CCTGGTCGTCCGCAGCCTTCT	36079	CCAGGAAGACCACAACCAAGC
7434	PGRVGPL	21757	CCTGGGAGGGTGGGGCCGTTG	36080	CCAGGAAGAGTCGGACCACTC
7435	PGSFPRG	21758	CCGGGGAGTTTTCCGAGGGGG	36081	CCAGGAAGCTTCCCAAGAGGA
7436	PGSNSGH	21759	CCTGGTAGTAATTCTGGGCAT	36082	CCAGGAAGCAACAGCGGACAC
7437	PGSQAVH	21760	CCTGGGTCGCAGGCTGTTCAT	36083	CCAGGAAGCCAAGCAGTCCAC
7438	PGSQRNS	21761	CCTGGTTCGCAGCGTAATAGT	36084	CCAGGAAGCCAAAGAAACAGC
7439	PGSRAPG	21762	CCTGGGTCGCGGGCTCCGGGT	36085	CCAGGAAGCAGAGCACCAGGA
7440	PGTARTN	21763	CCGGGTACTGCTCCGGACTAAT	36086	CCAGGAACAGCAAGAACAAAC
7441	PGTGRYV	21764	CCGGGTACGGGTAGGTATGTT	36087	CCAGGAACAGGAAGATACGTC
7442	PGTPLQS	21765	CCTGGGACTCCTCTGCAGTCG	36088	CCAGGAACACCACTCCAAAGC
7443	PGTSSTG	21766	CCGGGGACTAGTTCGACGGGG	36089	CCAGGAACAAGCAGCACAGGA
7444	PGVNPAI	21767	CCTGGTGTTAATCCTGCGATT	36090	CCAGGAGTCAACCCAGCAATC
7445	PGVRGSP	21768	CCGGGGGTTAGGGGTTCTCCG	36091	CCAGGAGTCAGAGGAAGCCCA
7446	PGVTDRG	21769	CCTGGGGTGACTGATCGGGGT	36092	CCAGGAGTCACAGACAGAGGA
7447	PGYPAVT	21770	CCGGGTTATCCTGCGGTGACG	36093	CCAGGATACCCAGCAGTCACA
7448	PHANSSL	21771	CCGCATGCTAATAGTTCGTTG	36094	CCACACGCAAACAGCAGCCTC
7449	PHDSPTP	21772	CCTCATGATTCTCCGACTCCT	36095	CCACACGACAGCCCAACACCA
7450	PHGVGDA	21773	CCGCATGGGGTTGGTGATGCG	36096	CCACACGGAGTCGGAGACGCA
7451	PHHDDEN	21774	CCTCATCATGATGATGAGAAT	36097	CCACACCACGACGACGAAAAC
7452	PHLECGM	21775	CCTCATCTTGAGTGTGGTATG	36098	CCACACCTCGAATGCGGAATG
7453	PHLGVST	21776	CCGCATTTGGGTGTGTCGACG	36099	CCACACCTCGGAGTCAGCACA
7454	PHLHNGL	21777	CCTCATTTGCATAATGGTCTG	36100	CCACACCTCCACAACGGACTC
7455	PHLKIAA	21778	CCGCATTTGAAGATTGCTGCG	36101	CCACACCTCAAAATCGCAGCA
7456	PHLPDHA	21779	CCGCATTTGCCTGATCATGCG	36102	CCACACCTCCCAGACCACGCA
7457	PHLPPAN	21780	CCTCATCTTCCGCCGGCGAAT	36103	CCACACCTCCCACCAGCAAAC
7458	PHLPQNM	21781	CCTCATCTGCCTCAGAATATG	36104	CCACACCTCCCACAAAACATG
7459	PHLSANA	21782	CCTCATCTGTCGGCGAATGCG	36105	CCACACCTCAGCGCAAACGCA

7460	PHMGRAD	21783	CCGCATATGGGGCGTGCTGAT	36106	CCACACATGGGAAGAGCAGAC
7461	PHNSTDT	21784	CCTCATAATAGTACGGATACT	36107	CCACACAACAGCACAGACACA
7462	PHPNSSP	21785	CCTCATCCTAATTCTTCTCCG	36108	CCACACCCAAACAGCAGCCCA
7463	PHPPEQS	21786	CCGCATCCTCCTGAGCAGTCG	36109	CCACACCCACCAGAACAAAGC
7464	PHPPSNR	21787	CCGCATCCTCCTTCTAATCGT	36110	CCACACCCACCAAGCAACAGA
7465	PHPSAQG	21788	CCGCATCCGTCTGCTCAGGGG	36111	CCACACCCAAGCGCACAAGGA
7466	PHPSSIP	21789	CCGCATCCTTCGTCGATTCCG	36112	CCACACCCAAGCAGCATCCCA
7467	PHQSIPP	21790	CCTCATCAGTCTATTCCTCCG	36113	CCACACCAAAGCATCCCACCA
7468	PHREYVV	21791	CCGCATCGGGAGTATGTTGTT	36114	CCACACAGAGAATACGTCGTC
7469	PHRPSNS	21792	CCTCATCGTCCGTCTAATTCT	36115	CCACACAGACCAAGCAACAGC
7470	PHRPTVV	21793	CCGCATCGGCCTACGGTTGTG	36116	CCACACAGACCAACAGTCGTC
7471	PHRVSVS	21794	CCTCATCGTGTGTCGGTTTCG	36117	CCACACAGAGTCAGCGTCAGC
7472	PHSNMNS	21795	CCTCATTCTAATATGAATTCG	36118	CCACACAGCAACATGAACAGC
7473	PHSSKEM	21796	CCGCATTCGTCGAAGGAGATG	36119	CCACACAGCAGCAAAGAAATG
7474	PHSSMLL	21797	CCTCATTCTTCTATGCTTTTG	36120	CCACACAGCAGCATGCTCCTC
7475	PHTGYTD	21798	CCGCATACTGGGTATACGGAT	36121	CCACACACAGGATACACAGAC
7476	PHTLVTR	21799	CCGCATACTTTGGTGACGAGG	36122	CCACACACACTCGTCACAAGA
7477	PHTSPPS	21800	CCTCATACTAGTCCGCCGTCT	36123	CCACACACAAGCCCACCAAGC
7478	PIAREYG	21801	CCTATTGCGCGTGAGTATGGG	36124	CCAATCGCAAGAGAATACGGA
7479	PIARGDF	21802	CCTATTGCGCGGGGTGATTTT	36125	CCAATCGCAAGAGGAGACTTC
7480	PIDREYA	21803	CCGATTGATCGGGAGTATGCG	36126	CCAATCGACAGAGAATACGCA
7481	PIDTGRE	21804	CCGATTGATACTGGTAGGGAG	36127	CCAATCGACACAGGAAGAGAA
7482	PIDYGVE	21805	CCGATTGATTATGGGGTTGAG	36128	CCAATCGACTACGGAGTCGAA
7483	PIEGRRV	21806	CCGATTGAGGGTAGGCGGGTG	36129	CCAATCGAAGGAAGAAGAGTC
7484	PIERTLP	21807	CCTATTGAGCGTACGCTTCCT	36130	CCAATCGAAAGAACACTCCCA
7485	PIGPPNS	21808	CCTATTGGTCCTCCTAATTCG	36131	CCAATCGGACCACCAAACAGC
7486	PIGSMLS	21809	CCGATTGGGTCTATGCTGAGT	36132	CCAATCGGAAGCATGCTCAGC
7487	PIGSNGK	21810	CCGATTGGTAGTAATGGGAAG	36133	CCAATCGGAAGCAACGGAAAA
7488	PIGVQEK	21811	CCTATTGGGGTTCAGGAGAAG	36134	CCAATCGGAGTCCAAGAAAAA
7489	PIHISSV	21812	CCTATTCATATTAGTTCTGTT	36135	CCAATCCACATCAGCAGCGTC
7490	PIHYSQD	21813	CCGATTCATTATTCTCAGGAT	36136	CCAATCCACTACAGCCAAGAC
7491	PIMGQKS	21814	CCTATTATGGGGCAGAAGTCT	36137	CCAATCATGGGACAAAAAAGC
7492	PINDSSS	21815	CCTATTAATGATTCGTCTTCG	36138	CCAATCAACGACAGCAGCAGC
7493	PINMRGP	21816	CCGATTAATATGCGGGGGCCT	36139	CCAATCAACATGAGAGGACCA
7494	PIPDKSS	21817	CCGATTCCTGATAAGAGTTCT	36140	CCAATCCCAGACAAAAGCAGC
7495	PIPGPGK	21818	CCTATTCCGGGTCCGGGTAAG	36141	CCAATCCCAGGACCAGGAAAA
7496	PIPNKGG	21819	CCGATTCCGAATAAGGGTGGT	36142	CCAATCCCAAACAAAGGAGGA
7497	PIQTRTY	21820	CCGATTCAGACGCGTACGTAT	36143	CCAATCCAAACAAGAACATAC
7498	PIRAAAS	21821	CCTATTCGTGCGGCTGCGTCG	36144	CCAATCAGAGCAGCAGCAAGC
7499	PIRAEAV	21822	CCTATTCGGGCGGAGGCTGTG	36145	CCAATCAGAGCAGAAGCAGTC
7500	PISEFNA	21823	CCTATTAGTGAGTTTAATGCG	36146	CCAATCAGCGAATTCAACGCA
7501	PISLSMP	21824	CCGATTTCGTTGTCGATGCCG	36147	CCAATCAGCCTCAGCATGCCA
7502	PISPLSY	21825	CCTATTTCTCCTTTGTCGTAT	36148	CCAATCAGCCCACTCAGCTAC
7503	PISQGRL	21826	CCTATTAGTCAGGGTCGTTTG	36149	CCAATCAGCCAAGGAAGACTC
7504	PISSKSS	21827	CCGATTAGTTCTAAGTCGTCG	36150	CCAATCAGCAGCAAAAGCAGC

7505	PISTLLA	21828	CCGATTAGTACTTTGCTTGCT	36151	CCAATCAGCACACTCCTCGCA
7506	PITNPRI	21829	CCTATTACTAATCCTAGGATT	36152	CCAATCACAAACCCAAGAATC
7507	PITNSNI	21830	CCGATTACGAATAGTAATATT	36153	CCAATCACAAACAGCAACATC
7508	PITNYSS	21831	CCGATTACTAATTATAGTAGT	36154	CCAATCACAAACTACAGCAGC
7509	PITPGNE	21832	CCGATTACTCCGGGGAATGAG	36155	CCAATCACACCAGGAAACGAA
7510	PITTVPA	21833	CCTATTACTACGGTGCCTGCG	36156	CCAATCACAACAGTCCCAGCA
7511	PIVGSHE	21834	CCTATTGTGGGGAGTCATGAG	36157	CCAATCGTCGGAAGCCACGAA
7512	PIVPVSA	21835	CCGATTGTGCCGGTGTCGGCT	36158	CCAATCGTCCCAGTCAGCGCA
7513	PIVTHAL	21836	CCGATTGTTACGCATGCGCTG	36159	CCAATCGTCACACACGCACTC
7514	PIYKGTG	21837	CCGATTTATAAGGGGACGGGT	36160	CCAATCTACAAAGGAACAGGA
7515	PKAAPNF	21838	CCTAAGGCGGCGCCTAATTTT	36161	CCAAAAGCAGCACCAAACTTC
7516	PKAILPS	21839	CCTAAGGCGATTTTGCCTTCT	36162	CCAAAAGCAATCCTCCCAAGC
7517	PKASDWH	21840	CCTAAGGCGTCGGATTGGCAT	36163	CCAAAAGCAAGCGACTGGCAC
7518	PKDDGQN	21841	CCTAAGGATGATGGTCAGAAT	36164	CCAAAAGACGACGGACAAAAC
7519	PKDIREF	21842	CCTAAGGATATTAGGGAGTTT	36165	CCAAAAGACATCAGAGAATTC
7520	PKDRNPV	21843	CCGAAGGATAGGAATCCGGTG	36166	CCAAAAGACAGAAACCCAGTC
7521	PKDSSRT	21844	CCTAAGGATAGTTCGCGGACG	36167	CCAAAAGACAGCAGCAGAACA
7522	PKERTHL	21845	CCGAAGGAGCGGACGCATTTG	36168	CCAAAAGAAAGAACACACCTC
7523	PKFGGVS	21846	CCGAAGTTTGGGGGTGTGAGT	36169	CCAAAATTCGGAGGAGTCAGC
7524	PKGAATM	21847	CCGAAGGGGGCTGCGACGATG	36170	CCAAAAGGAGCAGCAACAATG
7525	PKGETGR	21848	CCTAAGGGGGAGACTGGTCGT	36171	CCAAAAGGAGAAACAGGAAGA
7526	PKGTHFG	21849	CCTAAGGGTACGCATTTTGGG	36172	CCAAAAGGAACACACTTCGGA
7527	PKGYGAS	21850	CCTAAGGGGTATGGTGCGTCT	36173	CCAAAAGGATACGGAGCAAGC
7528	PKISTLG	21851	CCGAAGATTAGTACTCTGGGT	36174	CCAAAAATCAGCACACTCGGA
7529	PKKDPVP	21852	CCGAAGAAGGATCCGGTGCCT	36175	CCAAAAAAAGACCCAGTCCCA
7530	PKLKDVT	21853	CCGAAGCTGAAGGATGTTACT	36176	CCAAAACTCAAAGACGTCACA
7531	PKLSSST	21854	CCGAAGCTTAGTTCTTCTACT	36177	CCAAAACTCAGCAGCAGCACA
7532	PKLYDMM	21855	CCGAAGCTGTATGATATGATG	36178	CCAAAACTCTACGACATGATG
7533	PKMDDKN	21856	CCTAAGATGGATGATAAGAAT	36179	CCAAAAATGGACGACAAAAAC
7534	PKMLVTG	21857	CCTAAGATGCTTGTTACTGGT	36180	CCAAAAATGCTCGTCACAGGA
7535	PKMTGAR	21858	CCGAAGATGACTGGGGCTCGT	36181	CCAAAAATGACAGGAGCAAGA
7536	PKNMVPP	21859	CCGAAGAATATGGTTCCTCCG	36182	CCAAAAAACATGGTCCCACCA
7537	PKPEFAS	21860	CCGAAGCCTGAGTTTGCGTCT	36183	CCAAAACCAGAATTCGCAAGC
7538	PKPEFLA	21861	CCTAAGCCTGAGTTTCTTGCT	36184	CCAAAACCAGAATTCCTCGCA
7539	PKPEPHA	21862	CCGAAGCCGGAGCCGCATGCT	36185	CCAAAACCAGAACCACACGCA
7540	PKPITVT	21863	CCGAAGCCTATTACTGTGACG	36186	CCAAAACCAATCACAGTCACA
7541	PKPPNLL	21864	CCGAAGCCTCCTAATCTGTTG	36187	CCAAAACCACCAAACCTCCTC
7542	PKPPSLG	21865	CCTAAGCCTCCGTCTTTGGGG	36188	CCAAAACCACCAAGCCTCGGA
7543	PKQESYA	21866	CCGAAGCAGGAGTCTTATGCG	36189	CCAAAACAAGAAAGCTACGCA
7544	PKSMDGY	21867	CCGAAGTCGATGGATGGTTAT	36190	CCAAAAAGCATGGACGGATAC
7545	PKSNYYP	21868	CCGAAGTCGAATTATTATCCT	36191	CCAAAAAGCAACTACTACCCA
7546	PKTHVLS	21869	CCTAAGACGCATGTGCTGTCG	36192	CCAAAAACACACGTCCTCAGC
7547	PKTYETV	21870	CCTAAGACTTATGAGACTGTG	36193	CCAAAAACATACGAAACAGTC
7548	PLAAGSV	21871	CCGCTTGCGGCTGGGTCTGTT	36194	CCACTCGCAGCAGGAAGCGTC
7549	PLAGPLT	21872	CCTCTGGCGGGTCCTCTTACT	36195	CCACTCGCAGGACCACTCACA

7550	PLAHTTS	21873	CCTTTGGCTCATACTACTTCG	36196	CCACTCGCACACACAACAAGC
7551	PLAREEL	21874	CCGCTTGCTCGTGAGGAGCTG	36197	CCACTCGCAAGAGAAGAACTC
7552	PLASPIP	21875	CCGCTTGCTTCGCCTATTCCT	36198	CCACTCGCAAGCCCAATCCCA
7553	PLASTYP	21876	CCTCTTGCGAGTACGTATCCG	36199	CCACTCGCAAGCACATACCCA
7554	PLDAKMY	21877	CCTCTTGATGCGAAGATGTAT	36200	CCACTCGACGCAAAAATGTAC
7555	PLDDKPF	21878	CCTCTTGATGATAAGCCTTTT	36201	CCACTCGACGACAAACCATTC
7556	PLDPGIL	21879	CCGCTGGATCCTGGGATTTTG	36202	CCACTCGACCCAGGAATCCTC
7557	PLDSNVV	21880	CCGTTGGATTCTAATGTTGTG	36203	CCACTCGACAGCAACGTCGTC
7558	PLDTRFS	21881	CCTCTGGATACGCGTTTTTCT	36204	CCACTCGACACAAGATTCAGC
7559	PLDYRKG	21882	CCGCTGGATTATCGGAAGGGG	36205	CCACTCGACTACAGAAAAGGA
7560	PLEKSSF	21883	CCTCTGGAGAAGTCGTCTTTT	36206	CCACTCGAAAAAAGCAGCTTC
7561	PLESVDI	21884	CCTTTGGAGAGTGTGGATATT	36207	CCACTCGAAAGCGTCGACATC
7562	PLFNGSA	21885	CCGTTGTTTAATGGGTCTGCG	36208	CCACTCTTCAACGGAAGCGCA
7563	PLGAGKS	21886	CCGTTGGGTGCTGGGAAGAGT	36209	CCACTCGGAGCAGGAAAAAGC
7564	PLGAQHL	21887	CCTTTGGGTGCTCAGCATCTG	36210	CCACTCGGAGCACAACACCTC
7565	PLGDAWG	21888	CCTTTGGGTGATGCGTGGGGG	36211	CCACTCGGAGACGCATGGGGA
7566	PLGMVHT	21889	CCGCTGGGGATGGTGCATACG	36212	CCACTCGGAATGGTCCACACA
7567	PLHMTTM	21890	CCGCTGCATATGACGACTATG	36213	CCACTCCACATGACAACAATG
7568	PLHNRVP	21891	CCGCTGCATAATCGGGTTCCT	36214	CCACTCCACAACAGAGTCCCA
7569	PLHRANT	21892	CCGCTTCATCGGGCTAATACT	36215	CCACTCCACAGAGCAAACACA
7570	PLHRTLD	21893	CCGTTGCATCGGACGCTTGAT	36216	CCACTCCACAGAACACTCGAC
7571	PLIAVPT	21894	CCTCTTATTGCGGTGCCGACT	36217	CCACTCATCGCAGTCCCAACA
7572	PLIGKPN	21895	CCTTTGATTGGTAAGCCGAAT	36218	CCACTCATCGGAAAACCAAAC
7573	PLITPDL	21896	CCTCTTATTACTCCGGATCTT	36219	CCACTCATCACACCAGACCTC
7574	PLKAHMM	21897	CCGCTGAAGGCTCATATGATG	36220	CCACTCAAAGCACACATGATG
7575	PLKASGM	21898	CCGTTGAAGGCGTCGGGTATG	36221	CCACTCAAAGCAAGCGGAATG
7576	PLKLSYG	21899	CCGTTGAAGCTTAGTTATGGG	36222	CCACTCAAACTCAGCTACGGA
7577	PLKVSAS	21900	CCTTTGAAGGTGAGTGCTTCG	36223	CCACTCAAAGTCAGCGCAAGC
7578	PLLDSHS	21901	CCTTTGTTGGATAGTCATAGT	36224	CCACTCCTCGACAGCCACAGC
7579	PLLEHRG	21902	CCTCTGCTTGAGCATCGTGGT	36225	CCACTCCTCGAACACAGAGGA
7580	PLLHDKI	21903	CCGTTGTTGCATGATAAGATT	36226	CCACTCCTCCACGACAAAATC
7581	PLNAAPF	21904	CCGCTTAATGCTGCGCCTTTT	36227	CCACTCAACGCAGCACCATTC
7582	PLNGDAP	21905	CCTCTGAATGGTGATGCGCCT	36228	CCACTCAACGGAGACGCACCA
7583	PLNPSTG	21906	CCGCTGAATCCTAGTACGGGT	36229	CCACTCAACCCAAGCACAGGA
7584	PLNVRTV	21907	CCTCTGAATGTGAGGACTGTT	36230	CCACTCAACGTCAGAACAGTC
7585	PLPDYLV	21908	CCTCTTCCTGATTATCTTGTG	36231	CCACTCCCAGACTACCTCGTC
7586	PLPGNVG	21909	CCTCTGCCTGGTAATGTTGGG	36232	CCACTCCCAGGAAACGTCGGA
7587	PLPLRTG	21910	CCGTTGCCGCTGAGGACGGGG	36233	CCACTCCCACTCAGAACAGGA
7588	PLPPPEA	21911	CCGCTTCCTCCTCCGGAGGCG	36234	CCACTCCCACCACCAGAAGCA
7589	PLPRLAS	21912	CCGCTTCCGAGGCTGGCTTCT	36235	CCACTCCCAAGACTCGCAAGC
7590	PLPSDGH	21913	CCGCTGCCTAGTGATGGGCAT	36236	CCACTCCCAAGCGACGGACAC
7591	PLPVSRS	21914	CCGTTGCCGGTTTCTAGGTCT	36237	CCACTCCCAGTCAGCAGAAGC
7592	PLQSQTV	21915	CCTCTGCAGAGTCAGACTGTT	36238	CCACTCCAAAGCCAAACAGTC
7593	PLQSSQF	21916	CCTCTTCAGTCGTCGCAGTTT	36239	CCACTCCAAAGCAGCCAATTC
7594	PLQTMTL	21917	CCTCTGCAGACGATGACTCTG	36240	CCACTCCAAACAATGACACTC

7595	PLQVRLS	21918	CCTTTGCAGGTGCGGCTGTCG	36241	CCACTCCAAGTCAGACTCAGC
7596	PLRDGLV	21919	CCGCTTAGGGATGGGTTGGTT	36242	CCACTCAGAGACGGACTCGTC
7597	PLRLTSD	21920	CCGCTGAGGTTGACTTCTGAT	36243	CCACTCAGACTCACAAGCGAC
7598	PLRPGQL	21921	CCGCTGCGTCCGGGGCAGTTG	36244	CCACTCAGACCAGGACAACTC
7599	PLRVSTP	21922	CCTTTGCGGGTTTCGACGCCT	36245	CCACTCAGAGTCAGCACACCA
7600	PLSAINS	21923	CCTCTGTCGGCGATTAATTCG	36246	CCACTCAGCGCAATCAACAGC
7601	PLSDAMS	21924	CCGTTGTCTGATGCTATGTCT	36247	CCACTCAGCGACGCAATGAGC
7602	PLSDPNI	21925	CCTTTGTCTGATCCTAATATT	36248	CCACTCAGCGACCCAAACATC
7603	PLSEDKR	21926	CCTTTGTCTGAGGATAAGAGG	36249	CCACTCAGCGAAGACAAAAGA
7604	PLSFTVA	21927	CCTCTTAGTTTTACGGTTGCG	36250	CCACTCAGCTTCACAGTCGCA
7605	PLSMMEP	21928	CCTTTGAGTATGATGGAGCCG	36251	CCACTCAGCATGATGGAACCA
7606	PLSMRPD	21929	CCTCTTTCTATGCGGCCGGAT	36252	CCACTCAGCATGAGACCAGAC
7607	PLSNLQP	21930	CCTCTTTCGAATCTTCAGCCT	36253	CCACTCAGCAACCTCCAACCA
7608	PLSPAGA	21931	CCTCTGTCTCCTGCGGGTGCG	36254	CCACTCAGCCCAGCAGGAGCA
7609	PLSPIRN	21932	CCTTTGTCGCCTATTAGGAAT	36255	CCACTCAGCCCAATCAGAAAC
7610	PLSPTWK	21933	CCTCTGTCTCCGACTTGGAAG	36256	CCACTCAGCCCAACATGGAAA
7611	PLSRNQI	21934	CCTCTTTCTCGTAATCAGATT	36257	CCACTCAGCAGAAACCAAATC
7612	PLSSAAG	21935	CCTCTTTCTTCTGCTGCGGGT	36258	CCACTCAGCAGCGCAGCAGGA
7613	PLSSGGM	21936	CCTCTTAGTTCGGGTGGTATG	36259	CCACTCAGCAGCGGAGGAATG
7614	PLSSPAR	21937	CCTCTGTCTAGTCCGGCTCGG	36260	CCACTCAGCAGCCCAGCAAGA
7615	PLSSPNG	21938	CCGTTGTCGTCTCCGAATGGG	36261	CCACTCAGCAGCCCAAACGGA
7616	PLSSTLG	21939	CCGTTGTCTTCTACGCTTGGG	36262	CCACTCAGCAGCACACTCGGA
7617	PLSTNST	21940	CCTCTGAGTACGAATAGTACG	36263	CCACTCAGCACAAACAGCACA
7618	PLSYQKN	21941	CCGCTTTCGTATCAGAAGAAT	36264	CCACTCAGCTACCAAAAAAAC
7619	PLTAGLA	21942	CCTCTGACGGCGGGTTTGGCG	36265	CCACTCACAGCAGGACTCGCA
7620	PLTAHVS	21943	CCGCTGACTGCTCATGTGAGT	36266	CCACTCACAGCACACGTCAGC
7621	PLTQAVP	21944	CCGTTGACTCAGGCGGTGCCT	36267	CCACTCACACAAGCAGTCCCA
7622	PLTSLKL	21945	CCTCTTACGTCTTTGAAGTTG	36268	CCACTCACAAGCCTCAAACTC
7623	PLTSVAP	21946	CCTCTTACGAGTGTGGCGCCT	36269	CCACTCACAAGCGTCGCACCA
7624	PLTTRNQ	21947	CCTCTGACTACTCGTAATCAG	36270	CCACTCACAACAAGAAACCAA
7625	PLVAIST	21948	CCGTTGGTGGCGATTTCTACG	36271	CCACTCGTCGCAATCAGCACA
7626	PLVLSSH	21949	CCGTTGGTGTTGTCGTCTCAT	36272	CCACTCGTCCTCAGCAGCCAC
7627	PLVRGDS	21950	CCGCTTGTGCGTGGGGATTCG	36273	CCACTCGTCAGAGGAGACAGC
7628	PLVSTGI	21951	CCTTTGGTTAGTACGGGGATT	36274	CCACTCGTCAGCACAGGAATC
7629	PLVTMAS	21952	CCTTTGGTTACGATGGCGAGT	36275	CCACTCGTCACAATGGCAAGC
7630	PMAPPVQ	21953	CCTATGGCTCCTCCTGTTCAG	36276	CCAATGGCACCACCAGTCCAA
7631	PMAQVAP	21954	CCGATGGCGCAGGTGGCTCCG	36277	CCAATGGCACAAGTCGCACCA
7632	PMERTHM	21955	CCGATGGAGCGGACTCATATG	36278	CCAATGGAAAGAACACACATG
7633	PMGHQSA	21956	CCTATGGGTCATCAGTCGGCT	36279	CCAATGGGACACCAAAGCGCA
7634	PMINSSM	21957	CCGATGATTAATTCGTCGATG	36280	CCAATGATCAACAGCAGCATG
7635	PMKASSP	21958	CCTATGAAGGCGTCGAGTCCT	36281	CCAATGAAAGCAAGCAGCCCA
7636	PMKGSVY	21959	CCGATGAAGGGTTCTGTTTAT	36282	CCAATGAAAGGAAGCGTCTAC
7637	PMKMGPG	21960	CCTATGAAGATGGGTCCGGGG	36283	CCAATGAAAATGGGACCAGGA
7638	PMMQTPK	21961	CCTATGATGCAGACTCCGAAG	36284	CCAATGATGCAAACACCAAAA
7639	PMNRGKE	21962	CCGATGAATCGTGGTAAGGAG	36285	CCAATGAACAGAGGAAAAGAA

7640	PMNTNVS	21963	CCTATGAATACTAATGTTTCT	36286	CCAATGAACACAAACGTCAGC
7641	PMPASDF	21964	CCGATGCCGGCGAGTGATTTT	36287	CCAATGCCAGCAAGCGACTTC
7642	PMPEFNG	21965	CCGATGCCTGAGTTTAATGGG	36288	CCAATGCCAGAATTCAACGGA
7643	PMPEMAG	21966	CCTATGCCGGAGATGGCTGGT	36289	CCAATGCCAGAAATGGCAGGA
7644	PMPVRAV	21967	CCTATGCCTGTTCGGGCGGTT	36290	CCAATGCCAGTCAGAGCAGTC
7645	PMRGSTL	21968	CCTATGCGTGGGTCGACTCTT	36291	CCAATGAGAGGAAGCACACTC
7646	PMRNQVD	21969	CCTATGCGGAATCAGGTGGAT	36292	CCAATGAGAAACCAAGTCGAC
7647	PMRQIND	21970	CCGATGCGGCAGATTAATGAT	36293	CCAATGAGACAAATCAACGAC
7648	PMSELTP	21971	CCGATGTCGGAGCTTACTCCT	36294	CCAATGAGCGAACTCACACCA
7649	PMSGPSM	21972	CCTATGAGTGGTCCGTCGATG	36295	CCAATGAGCGGACCAAGCATG
7650	PMSGSNA	21973	CCGATGAGTGGTTCTAATGCG	36296	CCAATGAGCGGAAGCAACGCA
7651	PMSHMAP	21974	CCTATGTCTCATATGGCTCCG	36297	CCAATGAGCCACATGGCACCA
7652	PMSLPLS	21975	CCTATGAGTCTGCCTCTGAGT	36298	CCAATGAGCCTCCCACTCAGC
7653	PMSMKEP	21976	CCTATGTCTATGAAGGAGCCT	36299	CCAATGAGCATGAAAGAACCA
7654	PMSQTPG	21977	CCGATGTCTCAGACGCCTGGG	36300	CCAATGAGCCAAACACCAGGA
7655	PMSQTTS	21978	CCTATGTCGCAGACTACGAGT	36301	CCAATGAGCCAAACAACAAGC
7656	PMSSPLK	21979	CCTATGTCTTCGCCGCTTAAG	36302	CCAATGAGCAGCCCACTCAAA
7657	PMSSRVV	21980	CCGATGTCTTCGCGTGTTGTG	36303	CCAATGAGCAGCAGAGTCGTC
7658	PMSTSTP	21981	CCGATGTCTACTAGTACTCCG	36304	CCAATGAGCACAAGCACACCA
7659	PMVKGTS	21982	CCGATGGTTAAGGGGACGTCT	36305	CCAATGGTCAAAGGAACAAGC
7660	PMVTVRT	21983	CCTATGGTGACGGTTCGGACG	36306	CCAATGGTCACAGTCAGAACA
7661	PNAKTIP	21984	CCGAATGCTAAGACGATTCCT	36307	CCAAACGCAAAAACAATCCCA
7662	PNAQTVY	21985	CCGAATGCTCAGACTGTGTAT	36308	CCAAACGCACAAACAGTCTAC
7663	PNARMLV	21986	CCTAATGCTCGTATGCTGGTT	36309	CCAAACGCAAGAATGCTCGTC
7664	PNDGALP	21987	CCGAATGATGGGGCGCTTCCT	36310	CCAAACGACGGAGCACTCCCA
7665	PNDRAVV	21988	CCTAATGATCGGGCTGTGGTT	36311	CCAAACGACAGAGCAGTCGTC
7666	PNDRTRI	21989	CCTAATGATAGGACTCGTATT	36312	CCAAACGACAGAACAAGAATC
7667	PNEQALG	21990	CCGAATGAGCAGGCTCTTGGT	36313	CCAAACGAACAAGCACTCGGA
7668	PNESLVT	21991	CCGAATGAGTCTCTTGTTACT	36314	CCAAACGAAAGCCTCGTCACA
7669	PNFHRAE	21992	CCTAATTTTCATCGTGCTGAG	36315	CCAAACTTCCACAGAGCAGAA
7670	PNGPYNA	21993	CCGAATGGTCCTTATAATGCT	36316	CCAAACGGACCATACAACGCA
7671	PNGSAKS	21994	CCGAATGGTTCTGCTAAGTCT	36317	CCAAACGGAAGCGCAAAAAGC
7672	PNHDVPP	21995	CCGAATCATGATGTGCCGCCT	36318	CCAAACCACGACGTCCCACCA
7673	PNHKGFG	21996	CCGAATCATAAGGGTTTTGGG	36319	CCAAACCACAAAGGATTCGGA
7674	PNHNSDK	21997	CCGAATCATAATAGTGATAAG	36320	CCAAACCACAACAGCGACAAA
7675	PNHSQLL	21998	CCGAATCATTCTCAGCTTCTG	36321	CCAAACCACAGCCAACTCCTC
7676	PNIKNPS	21999	CCTAATATTAAGAATCCTTCT	36322	CCAAACATCAAAAACCCAAGC
7677	PNIPMRG	22000	CCGAATATTCCTATGCGGGGT	36323	CCAAACATCCCAATGAGAGGA
7678	PNITSTL	22001	CCGAATATTACTTCGACTCTT	36324	CCAAACATCACAAGCACACTC
7679	PNLILGP	22002	CCTAATCTGATTCTGGGTCCG	36325	CCAAACCTCATCCTCGGACCA
7680	PNLQRSP	22003	CCTAATCTGCAGAGGAGTCCT	36326	CCAAACCTCCAAAGAAGCCCA
7681	PNLSDES	22004	CCTAATCTTTCGGATGAGTCT	36327	CCAAACCTCAGCGACGAAAGC
7682	PNLTMAS	22005	CCGAATCTTACTATGGCTTCT	36328	CCAAACCTCACAATGGCAAGC
7683	PNLVTAA	22006	CCTAATCTTGTGACGGCTGCT	36329	CCAAACCTCGTCACAGCAGCA
7684	PNNNVPS	22007	CCTAATAATAATGTTCCTAGT	36330	CCAAACAACAACGTCCCAAGC

7685	PNNRDST	22008	CCTAATAATAGGGATAGTACG	36331	CCAAACAACAGAGACAGCACA
7686	PNNVISE	22009	CCTAATAATGTTATTTCGGAG	36332	CCAAACAACGTCATCAGCGAA
7687	PNNVPLA	22010	CCGAATAATGTTCCGCTTGCG	36333	CCAAACAACGTCCCACTCGCA
7688	PNPAAAA	22011	CCGAATCCGGCTGCTGCGGCT	36334	CCAAACCCAGCAGCAGCAGCA
7689	PNPARLT	22012	CCTAATCCTGCGCGTCTTACT	36335	CCAAACCCAGCAAGACTCACA
7690	PNPIFSS	22013	CCGAATCCGATTTTTAGTAGT	36336	CCAAACCCAATCTTCAGCAGC
7691	PNPTWSS	22014	CCGAATCCTACTTGGTCGTCG	36337	CCAAACCCAACATGGAGCAGC
7692	PNPVTRG	22015	CCGAATCCGGTGACTCGTGGT	36338	CCAAACCCAGTCACAAGAGGA
7693	PNQDTLD	22016	CCTAATCAGGATACTCTTGAT	36339	CCAAACCAAGACACACTCGAC
7694	PNQSVKP	22017	CCTAATCAGTCTGTGAAGCCG	36340	CCAAACCAAAGCGTCAAACCA
7695	PNRGHPS	22018	CCGAATAGGGGTCATCCGTCG	36341	CCAAACAGAGGACACCCAAGC
7696	PNRIAPI	22019	CCTAATAGGATTGCTCCTATT	36342	CCAAACAGAATCGCACCAATC
7697	PNSGVVT	22020	CCTAATTCGGGGGTTGTGACT	36343	CCAAACAGCGGAGTCGTCACA
7698	PNSLNAA	22021	CCGAATTCTCTTAATGCGGCG	36344	CCAAACAGCCTCAACGCAGCA
7699	PNSRTPY	22022	CCGAATAGTCGGACGCCGTAT	36345	CCAAACAGCAGAACACCATAC
7700	PNSSPRL	22023	CCTAATTCTTCGCCGAGGTTG	36346	CCAAACAGCAGCCCAAGACTC
7701	PNSTRVV	22024	CCTAATAGTACGAGGGTGGTT	36347	CCAAACAGCACAAGAGTCGTC
7702	PNTMTRL	22025	CCGAATACTATGACGAGGTTG	36348	CCAAACACAATGACAAGACTC
7703	PNVHPNI	22026	CCGAATGTTCATCCTAATATT	36349	CCAAACGTCCACCCAAACATC
7704	PNVNVST	22027	CCGAATGTGAATGTGTCTACG	36350	CCAAACGTCAACGTCAGCACA
7705	PNVVDMS	22028	CCTAATGTTGTTGATATGTCG	36351	CCAAACGTCGTCGACATGAGC
7706	PPADLRT	22029	CCTCCTGCTGATCTTAGGACG	36352	CCACCAGCAGACCTCAGAACA
7707	PPALSPV	22030	CCGCCGGCTCTTAGTCCGGTG	36353	CCACCAGCACTCAGCCCAGTC
7708	PPANSSS	22031	CCTCCGGCTAATTCGTCGTCT	36354	CCACCAGCAAACAGCAGCAGC
7709	PPDARSS	22032	CCGCCGGATGCTAGGTCTTCT	36355	CCACCAGACGCAAGAAGCAGC
7710	PPDGASR	22033	CCTCCGGATGGGGCGTCTCGG	36356	CCACCAGACGGAGCAAGCAGA
7711	PPDKMHS	22034	CCTCCTGATAAGATGCATTCG	36357	CCACCAGACAAAATGCACAGC
7712	PPDNLHK	22035	CCTCCGGATAATCTGCATAAG	36358	CCACCAGACAACCTCCACAAA
7713	PPEMILG	22036	CCTCCGGAGATGATTTTGGGT	36359	CCACCAGAAATGATCCTCGGA
7714	PPFNKSD	22037	CCTCCGTTTAATAAGTCGGAT	36360	CCACCATTCAACAAAAGCGAC
7715	PPFPERL	22038	CCTCCTTTTCCGGAGAGGCTT	36361	CCACCATTCCCAGAAAGACTC
7716	PPGHDAS	22039	CCTCCTGGGCATGATGCTTCT	36362	CCACCAGGACACGACGCAAGC
7717	PPGITTS	22040	CCGCCTGGTATTACGACGAGT	36363	CCACCAGGAATCACAACAAGC
7718	PPGQSLT	22041	CCGCCTGGGCAGTCTCTTACG	36364	CCACCAGGACAAAGCCTCACA
7719	PPGRVVA	22042	CCTCCGGGTAGGGTGGTTGCG	36365	CCACCAGGAAGAGTCGTCGCA
7720	PPGSHSS	22043	CCTCCTGGTAGTCATAGTTCG	36366	CCACCAGGAAGCCACAGCAGC
7721	PPGSSSR	22044	CCGCCGGGGTCTTCGTCTCGG	36367	CCACCAGGAAGCAGCAGCAGA
7722	PPGYRAS	22045	CCTCCGGGGTATAGGGCTAGT	36368	CCACCAGGATACAGAGCAAGC
7723	PPHQHLL	22046	CCTCCTCATCAGCATCTGCTG	36369	CCACCACACCAACACCTCCTC
7724	PPHRTFP	22047	CCTCCTCATAGGACGTTTCCG	36370	CCACCACACAGAACATTCCCA
7725	PPHTTFL	22048	CCGCCTCATACTACGTTTCTT	36371	CCACCACACACAACATTCCTC
7726	PPIDNRT	22049	CCTCCGATTGATAATCGGACT	36372	CCACCAATCGACAACAGAACA
7727	PPKAMPT	22050	CCGCCTAAGGCGATGCCGACT	36373	CCACCAAAAGCAATGCCAACA
7728	PPLEVKQ	22051	CCGCCTTTGGAGGTTAAGCAG	36374	CCACCACTCGAAGTCAAACAA
7729	PPLHTGE	22052	CCGCCTTTGCATACTGGGGAG	36375	CCACCACTCCACACAGGAGAA

7730	PPLKSPP	22053	CCTCCGCTTAAGTCTCCTCCT	36376	CCACCACTCAAAAGCCCACCA
7731	PPLPSNA	22054	CCGCCTCTTCCTTCGAATGCG	36377	CCACCACTCCCAAGCAACGCA
7732	PPMHGTR	22055	CCTCCTATGCATGGTACTCGT	36378	CCACCAATGCACGGAACAAGA
7733	PPMSPHV	22056	CCTCCTATGTCTCCTCATGTG	36379	CCACCAATGAGCCCACACGTC
7734	PPMVTNN	22057	CCTCCTATGGTTACGAATAAT	36380	CCACCAATGGTCACAAACAAC
7735	PPNNHAG	22058	CCTCCTAATAATCATGCTGGT	36381	CCACCAAACAACCACGCAGGA
7736	PPNYLNA	22059	CCGCCTAATTATCTGAATGCG	36382	CCACCAAACTACCTCAACGCA
7737	PPPAALS	22060	CCTCCGCCTGCGGCTCTTTCT	36383	CCACCACCAGCAGCACTCAGC
7738	PPPKSQS	22061	CCGCCGCCGAAGTCGCAGTCG	36384	CCACCACCAAAAAGCCAAAGC
7739	PPPNNNL	22062	CCTCCTCCTAATAATAATCTT	36385	CCACCACCAAACAACAACCTC
7740	PPPREVH	22063	CCTCCTCCTCGTGAGGTGCAT	36386	CCACCACCAAGAGAAGTCCAC
7741	PPPSCMV	22064	CCGCCGCCTTCTTGTATGGTT	36387	CCACCACCAAGCTGCATGGTC
7742	PPPSRMG	22065	CCGCCTCCGTCTCGGATGGGG	36388	CCACCACCAAGCAGAATGGGA
7743	PPQEMRY	22066	CCTCCGCAGGAGATGAGGTAT	36389	CCACCACAAGAAATGAGATAC
7744	PPQSAAV	22067	CCTCCTCAGAGTGCTGCTGTG	36390	CCACCACAAAGCGCAGCAGTC
7745	PPQSNRN	22068	CCTCCTCAGTCTAATAGGAAT	36391	CCACCACAAAGCAACAGAAAC
7746	PPRISDA	22069	CCGCCTCGGATTAGTGATGCT	36392	CCACCAAGAATCAGCGACGCA
7747	PPRLPSC	22070	CCTCCGCGGCTTCCTAGTTGT	36393	CCACCAAGACTCCCAAGCTGC
7748	PPRLVST	22071	CCGCCTAGGCTTGTTTCTACT	36394	CCACCAAGACTCGTCAGCACA
7749	PPRPNGI	22072	CCGCCTCGGCCTAATGGTATT	36395	CCACCAAGACCAAACGGAATC
7750	PPRRPME	22073	CCGCCTCGGAGGCCGATGGAG	36396	CCACCAAGAAGACCAATGGAA
7751	PPRSNVE	22074	CCTCCTCGTAGTAATGTGGAG	36397	CCACCAAGAAGCAACGTCGAA
7752	PPRTPSS	22075	CCGCCTCGGACGCCGTCTTCG	36398	CCACCAAGAACACCAAGCAGC
7753	PPRVSAV	22076	CCTCCTCGGGTTTCGGCGGTT	36399	CCACCAAGAGTCAGCGCAGTC
7754	PPSPSVT	22077	CCGCCTAGTCCTTCTGTGACG	36400	CCACCAAGCCCAAGCGTCACA
7755	PPSPTYM	22078	CCTCCTAGTCCGACTTATATG	36401	CCACCAAGCCCAACATACATG
7756	PPSTEIS	22079	CCGCCGTCTACTGAGATTTCT	36402	CCACCAAGCACAGAAATCAGC
7757	PPSTKLV	22080	CCTCCGTCTACGAAGCTTGTG	36403	CCACCAAGCACAAAACTCGTC
7758	PPSTNPK	22081	CCTCCTAGTACTAATCCGAAG	36404	CCACCAAGCACAAACCCAAAA
7759	PPSVPRE	22082	CCTCCTTCTGTGCCTAGGGAG	36405	CCACCAAGCGTCCCAAGAGAA
7760	PPTEPRA	22083	CCGCCGACGGAGCCGAGGGCG	36406	CCACCAACAGAACCAAGAGCA
7761	PPTGASF	22084	CCGCCGACGGGGGCGTCTTTT	36407	CCACCAACAGGAGCAAGCTTC
7762	PPTITSS	22085	CCTCCTACGATTACTTCGAGT	36408	CCACCAACAATCACAAGCAGC
7763	PPTKVDM	22086	CCGCCTACTAAGGTTGATATG	36409	CCACCAACAAAAGTCGACATG
7764	PPTLQSD	22087	CCTCCGACTCTTCAGAGTGAT	36410	CCACCAACACTCCAAAGCGAC
7765	PPTNPTV	22088	CCTCCTACTAATCCGACGGTG	36411	CCACCAACAAACCCAACAGTC
7766	PPTPAAH	22089	CCTCCTACGCCTGCTGCGCAT	36412	CCACCAACACCAGCAGCACAC
7767	PPTPVSW	22090	CCGCCTACGCCGGTTAGTTGG	36413	CCACCAACACCAGTCAGCTGG
7768	PPTRESP	22091	CCTCCTACGCGTGAGTCGCCT	36414	CCACCAACAAGAGAAAGCCCA
7769	PPTTNLN	22092	CCGCCTACTACGAATTTGAAT	36415	CCACCAACAACAAACCTCAAC
7770	PPVGTVL	22093	CCGCCTGTGGGTACGGTTTTG	36416	CCACCAGTCGGAACAGTCCTC
7771	PPYGAVT	22094	CCTCCTTATGGTGCGGTTACT	36417	CCACCATACGGAGCAGTCACA
7772	PPYTVSP	22095	CCTCCGTATACTGTGTCGCCG	36418	CCACCATACACAGTCAGCCCA
7773	PQARQPF	22096	CCGCAGGCGAGGCAGCCTTTT	36419	CCACAAGCAAGACAACCATTC
7774	PQEPGFD	22097	CCTCAGGAGCCGGGTTTTGAT	36420	CCACAAGAACCAGGATTCGAC

7775	PQERARS	22098	CCGCAGGAGCGTGCTAGGAGT	36421	CCACAAGAAAGAGCAAGAAGC
7776	PQHPSRN	22099	CCGCAGCATCCGAGTCGGAAT	36422	CCACAACACCCAAGCAGAAAC
7777	PQIHIMA	22100	CCTCAGATTCATATTATGGCT	36423	CCACAAATCCACATCATGGCA
7778	PQILPSA	22101	CCTCAGATTCTTCCTAGTGCT	36424	CCACAAATCCTCCCAAGCGCA
7779	PQLSQNV	22102	CCTCAGCTTAGTCAGAATGTT	36425	CCACAACTCAGCCAAAACGTC
7780	PQNASYR	22103	CCTCAGAATGCTAGTTATCGT	36426	CCACAAAACGCAAGCTACAGA
7781	PQNNPPG	22104	CCGCAGAATAATCCGCCGGGG	36427	CCACAAAACAACCCACCAGGA
7782	PQNRPPV	22105	CCGCAGAATAGGCCTCCTGTG	36428	CCACAAAACAGACCACCAGTC
7783	PQPRNVI	22106	CCGCAGCCTCGTAATGTTATT	36429	CCACAACCAAGAAACGTCATC
7784	PQPTETP	22107	CCGCAGCCTACTGAGACGCCG	36430	CCACAACCAACAGAAACACCA
7785	PQPTYTL	22108	CCGCAGCCGACTTATACGCTG	36431	CCACAACCAACATACACACTC
7786	PQRNAGA	22109	CCTCAGCGTAATGCTGGTGCT	36432	CCACAAAGAAACGCAGGAGCA
7787	PQRQGLL	22110	CCTCAGCGGCAGGGTTTGTTG	36433	CCACAAAGACAAGGACTCCTC
7788	PQRSAMP	22111	CCTCAGAGGAGTGCTATGCCG	36434	CCACAAAGAAGCGCAATGCCA
7789	PQRTQQE	22112	CCGCAGAGGACGCAGCAGGAG	36435	CCACAAAGAACACAACAAGAA
7790	PQRVHAA	22113	CCTCAGAGGGTTCATGCGGCG	36436	CCACAAAGAGTCCACGCAGCA
7791	PQSLHVR	22114	CCTCAGAGTTTGCATGTGAGG	36437	CCACAAAGCCTCCACGTCAGA
7792	PQSPNHS	22115	CCTCAGTCGCCTAATCATTCG	36438	CCACAAAGCCCAAACCACAGC
7793	PQSRDTY	22116	CCGCAGTCGCGTGATACTTAT	36439	CCACAAAGCAGAGACACATAC
7794	PQSRNTN	22117	CCGCAGTCGAGGAATACTAAT	36440	CCACAAAGCAGAAACACAAAC
7795	PQTLTSV	22118	CCGCAGACTCTGACTTCGGTG	36441	CCACAAACACTCACAAGCGTC
7796	PQTRSPS	22119	CCTCAGACGAGGAGTCCGTCG	36442	CCACAAACAAGAAGCCCAAGC
7797	PQTVTKV	22120	CCTCAGACGGTGACTAAGGTG	36443	CCACAAACAGTCACAAAAGTC
7798	PQVRASQ	22121	CCGCAGGTTAGGGCGTCTCAG	36444	CCACAAGTCAGAGCAAGCCAA
7799	PQVRQGP	22122	CCGCAGGTTCGTCAGGGGCCG	36445	CCACAAGTCAGACAAGGACCA
7800	PQVTTSA	22123	CCTCAGGTTACGACGTCGGCT	36446	CCACAAGTCACAACAAGCGCA
7801	PRANSGM	22124	CCTCGGGCGAATTCTGGTATG	36447	CCAAGAGCAAACAGCGGAATG
7802	PRANTFS	22125	CCTCGTGCTAATACGTTTTCG	36448	CCAAGAGCAAACACATTCAGC
7803	PRAPAVS	22126	CCTAGGGCTCCGGCTGTGTCT	36449	CCAAGAGCACCAGCAGTCAGC
7804	PRASGPY	22127	CCTCGTGCGTCGGGTCCGTAT	36450	CCAAGAGCAAGCGGACCATAC
7805	PRATTYS	22128	CCTCGTGCTACGACTTATTCT	36451	CCAAGAGCAACAACATACAGC
7806	PRDATRL	22129	CCTCGGGATGCTACTCGGTTG	36452	CCAAGAGACGCAACAAGACTC
7807	PRDKNPA	22130	CCGCGGGATAAGAATCCTGCT	36453	CCAAGAGACAAAAACCCAGCA
7808	PRDRLVI	22131	CCTCGTGATCGGTTGGTGATT	36454	CCAAGAGACAGACTCGTCATC
7809	PRDYQTS	22132	CCTCGTGATTATCAGACTTCG	36455	CCAAGAGACTACCAAACAAGC
7810	PREKAAT	22133	CCTCGTGAGAAGGCTGCGACG	36456	CCAAGAGAAAAAGCAGCAACA
7811	PREPYAE	22134	CCGCGGGAGCCTTATGCTGAG	36457	CCAAGAGAACCATACGCAGAA
7812	PRGEGTN	22135	CCGCGTGGGGAGGGTACGAAT	36458	CCAAGAGGAGAAGGAACAAAC
7813	PRGFETA	22136	CCTAGGGGTTTTGAGACTGCT	36459	CCAAGAGGATTCGAAACAGCA
7814	PRGLSSA	22137	CCTCGTGGGCTTTCTTCTGCT	36460	CCAAGAGGACTCAGCAGCGCA
7815	PRGQIAS	22138	CCGCGGGGTCAGATTGCGAGT	36461	CCAAGAGGACAAATCGCAAGC
7816	PRGSGSS	22139	CCTCGTGGTAGTGGGTCTAGT	36462	CCAAGAGGAAGCGGAAGCAGC
7817	PRGSSDY	22140	CCGCGTGGGTCGTCTGATTAT	36463	CCAAGAGGAAGCAGCGACTAC
7818	PRHTVYA	22141	CCTCGGCATACGGTGTATGCT	36464	CCAAGACACACAGTCTACGCA
7819	PRIEARN	22142	CCTCGGATTGAGGCTCGGAAT	36465	CCAAGAATCGAAGCAAGAAAC

7820	PRIINTI	22143	CCTAGGATTATTAATACTATT	36466	CCAAGAATCATCAACACAATC
7821	PRIPQTH	22144	CCTCGTATTCCTCAGACTCAT	36467	CCAAGAATCCCACAAACACAC
7822	PRKLPGD	22145	CCGCGTAAGTTGCCGGGTGAT	36468	CCAAGAAAACTCCCAGGAGAC
7823	PRKVGLS	22146	CCGCGGAAGGTTGGGCTGTCG	36469	CCAAGAAAAGTCGGACTCAGC
7824	PRLAGGI	22147	CCGAGGTTGGCGGGTGGTATT	36470	CCAAGACTCGCAGGAGGAATC
7825	PRLGGVV	22148	CCGCGTTTGGGTGGTGTGGTT	36471	CCAAGACTCGGAGGAGTCGTC
7826	PRLGLDN	22149	CCTCGGCTTGGGTTGGATAAT	36472	CCAAGACTCGGACTCGACAAC
7827	PRLNEMP	22150	CCTCGTCTGAATGAGATGCCT	36473	CCAAGACTCAACGAAATGCCA
7828	PRLTASI	22151	CCTCGTCTTACTGCTTCGATT	36474	CCAAGACTCACAGCAAGCATC
7829	PRMSASV	22152	CCTCGGATGAGTGCGAGTGTG	36475	CCAAGAATGAGCGCAAGCGTC
7830	PRNASTP	22153	CCTCGGAATGCGTCGACGCCG	36476	CCAAGAAACGCAAGCACACCA
7831	PRNPEFG	22154	CCGAGGAATCCGGAGTTTGGG	36477	CCAAGAAACCCAGAATTCGGA
7832	PRNQYAA	22155	CCGCGGAATCAGTATGCTGCT	36478	CCAAGAAACCAATACGCAGCA
7833	PRNRLSD	22156	CCGAGGAATCGGCTTTCTGAT	36479	CCAAGAAACAGACTCAGCGAC
7834	PRPAPVH	22157	CCGAGGCCTGCTCCGGTGCAT	36480	CCAAGACCAGCACCAGTCCAC
7835	PRPAVPA	22158	CCGCGGCCGGCTGTGCCGGCT	36481	CCAAGACCAGCAGTCCCAGCA
7836	PRPGMDK	22159	CCGCGTCCGGGTATGGATAAG	36482	CCAAGACCAGGAATGGACAAA
7837	PRPQANS	22160	CCTAGGCCTCAGGCTAATTCT	36483	CCAAGACCACAAGCAAACAGC
7838	PRPQSLT	22161	CCGCGTCCTCAGTCGCTGACT	36484	CCAAGACCACAAAGCCTCACA
7839	PRPSLDL	22162	CCTCGGCCGTCGCTTGATTTG	36485	CCAAGACCAAGCCTCGACCTC
7840	PRPTHAV	22163	CCTAGGCCTACGCATGCGGTT	36486	CCAAGACCAACACACGCAGTC
7841	PRQTEGM	22164	CCTCGTCAGACTGAGGGTATG	36487	CCAAGACAAACAGAAGGAATG
7842	PRQTTNG	22165	CCGCGGCAGACTACGAATGGT	36488	CCAAGACAAACAACAAACGGA
7843	PRRDQET	22166	CCGAGGCGTGATCAGGAGACT	36489	CCAAGAAGAGACCAAGAAACA
7844	PRRIEFP	22167	CCGCGGCGGATTGAGTTTCCG	36490	CCAAGAAGAATCGAATTCCCA
7845	PRSADLE	22168	CCGCGTAGTGCGGATTTGGAG	36491	CCAAGAAGCGCAGACCTCGAA
7846	PRSGTAS	22169	CCGCGTAGTGGTACGGCTTCT	36492	CCAAGAAGCGGAACAGCAAGC
7847	PRSHPTS	22170	CCTAGGAGTCATCCGACGTCG	36493	CCAAGAAGCCACCCAACAAGC
7848	PRSIPGL	22171	CCTAGGTCGATTCCTGGGCTT	36494	CCAAGAAGCATCCCAGGACTC
7849	PRSLPLT	22172	CCTCGGTCTCTGCCTCTGACT	36495	CCAAGAAGCCTCCCACTCACA
7850	PRSMNQT	22173	CCTAGGTCTATGAATCAGACG	36496	CCAAGAAGCATGAACCAAACA
7851	PRSNSDT	22174	CCTCGTTCTAATTCTGATACT	36497	CCAAGAAGCAACAGCGACACA
7852	PRSPNPP	22175	CCTCGTAGTCCGAATCCGCCT	36498	CCAAGAAGCCCAAACCCACCA
7853	PRSPSDK	22176	CCTAGGTCGCCTAGTGATAAG	36499	CCAAGAAGCCCAAGCGACAAA
7854	PRSSFTE	22177	CCGAGGAGTAGTTTTACTGAG	36500	CCAAGAAGCAGCTTCACAGAA
7855	PRSSSSL	22178	CCTAGGTCTTCTTCTTCGTTG	36501	CCAAGAAGCAGCAGCAGCCTC
7856	PRTEPFL	22179	CCTCGGACGGAGCCTTTTCTT	36502	CCAAGAACAGAACCATTCCTC
7857	PRTHTDA	22180	CCGCGGACTCATACGGATGCT	36503	CCAAGAACACACACAGACGCA
7858	PRTSGTM	22181	CCTCGTACTTCTGGGACTATG	36504	CCAAGAACAAGCGGAACAATG
7859	PRTSSTH	22182	CCTCGTACTAGTTCTACTCAT	36505	CCAAGAACAAGCAGCACACAC
7860	PRTTMTE	22183	CCGCGGACTACTATGACTGAG	36506	CCAAGAACAACAATGACAGAA
7861	PRTTYSD	22184	CCTAGGACGACGTATAGTGAT	36507	CCAAGAACAACATACAGCGAC
7862	PRVGSPQ	22185	CCGCGGGTGGGTAGTCCGCAG	36508	CCAAGAGTCGGAAGCCCACAA
7863	PRVLSSG	22186	CCTAGGGTGCTGTCGAGTGGG	36509	CCAAGAGTCCTCAGCAGCGGA
7864	PRVPTHD	22187	CCGCGGGTGCCTACTCATGAT	36510	CCAAGAGTCCCAACACACGAC

7865	PRVSIAN	22188	CCGCGTGTTTCTATTGCGAAT	36511	CCAAGAGTCAGCATCGCAAAC
7866	PRVSVAP	22189	CCGAGGGTGTCGGTTGCGCCG	36512	CCAAGAGTCAGCGTCGCACCA
7867	PRYDAAG	22190	CCGCGTTATGATGCTGCTGGT	36513	CCAAGATACGACGCAGCAGGA
7868	PSAAHPP	22191	CCGTCGGCGGCTCATCCTCCT	36514	CCAAGCGCAGCACACCCACCA
7869	PSANMRS	22192	CCGAGTGCGAATATGCGGTCG	36515	CCAAGCGCAAACATGAGAAGC
7870	PSANRLS	22193	CCGAGTGCGAATCGTTTGTCT	36516	CCAAGCGCAAACAGACTCAGC
7871	PSAQSHS	22194	CCTTCTGCGCAGTCTCATAGT	36517	CCAAGCGCACAAAGCCACAGC
7872	PSASNSM	22195	CCTTCGGCTAGTAATAGTATG	36518	CCAAGCGCAAGCAACAGCATG
7873	PSATGVK	22196	CCTAGTGCGACTGGGGTGAAG	36519	CCAAGCGCAACAGGAGTCAAA
7874	PSCDNNT	22197	CCTTCTTGTGATAATAATACG	36520	CCAAGCTGCGACAACAACACA
7875	PSDDAGG	22198	CCTAGTGATGATGCTGGGGGT	36521	CCAAGCGACGACGCAGGAGGA
7876	PSDKNTG	22199	CCTAGTGATAAGAATACTGGG	36522	CCAAGCGACAAAAACACAGGA
7877	PSDKSFR	22200	CCTTCTGATAAGAGTTTTCGT	36523	CCAAGCGACAAAAGCTTCAGA
7878	PSDMPSS	22201	CCGTCGGATATGCCTTCGTCG	36524	CCAAGCGACATGCCAAGCAGC
7879	PSDPSAG	22202	CCGTCGGATCCTTCGGCTGGT	36525	CCAAGCGACCCAAGCGCAGGA
7880	PSDPVTR	22203	CCTTCGGATCCGGTGACGAGG	36526	CCAAGCGACCCAGTCACAAGA
7881	PSDRVHT	22204	CCTTCGGATCGTGTGCATACG	36527	CCAAGCGACAGAGTCCACACA
7882	PSDSAYP	22205	CCTTCTGATTCTGCGTATCCT	36528	CCAAGCGACAGCGCATACCCA
7883	PSDSVHS	22206	CCGTCTGATTCGGTTCATTCG	36529	CCAAGCGACAGCGTCCACAGC
7884	PSDTHRS	22207	CCTTCGGATACGCATAGGAGT	36530	CCAAGCGACACACACAGAAGC
7885	PSDTPTR	22208	CCGAGTGATACTCCTACGAGG	36531	CCAAGCGACACACCAACAAGA
7886	PSELNSR	22209	CCGTCGGAGCTTAATTCTCGG	36532	CCAAGCGAACTCAACAGCAGA
7887	PSEQPVR	22210	CCGTCTGAGCAGCCGGTGAGG	36533	CCAAGCGAACAACCAGTCAGA
7888	PSESTIV	22211	CCGTCGGAGTCTACTATTGTT	36534	CCAAGCGAAAGCACAATCGTC
7889	PSEYTLD	22212	CCGAGTGAGTATACTCTGGAT	36535	CCAAGCGAATACACACTCGAC
7890	PSFLEGI	22213	CCGTCGTTTTTGGAGGGGATT	36536	CCAAGCTTCCTCGAAGGAATC
7891	PSFNPMT	22214	CCTTCTTTTAATCCTATGACT	36537	CCAAGCTTCAACCCAATGACA
7892	PSFPSMT	22215	CCTTCGTTTCCGTCTATGACT	36538	CCAAGCTTCCCAAGCATGACA
7893	PSGKSPY	22216	CCGTCTGGGAAGTCTCCTTAT	36539	CCAAGCGGAAAAAGCCCATAC
7894	PSGMKPT	22217	CCTAGTGGGATGAAGCCTACT	36540	CCAAGCGGAATGAAACCAACA
7895	PSGMPSS	22218	CCTAGTGGTATGCCTAGTTCG	36541	CCAAGCGGAATGCCAAGCAGC
7896	PSGQVTG	22219	CCGTCTGGGCAGGTGACTGGT	36542	CCAAGCGGACAAGTCACAGGA
7897	PSGSDNL	22220	CCGTCGGGTAGTGATAATCTG	36543	CCAAGCGGAAGCGACAACCTC
7898	PSGTLTM	22221	CCGAGTGGGACTCTTACTATG	36544	CCAAGCGGAACACTCACAATG
7899	PSHDSFL	22222	CCTTCGCATGATTCTTTTCTG	36545	CCAAGCCACGACAGCTTCCTC
7900	PSHGLDK	22223	CCGTCTCATGGGCTTGATAAG	36546	CCAAGCCACGGACTCGACAAA
7901	PSHKAVF	22224	CCTTCTCATAAGGCGGTTTTT	36547	CCAAGCCACAAAGCAGTCTTC
7902	PSHPHER	22225	CCTTCTCATCCTCATGAGCGT	36548	CCAAGCCACCCACACGAAAGA
7903	PSHRTSL	22226	CCTTCTCATAGGACTAGTCTT	36549	CCAAGCCACAGAACAAGCCTC
7904	PSHSGTT	22227	CCGTCTCATAGTGGTACTACT	36550	CCAAGCCACAGCGGAACAACA
7905	PSHTRPV	22228	CCGTCGCATACTAGGCCGGTT	36551	CCAAGCCACACAAGACCAGTC
7906	PSIAQPP	22229	CCGTCGATTGCTCAGCCGCCT	36552	CCAAGCATCGCACAACCACCA
7907	PSIKLSE	22230	CCTTCGATTAAGTTGAGTGAG	36553	CCAAGCATCAAACTCAGCGAA
7908	PSISKPM	22231	CCGAGTATTAGTAAGCCTATG	36554	CCAAGCATCAGCAAACCAATG
7909	PSKASTE	22232	CCTTCTAAGGCTTCGACGGAG	36555	CCAAGCAAAGCAAGCACAGAA

7910	PSKSPST	22233	CCGAGTAAGTCTCCTAGTACT	36556	CCAAGCAAAAGCCCAAGCACA
7911	PSKSSAA	22234	CCGAGTAAGTCGTCTGCTGCT	36557	CCAAGCAAAAGCAGCGCAGCA
7912	PSKVGRE	22235	CCGTCGAAGGTGGGGCGGGAG	36558	CCAAGCAAAGTCGGAAGAGAA
7913	PSLEGAP	22236	CCTTCTTTGGAGGGTGCTCCT	36559	CCAAGCCTCGAAGGAGCACCA
7914	PSLRAAL	22237	CCGAGTCTTCGGGCTGCTCTT	36560	CCAAGCCTCAGAGCAGCACTC
7915	PSLSNKV	22238	CCTAGTCTGTCGAATAAGGTG	36561	CCAAGCCTCAGCAACAAAGTC
7916	PSLSSSP	22239	CCTTCGCTTTCGAGTAGTCCG	36562	CCAAGCCTCAGCAGCAGCCCA
7917	PSMSPHT	22240	CCGTCGATGAGTCCGCATACG	36563	CCAAGCATGAGCCCACACACA
7918	PSMTAQE	22241	CCGTCTATGACGGCGCAGGAG	36564	CCAAGCATGACAGCACAAGAA
7919	PSNAGRF	22242	CCGTCTAATGCGGGGCGGTTT	36565	CCAAGCAACGCAGGAAGATTC
7920	PSNGKSI	22243	CCTTCTAATGGTAAGTCTATT	36566	CCAAGCAACGGAAAAAGCATC
7921	PSNHLKS	22244	CCTAGTAATCATTTGAAGAGT	36567	CCAAGCAACCACCTCAAAAGC
7922	PSNNTEG	22245	CCGTCGAATAATACTGAGGGT	36568	CCAAGCAACAACACAGAAGGA
7923	PSNPSFR	22246	CCTTCGAATCCTTCTTTTCGT	36569	CCAAGCAACCCAAGCTTCAGA
7924	PSNQLVR	22247	CCGTCTAATCAGTTGGTTCGT	36570	CCAAGCAACCAACTCGTCAGA
7925	PSPAVKS	22248	CCTAGTCCGGCGGTTAAGAGT	36571	CCAAGCCCAGCAGTCAAAAGC
7926	PSPDVRG	22249	CCGTCTCCTGATGTTAGGGGG	36572	CCAAGCCCAGACGTCAGAGGA
7927	PSPKTCP	22250	CCTAGTCCTAAGACTTGTCCT	36573	CCAAGCCCAAAAACATGCCCA
7928	PSPLRLG	22251	CCTTCTCCGCTTCGTCTTGGG	36574	CCAAGCCCACTCAGACTCGGA
7929	PSPVKGG	22252	CCGAGTCCGGTTAAGGGGGGT	36575	CCAAGCCCAGTCAAAGGAGGA
7930	PSQDPHL	22253	CCTTCTCAGGATCCTCATCTT	36576	CCAAGCCAAGACCCACACCTC
7931	PSQDRQA	22254	CCTTCTCAGGATCGGCAGGCT	36577	CCAAGCCAAGACAGACAAGCA
7932	PSQFKEN	22255	CCTAGTCAGTTTAAGGAGAAT	36578	CCAAGCCAATTCAAAGAAAAC
7933	PSQGHSM	22256	CCTTCTCAGGGTCATTCGATG	36579	CCAAGCCAAGGACACAGCATG
7934	PSQGPWT	22257	CCGAGTCAGGGTCCGTGGACT	36580	CCAAGCCAAGGACCATGGACA
7935	PSQLASN	22258	CCGTCTCAGCTTGCGTCGAAT	36581	CCAAGCCAACTCGCAAGCAAC
7936	PSQLVVA	22259	CCGTCGCAGCTTGTTGTTGCT	36582	CCAAGCCAACTCGTCGTCGCA
7937	PSQPGAI	22260	CCTTCTCAGCCGGGGGCGATT	36583	CCAAGCCAACCAGGAGCAATC
7938	PSQREMK	22261	CCTAGTCAGAGGGAGATGAAG	36584	CCAAGCCAAAGAGAAATGAAA
7939	PSQSNLR	22262	CCGTCTCAGTCGAATCTTCGT	36585	CCAAGCCAAAGCAACCTCAGA
7940	PSQSSKL	22263	CCGTCTCAGTCGTCTAAGCTT	36586	CCAAGCCAAAGCAGCAAACTC
7941	PSQTATP	22264	CCGTCGCAGACGGCGACGCCT	36587	CCAAGCCAAACAGCAACACCA
7942	PSQTHSP	22265	CCTTCGCAGACTCATTCTCCT	36588	CCAAGCCAAACACACAGCCCA
7943	PSREISL	22266	CCGTCGAGGGAGATTTCGCTG	36589	CCAAGCAGAGAAATCAGCCTC
7944	PSRERSN	22267	CCTTCGCGTGAGCGTTCGAAT	36590	CCAAGCAGAGAAAGAAGCAAC
7945	PSRFSTP	22268	CCTAGTCGTTTTAGTACGCCT	36591	CCAAGCAGATTCAGCACACCA
7946	PSRGDIG	22269	CCTTCGAGGGGGGATATTGGT	36592	CCAAGCAGAGGAGACATCGGA
7947	PSRGVLP	22270	CCTTCGCGTGGGGTGCTTCCT	36593	CCAAGCAGAGGAGTCCTCCCA
7948	PSRLGSA	22271	CCTTCTCGTTTGGGGAGTGCT	36594	CCAAGCAGACTCGGAAGCGCA
7949	PSRLTND	22272	CCTTCGCGGTTGACTAATGAT	36595	CCAAGCAGACTCACAAACGAC
7950	PSRLVSE	22273	CCTTCTAGGCTGGTGTCGGAG	36596	CCAAGCAGACTCGTCAGCGAA
7951	PSRPMMS	22274	CCTAGTCGTCCGATGATGAGT	36597	CCAAGCAGACCAATGATGAGC
7952	PSRSMSE	22275	CCTTCGAGGAGTATGTCGGAG	36598	CCAAGCAGAAGCATGAGCGAA
7953	PSRTEPP	22276	CCTTCTAGGACTGAGCCTCCG	36599	CCAAGCAGAACAGAACCACCA
7954	PSRTHLH	22277	CCTAGTCGGACTCATCTGCAT	36600	CCAAGCAGAACACACCTCCAC

7955	PSRVVEA	22278	CCTTCTCGGGTGGTTGAGGCT	36601	CCAAGCAGAGTCGTCGAAGCA
7956	PSSESDF	22279	CCTTCGAGTGAGTCTGATTTT	36602	CCAAGCAGCGAAAGCGACTTC
7957	PSSGGLV	22280	CCTTCTTCGGGTGGGCTGGTT	36603	CCAAGCAGCGGAGGACTCGTC
7958	PSSGLHL	22281	CCTAGTTCGGGTCTTCATTTG	36604	CCAAGCAGCGGACTCCACCTC
7959	PSSKGLL	22282	CCGTCTTCGAAGGGTTTGCTT	36605	CCAAGCAGCAAAGGACTCCTC
7960	PSSKVGD	22283	CCGAGTTCTAAGGTTGGTGAT	36606	CCAAGCAGCAAAGTCGGAGAC
7961	PSSLDDG	22284	CCTTCTAGTTTGGATGATGGT	36607	CCAAGCAGCCTCGACGACGGA
7962	PSSLNRL	22285	CCTTCTAGTCTTAATCGGCTT	36608	CCAAGCAGCCTCAACAGACTC
7963	PSSLSAG	22286	CCGAGTAGTTTGTCTGCGGGG	36609	CCAAGCAGCCTCAGCGCAGGA
7964	PSSMAHP	22287	CCTTCTTCGATGGCTCATCCT	36610	CCAAGCAGCATGGCACACCCA
7965	PSSMIAE	22288	CCTTCTTCGATGATTGCTGAG	36611	CCAAGCAGCATGATCGCAGAA
7966	PSSPAVR	22289	CCTTCGTCGCCGGCTGTTCGG	36612	CCAAGCAGCCCAGCAGTCAGA
7967	PSSPLMT	22290	CCTTCGTCTCCTTTGATGACT	36613	CCAAGCAGCCCACTCATGACA
7968	PSSPPFF	22291	CCGTCGAGTCCTCCTTTTTTT	36614	CCAAGCAGCCCACCATTCTTC
7969	PSSPVFI	22292	CCTAGTTCTCCTGTGTTTATT	36615	CCAAGCAGCCCAGTCTTCATC
7970	PSSRGAL	22293	CCTTCGTCGCGGGGGGCTCTT	36616	CCAAGCAGCAGAGGAGCACTC
7971	PSSSINR	22294	CCTAGTAGTAGTATTAATCGT	36617	CCAAGCAGCAGCATCAACAGA
7972	PSSSSGN	22295	CCGTCTTCGAGTAGTGGGAAT	36618	CCAAGCAGCAGCAGCGGAAAC
7973	PSSSYPL	22296	CCGTCTTCGTCGTATCCGCTG	36619	CCAAGCAGCAGCTACCCACTC
7974	PSSTPGQ	22297	CCTTCGTCTACTCCTGGGCAG	36620	CCAAGCAGCACACCAGGACAA
7975	PSTAGSK	22298	CCTTCTACTGCTGGGTCGAAG	36621	CCAAGCACAGCAGGAAGCAAA
7976	PSTAHST	22299	CCTAGTACGGCTCATAGTACT	36622	CCAAGCACAGCACACAGCACA
7977	PSTAIKT	22300	CCTTCTACGGCTATTAAGACT	36623	CCAAGCACAGCAATCAAAACA
7978	PSTARTS	22301	CCTAGTACTGCGCGGACGTCT	36624	CCAAGCACAGCAAGAACAAGC
7979	PSTGPFH	22302	CCGTCTACGGGGCCTTTTCAT	36625	CCAAGCACAGGACCATTCCAC
7980	PSTGRPL	22303	CCGTCGACGGGTCGTCCGTTG	36626	CCAAGCACAGGAAGACCACTC
7981	PSTKEFI	22304	CCGTCTACTAAGGAGTTTATT	36627	CCAAGCACAAAAGAATTCATC
7982	PSTNAYA	22305	CCGTCGACTAATGCTTATGCT	36628	CCAAGCACAAACGCATACGCA
7983	PSTNGSH	22306	CCGTCTACGAATGGGTCGCAT	36629	CCAAGCACAAACGGAAGCCAC
7984	PSTPAAN	22307	CCTTCTACTCCGGCGGCGAAT	36630	CCAAGCACACCAGCAGCAAAC
7985	PSTPAAS	22308	CCGTCTACTCCTGCTGCGAGT	36631	CCAAGCACACCAGCAGCAAGC
7986	PSTSLSE	22309	CCTTCTACTAGTCTTTCGGAG	36632	CCAAGCACAAGCCTCAGCGAA
7987	PSVDSWS	22310	CCTTCTGTGGATTCTTGGAGT	36633	CCAAGCGTCGACAGCTGGAGC
7988	PSVDSYL	22311	CCTTCTGTGGATAGTTATCTT	36634	CCAAGCGTCGACAGCTACCTC
7989	PSVEHVP	22312	CCGAGTGTTGAGCATGTGCCG	36635	CCAAGCGTCGAACACGTCCCA
7990	PSVESWS	22313	CCTTCTGTGGAGTCTTGGAGT	36636	CCAAGCGTCGAAAGCTGGAGC
7991	PSVLHPS	22314	CCGAGTGTGTTGCATCCGTCG	36637	CCAAGCGTCCTCCACCCAAGC
7992	PSVPLMT	22315	CCTTCGGTGCCGTTGATGACT	36638	CCAAGCGTCCCACTCATGACA
7993	PSVPRGP	22316	CCTTCTGTTCCGCGTGGGCCG	36639	CCAAGCGTCCCAAGAGGACCA
7994	PSVQHFP	22317	CCGTCGGTGCAGCATTTTCCT	36640	CCAAGCGTCCAACACTTCCCA
7995	PSVRDPA	22318	CCGAGTGTGCGGGATCCTGCT	36641	CCAAGCGTCAGAGACCCAGCA
7996	PSVTGTM	22319	CCGTCGGTGACGGGGACTATG	36642	CCAAGCGTCACAGGAACAATG
7997	PSYDKLK	22320	CCTTCTTATGATAAGCTGAAG	36643	CCAAGCTACGACAAACTCAAA
7998	PSYPGLD	22321	CCTTCGTATCCTGGTTTGGAT	36644	CCAAGCTACCCAGGACTCGAC
7999	PSYSHME	22322	CCGTCGTATTCTCATATGGAG	36645	CCAAGCTACAGCCACATGGAA

8000	PSYSVTE	22323	CCGTCTTATTCTGTTACTGAG	36646	CCAAGCTACAGCGTCACAGAA
8001	PTAARPP	22324	CCTACTGCTGCTAGGCCTCCG	36647	CCAACAGCAGCAAGACCACCA
8002	PTALASF	22325	CCGACGGCTCTTGCGAGTTTT	36648	CCAACAGCACTCGCAAGCTTC
8003	PTALGKS	22326	CCTACGGCGCTTGGGAAGTCG	36649	CCAACAGCACTCGGAAAAAGC
8004	PTAPTIP	22327	CCTACTGCTCCTACGATTCCT	36650	CCAACAGCACCAACAATCCCA
8005	PTASPNT	22328	CCGACGGCGAGTCCTAATACG	36651	CCAACAGCAAGCCCAAACACA
8006	PTDNTSP	22329	CCGACTGATAATACTAGTCCG	36652	CCAACAGACAACACAAGCCCA
8007	PTDPRAP	22330	CCTACTGATCCGCGTGCGCCT	36653	CCAACAGACCCAAGAGCACCA
8008	PTDRHSI	22331	CCTACTGATCGTCATTCTATT	36654	CCAACAGACAGACACAGCATC
8009	PTDRREM	22332	CCTACTGATAGGCGTGAGATG	36655	CCAACAGACAGAAGAGAAATG
8010	PTDTVPP	22333	CCTACGGATACGGTTCCGCCT	36656	CCAACAGACACAGTCCCACCA
8011	PTDVNRG	22334	CCTACTGATGTGAATCGTGGT	36657	CCAACAGACGTCAACAGAGGA
8012	PTDYARG	22335	CCTACTGATTATGCTAGGGGT	36658	CCAACAGACTACGCAAGAGGA
8013	PTEAAGV	22336	CCTACTGAGGCTGCTGGGGTT	36659	CCAACAGAAGCAGCAGGAGTC
8014	PTETNGY	22337	CCTACTGAGACGAATGGTTAT	36660	CCAACAGAAACAAACGGATAC
8015	PTFLTTN	22338	CCGACGTTTTTGACGACGAAT	36661	CCAACATTCCTCACAACAAAC
8016	PTFTRST	22339	CCGACGTTTACTAGGTCGACT	36662	CCAACATTCACAAGAAGCACA
8017	PTGATSS	22340	CCGACTGGGGCGACTTCTTCG	36663	CCAACAGGAGCAACAAGCAGC
8018	PTGGAHT	22341	CCGACGGGGGGTGCTCATACT	36664	CCAACAGGAGGAGCACACACA
8019	PTGPGSP	22342	CCTACTGGTCCTGGGTCGCCG	36665	CCAACAGGACCAGGAAGCCCA
8020	PTGPHDL	22343	CCGACTGGGCCGCATGATTTG	36666	CCAACAGGACCACACGACCTC
8021	PTGQPRP	22344	CCTACGGGGCAGCCGCGGCCT	36667	CCAACAGGACAACCAAGACCA
8022	PTGRALA	22345	CCGACGGGGAGGGCTTTGGCT	36668	CCAACAGGAAGAGCACTCGCA
8023	PTGSIQI	22346	CCTACGGGTTCTATTCAGATT	36669	CCAACAGGAAGCATCCAAATC
8024	PTGTPEI	22347	CCGACTGGGACTCCTGAGATT	36670	CCAACAGGAACACCAGAAATC
8025	PTGTSPL	22348	CCTACTGGGACGTCGCCTTTG	36671	CCAACAGGAACAAGCCCACTC
8026	PTGVGSL	22349	CCTACGGGTGTGGGGTCTCTG	36672	CCAACAGGAGTCGGAAGCCTC
8027	PTHPNSF	22350	CCTACTCATCCTAATTCTTTT	36673	CCAACACACCCAAACAGCTTC
8028	PTHSGIT	22351	CCTACGCATTCGGGGATTACG	36674	CCAACACACAGCGGAATCACA
8029	PTHSLIS	22352	CCTACTCATTCGCTGATTTCT	36675	CCAACACACAGCCTCATCAGC
8030	PTHSTNK	22353	CCTACTCATAGTACGAATAAG	36676	CCAACACACAGCACAAACAAA
8031	PTIPKKD	22354	CCTACGATTCCTAAGAAGGAT	36677	CCAACAATCCCAAAAAAAGAC
8032	PTIPLDR	22355	CCGACGATTCCTTTGGATAGG	36678	CCAACAATCCCACTCGACAGA
8033	PTKPLGD	22356	CCTACTAAGCCTTTGGGTGAT	36679	CCAACAAAACCACTCGGAGAC
8034	PTLDDPK	22357	CCGACGCTGGATGATCCGAAG	36680	CCAACACTCGACGACCCAAAA
8035	PTLDGKP	22358	CCGACTCTTGATGGGAAGCCG	36681	CCAACACTCGACGGAAAACCA
8036	PTLKSDM	22359	CCTACGTTGAAGAGTGATATG	36682	CCAACACTCAAAAGCGACATG
8037	PTLPSTV	22360	CCTACTCTTCCGAGTACTGTT	36683	CCAACACTCCCAAGCACAGTC
8038	PTLSMAH	22361	CCTACTTTGAGTATGGCTCAT	36684	CCAACACTCAGCATGGCACAC
8039	PTLSRTH	22362	CCGACGTTGTCTCGGACGCAT	36685	CCAACACTCAGCAGAACACAC
8040	PTLSTLL	22363	CCTACTCTTTCGACTTTGTTG	36686	CCAACACTCAGCACACTCCTC
8041	PTMHMLS	22364	CCGACTATGCATATGCTGTCT	36687	CCAACAATGCACATGCTCAGC
8042	PTMNRNE	22365	CCTACTATGAATCGGAATGAG	36688	CCAACAATGAACAGAAACGAA
8043	PTMSDSR	22366	CCTACGATGTCTGATAGTAGG	36689	CCAACAATGAGCGACAGCAGA
8044	PTNALHL	22367	CCGACGAATGCTCTTCATTTG	36690	CCAACAAACGCACTCCACCTC

8045	PTNAVDN	22368	CCTACTAATGCTGTGGATAAT	36691	CCAACAAACGCAGTCGACAAC
8046	PTNLGRA	22369	CCTACTAATCTTGGTCGTGCG	36692	CCAACAAACCTCGGAAGAGCA
8047	PTNPRLM	22370	CCTACTAATCCTCGTTTGATG	36693	CCAACAAACCCAAGACTCATG
8048	PTNRPSS	22371	CCTACTAATAGGCCGTCGTCG	36694	CCAACAAACAGACCAAGCAGC
8049	PTPAAHG	22372	CCTACTCCGGCGGCGCATGGT	36695	CCAACACCAGCAGCACACGGA
8050	PTPPTVT	22373	CCGACGCCTCCTACGGTGACG	36696	CCAACACCACCAACAGTCACA
8051	PTPQGSA	22374	CCGACGCCGCAGGGGTCTGCG	36697	CCAACACCACAAGGAAGCGCA
8052	PTPRPSP	22375	CCTACGCCTAGGCCGTCGCCG	36698	CCAACACCAAGACCAAGCCCA
8053	PTPRSVP	22376	CCTACGCCGAGGTCTGTTCCT	36699	CCAACACCAAGAAGCGTCCCA
8054	PTQSGVS	22377	CCGACTCAGTCTGGTGTGAGT	36700	CCAACACAAAGCGGAGTCAGC
8055	PTRAEFY	22378	CCTACTCGGGCTGAGTTTTAT	36701	CCAACAAGAGCAGAATTCTAC
8056	PTRQPVL	22379	CCTACGCGTCAGCCGGTTCTG	36702	CCAACAAGACAACCAGTCCTC
8057	PTRTINA	22380	CCTACTCGTACGATTAATGCT	36703	CCAACAAGAACAATCAACGCA
8058	PTRTPAS	22381	CCTACGCGGACTCCGGCGAGT	36704	CCAACAAGAACACCAGCAAGC
8059	PTSDFKC	22382	CCGACGAGTGATTTTAAGTGT	36705	CCAACAAGCGACTTCAAATGC
8060	PTSEALR	22383	CCTACTTCTGAGGCGCTTAGG	36706	CCAACAAGCGAAGCACTCAGA
8061	PTSIHRN	22384	CCGACTTCGATTCATAGGAAT	36707	CCAACAAGCATCCACAGAAAC
8062	PTSIVRS	22385	CCTACTTCGATTGTGCGTTCT	36708	CCAACAAGCATCGTCAGAAGC
8063	PTSKGPL	22386	CCGACGTCGAAGGGTCCGTTG	36709	CCAACAAGCAAAGGACCACTC
8064	PTSPTDM	22387	CCTACGTCTCCTACGGATATG	36710	CCAACAAGCCCAACAGACATG
8065	PTSPTTC	22388	CCGACGTCGCCTACTACTTGT	36711	CCAACAAGCCCAACAACATGC
8066	PTSRPSL	22389	CCTACGAGTCGTCCTTCGCTG	36712	CCAACAAGCAGACCAAGCCTC
8067	PTSSIGG	22390	CCTACTTCGTCTATTGGGGGT	36713	CCAACAAGCAGCATCGGAGGA
8068	PTSTNPL	22391	CCTACTAGTACGAATCCTCTG	36714	CCAACAAGCACAAACCCACTC
8069	PTSVGTG	22392	CCGACTTCGGTGGGTACTGGG	36715	CCAACAAGCGTCGGAACAGGA
8070	PTSVPKT	22393	CCTACGTCTGTGCCGAAGACG	36716	CCAACAAGCGTCCCAAAAACA
8071	PTTHLSD	22394	CCGACGACGCATCTTTCTGAT	36717	CCAACAACACACCTCAGCGAC
8072	PTTHSAR	22395	CCGACTACGCATTCTGCTCGT	36718	CCAACAACACACAGCGCAAGA
8073	PTTLAVA	22396	CCTACTACTCTGGCTGTGGCT	36719	CCAACAACACTCGCAGTCGCA
8074	PTTNGST	22397	CCGACGACGAATGGTTCTACG	36720	CCAACAACAAACGGAAGCACA
8075	PTTPVAI	22398	CCTACTACTCCTGTTGCGATT	36721	CCAACAACACCAGTCGCAATC
8076	PTTRGPP	22399	CCGACGACTAGGGGTCCGCCG	36722	CCAACAACAAGAGGACCACCA
8077	PTVKLLG	22400	CCTACTGTGAAGTTGTTGGGT	36723	CCAACAGTCAAACTCCTCGGA
8078	PTVPDLN	22401	CCTACTGTGCCGGATCTGAAT	36724	CCAACAGTCCCAGACCTCAAC
8079	PTVPRPG	22402	CCGACTGTGCCTCGTCCGGGG	36725	CCAACAGTCCCAAGACCAGGA
8080	PTVPVGL	22403	CCTACTGTTCCGGTTGGTTTG	36726	CCAACAGTCCCAGTCGGACTC
8081	PTVRGQY	22404	CCTACTGTGCGGGGGCAGTAT	36727	CCAACAGTCAGAGGACAATAC
8082	PTYPKAT	22405	CCTACTTATCCTAAGGCTACT	36728	CCAACATACCCAAAAGCAACA
8083	PTYRDTA	22406	CCTACGTATAGGGATACTGCT	36729	CCAACATACAGAGACACAGCA
8084	PVARSMS	22407	CCTGTTGCTAGGTCGATGAGT	36730	CCAGTCGCAAGAAGCATGAGC
8085	PVATCRV	22408	CCGGTTGCTACTTGTCGTGTT	36731	CCAGTCGCAACATGCAGAGTC
8086	PVATSYD	22409	CCTGTTGCTACTTCTTATGAT	36732	CCAGTCGCAACAAGCTACGAC
8087	PVDALPR	22410	CCGGTTGATGCTCTTCCGCGT	36733	CCAGTCGACGCACTCCCAAGA
8088	PVDHARS	22411	CCTGTGGATCATGCTAGGAGT	36734	CCAGTCGACCACGCAAGAAGC
8089	PVDLGRG	22412	CCTGTTGATCTTGGGCGTGGT	36735	CCAGTCGACCTCGGAAGAGGA

8090	PVEATVL	22413	CCGGTTGAGGCTACGGTGCTG	36736	CCAGTCGAAGCAACAGTCCTC
8091	PVEKYDK	22414	CCGGTTGAGAAGTATGATAAG	36737	CCAGTCGAAAAATACGACAAA
8092	PVEPGMS	22415	CCTGTTGAGCCGGGTATGTCG	36738	CCAGTCGAACCAGGAATGAGC
8093	PVESHRL	22416	CCTGTGGAGTCTCATCGTTTG	36739	CCAGTCGAAAGCCACAGACTC
8094	PVFHEAS	22417	CCGGTTTTTCATGAGGCTTCG	36740	CCAGTCTTCCACGAAGCAAGC
8095	PVFPQSS	22418	CCGGTGTTTCCTCAGAGTTCT	36741	CCAGTCTTCCCACAAAGCAGC
8096	PVGFTEN	22419	CCTGTGGGTTTTACTGAGAAT	36742	CCAGTCGGATTCACAGAAAAC
8097	PVGSNSA	22420	CCTGTGGGGTCGAATTCTGCG	36743	CCAGTCGGAAGCAACAGCGCA
8098	PVHIHTS	22421	CCTGTTCATATTCATACTTCG	36744	CCAGTCCACATCCACACAAGC
8099	PVHSGRP	22422	CCGGTTCATAGTGGGCGTCCT	36745	CCAGTCCACAGCGGAAGACCA
8100	PVISTIA	22423	CCGGTTATTTCGACGATTGCG	36746	CCAGTCATCAGCACAATCGCA
8101	PVKEVGD	22424	CCGGTTAAGGAGGTGGGTGAT	36747	CCAGTCAAAGAAGTCGGAGAC
8102	PVKSAAP	22425	CCTGTTAAGTCTGCGGCGCCG	36748	CCAGTCAAAAGCGCAGCACCA
8103	PVLPSDH	22426	CCTGTGCTGCCGTCTGATCAT	36749	CCAGTCCTCCCAAGCGACCAC
8104	PVMGTSV	22427	CCTGTTATGGGTACGAGTGTT	36750	CCAGTCATGGGAACAAGCGTC
8105	PVMSGAS	22428	CCTGTGATGAGTGGGGCGTCG	36751	CCAGTCATGAGCGGAGCAAGC
8106	PVNSERM	22429	CCTGTGAATAGTGAGCGTATG	36752	CCAGTCAACAGCGAAAGAATG
8107	PVPGKLA	22430	CCGGTGCCGGGTAAGCTGGCT	36753	CCAGTCCCAGGAAAACTCGCA
8108	PVPPPLR	22431	CCGGTTCCGCCTCCTTTGCGT	36754	CCAGTCCCACCACCACTCAGA
8109	PVPRSVN	22432	CCGGTGCCTAGGTCTGTTAAT	36755	CCAGTCCCAAGAAGCGTCAAC
8110	PVQMTAS	22433	CCTGTGCAGATGACTGCTTCT	36756	CCAGTCCAAATGACAGCAAGC
8111	PVQVSLG	22434	CCTGTTCAGGTGTCGTTGGGT	36757	CCAGTCCAAGTCAGCCTCGGA
8112	PVRAIEH	22435	CCGGTTCGTGCGATTGAGCAT	36758	CCAGTCAGAGCAATCGAACAC
8113	PVRAMDG	22436	CCGGTGAGGGCGATGGATGGT	36759	CCAGTCAGAGCAATGGACGGA
8114	PVSGNFT	22437	CCGGTTAGTGGGAATTTTACG	36760	CCAGTCAGCGGAAACTTCACA
8115	PVSKDRP	22438	CCTGTTTCTAAGGATCGGCCT	36761	CCAGTCAGCAAAGACAGACCA
8116	PVSMAAR	22439	CCGGTGTCTATGGCGGCTAGG	36762	CCAGTCAGCATGGCAGCAAGA
8117	PVSMPRE	22440	CCTGTGTCTATGCCGCGGGAG	36763	CCAGTCAGCATGCCAAGAGAA
8118	PVSPAIP	22441	CCTGTGTCGCCGGCTATTCCT	36764	CCAGTCAGCCCAGCAATCCCA
8119	PVSPVPA	22442	CCGGTGTCGCCGGTTCCTGCT	36765	CCAGTCAGCCCAGTCCCAGCA
8120	PVSQHSK	22443	CCGGTGTCTCAGCATAGTAAG	36766	CCAGTCAGCCAACACAGCAAA
8121	PVSSPTM	22444	CCGGTGTCTTCTCCGACTATG	36767	CCAGTCAGCAGCCCAACAATG
8122	PVSTSAD	22445	CCTGTGTCGACTAGTGCGGAT	36768	CCAGTCAGCACAAGCGCAGAC
8123	PVTAGER	22446	CCTGTTACTGCGGGGGAGCGG	36769	CCAGTCACAGCAGGAGAAAGA
8124	PVTGPGQ	22447	CCTGTGACGGGGCCGGGGCAG	36770	CCAGTCACAGGACCAGGACAA
8125	PVTKSLL	22448	CCTGTGACTAAGAGTCTTCTG	36771	CCAGTCACAAAAAGCCTCCTC
8126	PVTKSVL	22449	CCGGTGACTAAGAGTGTTCTT	36772	CCAGTCACAAAAAGCGTCCTC
8127	PVTNDRH	22450	CCTGTTACTAATGATCGGCAT	36773	CCAGTCACAAACGACAGACAC
8128	PVTTNAG	22451	CCGGTTACTACGAATGCTGGT	36774	CCAGTCACAACAAACGCAGGA
8129	PVVNVWS	22452	CCGGTTGTTAATGTGTGGTCG	36775	CCAGTCGTCAACGTCTGGAGC
8130	PVVSDTL	22453	CCTGTGGTGTCGGATACGCTT	36776	CCAGTCGTCAGCGACACACTC
8131	PVVTTTL	22454	CCGGTTGTGACGACTACTCTT	36777	CCAGTCGTCACAACAACACTC
8132	PVYVGEI	22455	CCTGTGTATGTTGGTGAGATT	36778	CCAGTCTACGTCGGAGAAATC
8133	PWATMQG	22456	CCTTGGGCTACTATGCAGGGT	36779	CCATGGGCAACAATGCAAGGA
8134	PWKDNRG	22457	CCTTGGAAGGATAATCGTGGG	36780	CCATGGAAAGACAACAGAGGA

8135	PWSEDGM	22458	CCTTGGAGTGAGGATGGGATG	36781	CCATGGAGCGAAGACGGAATG
8136	PYATALT	22459	CCTTATGCTACTGCTCTGACG	36782	CCATACGCAACAGCACTCACA
8137	PYDRPSA	22460	CCGTATGATAGGCCGTCTGCT	36783	CCATACGACAGACCAAGCGCA
8138	PYEARAL	22461	CCTTATGAGGCTCGGGCTTTG	36784	CCATACGAAGCAAGAGCACTC
8139	PYEMVAM	22462	CCGTATGAGATGGTGGCTATG	36785	CCATACGAAATGGTCGCAATG
8140	PYGTRET	22463	CCTTATGGTACGCGGGAGACG	36786	CCATACGGAACAAGAGAAACA
8141	PYHNHSA	22464	CCGTATCATAATCATTCGGCT	36787	CCATACCACAACCACAGCGCA
8142	PYIGGMS	22465	CCTTATATTGGGGGTATGTCG	36788	CCATACATCGGAGGAATGAGC
8143	PYLDPLR	22466	CCGTATTTGGATCCTCTGAGG	36789	CCATACCTCGACCCACTCAGA
8144	PYLSNRP	22467	CCGTATCTGTCTAATCGTCCG	36790	CCATACCTCAGCAACAGACCA
8145	PYLYPEE	22468	CCGTATCTGTATCCGGAGGAG	36791	CCATACCTCTACCCAGAAGAA
8146	PYPDPSK	22469	CCTTATCCTGATCCGTCGAAG	36792	CCATACCCAGACCCAAGCAAA
8147	PYPETSH	22470	CCGTATCCTGAGACTTCGCAT	36793	CCATACCCAGAAACAAGCCAC
8148	PYPSDKF	22471	CCTTATCCTAGTGATAAGTTT	36794	CCATACCCAAGCGACAAATTC
8149	PYPTSNE	22472	CCGTATCCGACGTCTAATGAG	36795	CCATACCCAACAAGCAACGAA
8150	PYQRNSV	22473	CCTTATCAGCGTAATTCGGTG	36796	CCATACCAAAGAAACAGCGTC
8151	PYREHTV	22474	CCGTATAGGGAGCATACTGTT	36797	CCATACAGAGAACACACAGTC
8152	PYRESSP	22475	CCGTATCGGGAGAGTAGTCCG	36798	CCATACAGAGAAAGCAGCCCA
8153	PYRSEPA	22476	CCTTATCGTAGTGAGCCGGCG	36799	CCATACAGAAGCGAACCAGCA
8154	PYSAGYH	22477	CCTTATAGTGCTGGTTATCAT	36800	CCATACAGCGCAGGATACCAC
8155	PYSGMTL	22478	CCTTATAGTGGGATGACTTTG	36801	CCATACAGCGGAATGACACTC
8156	PYSVAVS	22479	CCGTATTCTGTTGCGGTGTCT	36802	CCATACAGCGTCGCAGTCAGC
8157	PYTSALL	22480	CCTTATACTAGTGCTTTGCTG	36803	CCATACACAAGCGCACTCCTC
8158	PYVIDRV	22481	CCTTATGTTACTGATCGTGTT	36804	CCATACGTCACAGACAGAGTC
8159	PYVIEVY	22482	CCTTATGTTACGGAGGTTTAT	36805	CCATACGTCACAGAAGTCTAC
8160	QAASLLA	22483	CAGGCGGCGTCTCTTCTGGCG	36806	CAAGCAGCAAGCCTCCTCGCA
8161	QAELPYG	22484	CAGGCGGAGTTGCCTTATGGG	36807	CAAGCAGAACTCCCATACGGA
8162	QAFDVEM	22485	CAGGCTTTTGATGTTGAGATG	36808	CAAGCATTCGACGTCGAAATG
8163	QAGMQGA	22486	CAGGCTGGGATGCAGGGTGCT	36809	CAAGCAGGAATGCAAGGAGCA
8164	QAGNLRD	22487	CAGGCGGGTAATCTGCGTGAT	36810	CAAGCAGGAAACCTCAGAGAC
8165	QAGNNGA	22488	CAGGCTGGTAATAATGGTGCT	36811	CAAGCAGGAAACAACGGAGCA
8166	QAGVTNS	22489	CAGGCTGGTGTGACGAATTCG	36812	CAAGCAGGAGTCACAAACAGC
8167	QAHGGAL	22490	CAGGCGCATGGGGGGGCGTTG	36813	CAAGCACACGGAGGAGCACTC
8168	QAIQQRQ	22491	CAGGCGATTCAGCAGCGTCAG	36814	CAAGCAATCCAACAAAGACAA
8169	QAIRNEP	22492	CAGGCGATTCGTAATGAGCCT	36815	CAAGCAATCAGAAACGAACCA
8170	QAKAYAT	22493	CAGGCTAAGGCGTATGCGACT	36816	CAAGCAAAAGCATACGCAACA
8171	QAKSPSL	22494	CAGGCGAAGTCTCCTTCTTTG	36817	CAAGCAAAAAGCCCAAGCCTC
8172	QALAPTN	22495	CAGGCGCTGGCGCCGACTAAT	36818	CAAGCACTCGCACCAACAAAC
8173	QALPTMH	22496	CAGGCTTTGCCTACTATGCAT	36819	CAAGCACTCCCAACAATGCAC
8174	QANGSVG	22497	CAGGCTAATGGTAGTGTTGGG	36820	CAAGCAAACGGAAGCGTCGGA
8175	QANVSQP	22498	CAGGCGAATGTTAGTCAGCCG	36821	CAAGCAAACGTCAGCCAACCA
8176	QAPGHRE	22499	CAGGCTCCGGGTCATCGGGAG	36822	CAAGCACCAGGACACAGAGAA
8177	QAPGILL	22500	CAGGCTCCTGGTATTCTTCTT	36823	CAAGCACCAGGAATCCTCCTC
8178	QAPGLLV	22501	CAGGCGCCGGGGCTGCTGGTT	36824	CAAGCACCAGGACTCCTCGTC
8179	QAPLASL	22502	CAGGCGCCGCTTGCTTCTTTG	36825	CAAGCACCACTCGCAAGCCTC

8180	QAPRSDV	22503	CAGGCGCCGCGTAGTGATGTG	36826	CAAGCACCAAGAAGCGACGTC
8181	QAQLQGR	22504	CAGGCTCAGCTGCAGGGTCGG	36827	CAAGCACAACTCCAAGGAAGA
8182	QAQRALS	22505	CAGGCGCAGCGGGCTTTGAGT	36828	CAAGCACAAAGAGCACTCAGC
8183	QAQYPAM	22506	CAGGCGCAGTATCCGGCTATG	36829	CAAGCACAATACCCAGCAATG
8184	QARAVTS	22507	CAGGCTCGGGCTGTTACGTCG	36830	CAAGCAAGAGCAGTCACAAGC
8185	QARDPSL	22508	CAGGCGCGTGATCCGTCTTTG	36831	CAAGCAAGAGACCCAAGCCTC
8186	QAREVSP	22509	CAGGCTCGTGAGGTTAGTCCT	36832	CAAGCAAGAGAAGTCAGCCCA
8187	QARGNVS	22510	CAGGCGAGGGGTAATGTTTCT	36833	CAAGCAAGAGGAAACGTCAGC
8188	QARNTSL	22511	CAGGCGCGGAATACTTCTTTG	36834	CAAGCAAGAAACACAAGCCTC
8189	QARPGIL	22512	CAGGCTAGGCCGGGTATTCTT	36835	CAAGCAAGACCAGGAATCCTC
8190	QARVFDS	22513	CAGGCTCGTGTGTTTGATTCT	36836	CAAGCAAGAGTCTTCGACAGC
8191	QASANRA	22514	CAGGCTAGTGCGAATCGGGCG	36837	CAAGCAAGCGCAAACAGAGCA
8192	QASIIRA	22515	CAGGCGTCGATTATTAGGGCG	36838	CAAGCAAGCATCATCAGAGCA
8193	QASKLPS	22516	CAGGCGTCGAAGCTGCCTTCT	36839	CAAGCAAGCAAACTCCCAAGC
8194	QASPAYG	22517	CAGGCTAGTCCTGCTTATGGT	36840	CAAGCAAGCCCAGCATACGGA
8195	QASQSLS	22518	CAGGCTAGTCAGTCTCTTTCG	36841	CAAGCAAGCCAAAGCCTCAGC
8196	QATANSL	22519	CAGGCGACTGCTAATTCTTTG	36842	CAAGCAACAGCAAACAGCCTC
8197	QATFGDD	22520	CAGGCTACTTTTGGGGATGAT	36843	CAAGCAACATTCGGAGACGAC
8198	QATNQSL	22521	CAGGCGACTAATCAGTCTTTG	36844	CAAGCAACAAACCAAAGCCTC
8199	QATPLTT	22522	CAGGCTACTCCGCTTACGACT	36845	CAAGCAACACCACTCACAACA
8200	QATQLGH	22523	CAGGCGACGCAGCTGGGGCAT	36846	CAAGCAACACAACTCGGACAC
8201	QAVRDKD	22524	CAGGCGGTTAGGGATAAGGAT	36847	CAAGCAGTCAGAGACAAAGAC
8202	QAVRPDS	22525	CAGGCGGTTAGGCCTGATTCT	36848	CAAGCAGTCAGACCAGACAGC
8203	QAYHNSL	22526	CAGGCGTATCATAATTCTTTG	36849	CAAGCATACCACAACAGCCTC
8204	QAYVNSL	22527	CAGGCGTATGTTAATTCTTTG	36850	CAAGCATACGTCAACAGCCTC
8205	QCSDRRA	22528	CAGTGTTCGGATCGTAGGGCT	36851	CAATGCAGCGACAGAAGAGCA
8206	QDADPAH	22529	CAGGATGCTGATCCGGCGCAT	36852	CAAGACGCAGACCCAGCACAC
8207	QDDFRSK	22530	CAGGATGATTTTCGGTCGAAG	36853	CAAGACGACTTCAGAAGCAAA
8208	QDDVQKL	22531	CAGGATGATGTGCAGAAGTTG	36854	CAAGACGACGTCCAAAAACTC
8209	QDFDDVH	22532	CAGGATTTTGATGATGTTCAT	36855	CAAGACTTCGACGACGTCCAC
8210	QDGIRIM	22533	CAGGATGGTATTCGGATTATG	36856	CAAGACGGAATCAGAATCATG
8211	QDIRAFA	22534	CAGGATATTCGGGCTTTTGCG	36857	CAAGACATCAGAGCATTCGCA
8212	QDRALQP	22535	CAGGATCGTGCTCTTCAGCCG	36858	CAAGACAGAGCACTCCAACCA
8213	QDRLADT	22536	CAGGATCGGCTGGCGGATACT	36859	CAAGACAGACTCGCAGACACA
8214	QDRMSLR	22537	CAGGATCGTATGAGTCTGAGG	36860	CAAGACAGAATGAGCCTCAGA
8215	QDRSTNF	22538	CAGGATCGTTCTACGAATTTT	36861	CAAGACAGAAGCACAAACTTC
8216	QDSCLLP	22539	CAGGATAGTTGTCTTTTGCCT	36862	CAAGACAGCTGCCTCCTCCCA
8217	QDSYLGY	22540	CAGGATAGTTATCTGGGTTAT	36863	CAAGACAGCTACCTCGGATAC
8218	QDTLTRF	22541	CAGGATACTTTGACTAGGTTT	36864	CAAGACACACTCACAAGATTC
8219	QDTTSLD	22542	CAGGATACGACGTCGCTGGAT	36865	CAAGACACAACAAGCCTCGAC
8220	QDTYTHK	22543	CAGGATACTTATACTCATAAG	36866	CAAGACACATACACACACAAA
8221	QDVGLTV	22544	CAGGATGTTGGTCTTACTGTG	36867	CAAGACGTCGGACTCACAGTC
8222	QDVPSCG	22545	CAGGATGTTCCGAGTTGTGGG	36868	CAAGACGTCCCAAGCTGCGGA
8223	QDYKKPS	22546	CAGGATTATAAGAAGCCTTCT	36869	CAAGACTACAAAAAACCAAGC
8224	QDYRLPE	22547	CAGGATTATCGGCTGCCTGAG	36870	CAAGACTACAGACTCCCAGAA

8225	QEAARVE	22548	CAGGAGGCTGCTAGGGTGGAG	36871	CAAGAAGCAGCAAGAGTCGAA
8226	QEDTWSG	22549	CAGGAGGATACGTGGTCGGGG	36872	CAAGAAGACACATGGAGCGGA
8227	QEGAVMN	22550	CAGGAGGGTGCGGTGATGAAT	36873	CAAGAAGGAGCAGTCATGAAC
8228	QELLKGY	22551	CAGGAGTTGCTGAAGGGTTAT	36874	CAAGAACTCCTCAAAGGATAC
8229	QELVLTR	22552	CAGGAGTTGGTGTTGACTCGG	36875	CAAGAACTCGTCCTCACAAGA
8230	QEPAVSI	22553	CAGGAGCCTGCTGTTTCTATT	36876	CAAGAACCAGCAGTCAGCATC
8231	QEPMSGA	22554	CAGGAGCCGATGTCTGGTGCG	36877	CAAGAACCAATGAGCGGAGCA
8232	QEPRGMH	22555	CAGGAGCCGCGGGGGATGCAT	36878	CAAGAACCAAGAGGAATGCAC
8233	QERRMGP	22556	CAGGAGAGGAGGATGGGTCCG	36879	CAAGAAAGAAGAATGGGACCA
8234	QESSHGP	22557	CAGGAGTCGAGTCATGGTCCT	36880	CAAGAAAGCAGCCACGGACCA
8235	QESTGVW	22558	CAGGAGTCGACGGGGGTTTGG	36881	CAAGAAAGCACAGGAGTCTGG
8236	QEVANNP	22559	CAGGAGGTGGCTAATAATCCG	36882	CAAGAAGTCGCAAACAACCCA
8237	QEVHITG	22560	CAGGAGGTTCATATTACGGGG	36883	CAAGAAGTCCACATCACAGGA
8238	QEVPGRI	22561	CAGGAGGTTCCGGGTAGGATT	36884	CAAGAAGTCCCAGGAAGAATC
8239	QEWNATA	22562	CAGGAGTGGAATGCTACGGCT	36885	CAAGAATGGAACGCAACAGCA
8240	QEYVSKS	22563	CAGGAGTATGTTTCTAAGTCG	36886	CAAGAATACGTCAGCAAAAGC
8241	QFDKMMP	22564	CAGTTTGATAAGATGATGCCT	36887	CAATTCGACAAAATGATGCCA
8242	QFDLSPA	22565	CAGTTTGATCTGTCTCCTGCT	36888	CAATTCGACCTCAGCCCAGCA
8243	QFENACV	22566	CAGTTTGAGAATGCTTGTGTG	36889	CAATTCGAAAACGCATGCGTC
8244	QFGMPRD	22567	CAGTTTGGGATGCCGCGGGAT	36890	CAATTCGGAATGCCAAGAGAC
8245	QFLKHEE	22568	CAGTTTCTTAAGCATGAGGAG	36891	CAATTCCTCAAACACGAAGAA
8246	QFMGGVN	22569	CAGTTTATGGGTGGTGTGAAT	36892	CAATTCATGGGAGGAGTCAAC
8247	QFNETLT	22570	CAGTTTAATGAGACTTTGACG	36893	CAATTCAACGAAACACTCACA
8248	QFNPSIR	22571	CAGTTTAATCCGAGTATTCGT	36894	CAATTCAACCCAAGCATCAGA
8249	QFNSPMP	22572	CAGTTTAATTCTCCGATGCCG	36895	CAATTCAACAGCCCAATGCCA
8250	QFPGSMP	22573	CAGTTTCCTGGGTCTATGCCT	36896	CAATTCCCAGGAAGCATGCCA
8251	QFPPANS	22574	CAGTTTCCTCCTGCGAATTCT	36897	CAATTCCCACCAGCAAACAGC
8252	QFQSSQA	22575	CAGTTTCAGTCTTCGCAGGCT	36898	CAATTCCAAAGCAGCCAAGCA
8253	QFRAEIT	22576	CAGTTTCGTGCTGAGATTACT	36899	CAATTCAGAGCAGAAATCACA
8254	QFSLNAE	22577	CAGTTTTCGTTGAATGCGGAG	36900	CAATTCAGCCTCAACGCAGAA
8255	QFSPTSR	22578	CAGTTTAGTCCGACGTCGCGG	36901	CAATTCAGCCCAACAAGCAGA
8256	QFSSGSP	22579	CAGTTTTCGTCGGGGTCGCCG	36902	CAATTCAGCAGCGGAAGCCCA
8257	QGADSRL	22580	CAGGGGGCTGATAGTCGGTTG	36903	CAAGGAGCAGACAGCAGACTC
8258	QGEHFAV	22581	CAGGGGGAGCATTTTGCGGTT	36904	CAAGGAGAACACTTCGCAGTC
8259	QGEKPDA	22582	CAGGGGGAGAAGCCTGATGCG	36905	CAAGGAGAAAAACCAGACGCA
8260	QGGSGPY	22583	CAGGGTGGTTCTGGTCCGTAT	36906	CAAGGAGGAAGCGGACCATAC
8261	QGHDDDI	22584	CAGGGTCATGATGATGATATT	36907	CAAGGACACGACGACGACATC
8262	QGIEHRP	22585	CAGGGTATTGAGCATAGGCCG	36908	CAAGGAATCGAACACAGACCA
8263	QGITCSP	22586	CAGGGGATTACTTGTTCGCCT	36909	CAAGGAATCACATGCAGCCCA
8264	QGKQLTA	22587	CAGGGTAAGCAGCTGACGGCT	36910	CAAGGAAAACAACTCACAGCA
8265	QGKVDQR	22588	CAGGGTAAGGTTGATCAGCGT	36911	CAAGGAAAAGTCGACCAAAGA
8266	QGLVANF	22589	CAGGGTCTGGTTGCGAATTTT	36912	CAAGGACTCGTCGCAAACTTC
8267	QGMSFGP	22590	CAGGGTATGTCGTTTGGTCCT	36913	CAAGGAATGAGCTTCGGACCA
8268	QGNRSPH	22591	CAGGGGAATAGGAGTCCTCAT	36914	CAAGGAAACAGAAGCCCACAC
8269	QGPANVV	22592	CAGGGTCCGGCGAATGTTGTG	36915	CAAGGACCAGCAAACGTCGTC

8270	QGPPVTN	22593	CAGGGTCCGCCTGTTACGAAT	36916	CAAGGACCACCAGTCACAAAC
8271	QGPRAAP	22594	CAGGGGCCGCGGGCTGCTCCT	36917	CAAGGACCAAGAGCAGCACCA
8272	QGPSMLT	22595	CAGGGTCCTTCTATGTTGACT	36918	CAAGGACCAAGCATGCTCACA
8273	QGQHPMT	22596	CAGGGTCAGCATCCTATGACT	36919	CAAGGACAACACCCAATGACA
8274	QGQPIDR	22597	CAGGGTCAGCCGATTGATAGG	36920	CAAGGACAACCAATCGACAGA
8275	QGREWVQ	22598	CAGGGTAGGGAGTGGGTGCAG	36921	CAAGGAAGAGAATGGGTCCAA
8276	QGRSLPA	22599	CAGGGTCGTTCGTTGCCGGCG	36922	CAAGGAAGAAGCCTCCCAGCA
8277	QGRTPQA	22600	CAGGGGCGGACTCCTCAGGCG	36923	CAAGGAAGAACACCACAAGCA
8278	QGSHSST	22601	CAGGGGTCTCATTCGAGTACT	36924	CAAGGAAGCCACAGCAGCACA
8279	QGSRTNP	22602	CAGGGTTCGCGTACGAATCCG	36925	CAAGGAAGCAGAACAAACCCA
8280	QGSTAVT	22603	CAGGGGTCTACTGCGGTGACG	36926	CAAGGAAGCACAGCAGTCACA
8281	QGSTWSP	22604	CAGGGGAGTACTTGGAGTCCG	36927	CAAGGAAGCACATGGAGCCCA
8282	QGTLKNI	22605	CAGGGGACTCTTAAGAATATT	36928	CAAGGAACACTCAAAAACATC
8283	QGVAGHA	22606	CAGGGGGTTGCGGGGCATGCT	36929	CAAGGAGTCGCAGGACACGCA
8284	QGVLLVT	22607	CAGGGTGTTTTGCTGGTTACT	36930	CAAGGAGTCCTCCTCGTCACA
8285	QGVRQAV	22608	CAGGGTGTTCGTCAGGCTGTT	36931	CAAGGAGTCAGACAAGCAGTC
8286	QGVRTTS	22609	CAGGGTGTGCGTACGACGTCT	36932	CAAGGAGTCAGAACAACAAGC
8287	QHERMPS	22610	CAGCATGAGCGGATGCCTTCG	36933	CAACACGAAAGAATGCCAAGC
8288	QHFNQAE	22611	CAGCATTTTAATCAGGCTGAG	36934	CAACACTTCAACCAAGCAGAA
8289	QHGAPTW	22612	CAGCATGGTGCTCCGACTTGG	36935	CAACACGGAGCACCAACATGG
8290	QHLHTLK	22613	CAGCATCTGCATACGCTGAAG	36936	CAACACCTCCACACACTCAAA
8291	QHLNSYV	22614	CAGCATTTGAATTCGTATGTG	36937	CAACACCTCAACAGCTACGTC
8292	QHLPRTT	22615	CAGCATTTGCCGAGGACTACG	36938	CAACACCTCCCAAGAACAACA
8293	QHLVHDA	22616	CAGCATCTTGTTCATGATGCT	36939	CAACACCTCGTCCACGACGCA
8294	QHSLAVT	22617	CAGCATTCTCTTGCTGTTACT	36940	CAACACAGCCTCGCAGTCACA
8295	QHSSLGI	22618	CAGCATTCGTCGCTGGGGATT	36941	CAACACAGCAGCCTCGGAATC
8296	QHSSMAR	22619	CAGCATTCGAGTATGGCGAGG	36942	CAACACAGCAGCATGGCAAGA
8297	QHTAAAL	22620	CAGCATACTGCTGCTGCGCTT	36943	CAACACACAGCAGCAGCACTC
8298	QHTLTIS	22621	CAGCATACTTTGACTATTAGT	36944	CAACACACACTCACAATCAGC
8299	QHTRVVF	22622	CAGCATACTAGGGTGGTTTTT	36945	CAACACACAAGAGTCGTCTTC
8300	QHTTKQS	22623	CAGCATACGACTAAGCAGTCT	36946	CAACACACAACAAAACAAAGC
8301	QHVSSTG	22624	CAGCATGTGTCTTCGACTGGT	36947	CAACACGTCAGCAGCACAGGA
8302	QIARSSI	22625	CAGATTGCTCGTAGTTCTATT	36948	CAAATCGCAAGAAGCAGCATC
8303	QIDYRAP	22626	CAGATTGATTATCGGGCGCCG	36949	CAAATCGACTACAGAGCACCA
8304	QIETLAH	22627	CAGATTGAGACTCTGGCTCAT	36950	CAAATCGAAACACTCGCACAC
8305	QIFGRTP	22628	CAGATTTTTGGGAGGACTCCT	36951	CAAATCTTCGGAAGAACACCA
8306	QIGFGTS	22629	CAGATTGGGTTTGGGACTAGT	36952	CAAATCGGATTCGGAACAAGC
8307	QIGTYLA	22630	CAGATTGGTACGTATTTGGCT	36953	CAAATCGGAACATACCTCGCA
8308	QIHESGE	22631	CAGATTCATGAGTCTGGTGAG	36954	CAAATCCACGAAAGCGGAGAA
8309	QIMADTR	22632	CAGATTATGGCGGATACTCGG	36955	CAAATCATGGCAGACACAAGA
8310	QINFPMD	22633	CAGATTAATTTTCCGATGGAT	36956	CAAATCAACTTCCCAATGGAC
8311	QINSNKT	22634	CAGATTAATTCGAATAAGACT	36957	CAAATCAACAGCAACAAAACA
8312	QINSTTG	22635	CAGATTAATTCGACGACGGGT	36958	CAAATCAACAGCACAACAGGA
8313	QIPIIES	22636	CAGATTCCGATTATTGAGTCG	36959	CAAATCCCAATCATCGAAAGC
8314	QIPKAPG	22637	CAGATTCCTAAGGCGCCGGGT	36960	CAAATCCCAAAAGCACCAGGA

8315	QIPNSFS	22638	CAGATTCCTAATTCTTTTAGT	36961	CAAATCCCAAACAGCTTCAGC
8316	QIPTTLA	22639	CAGATTCCTACTACTTTGGCT	36962	CAAATCCCAACAACACTCGCA
8317	QIRNSTE	22640	CAGATTCGGAATTCTACGGAG	36963	CAAATCAGAAACAGCACAGAA
8318	QISQPKI	22641	CAGATTAGTCAGCCGAAGATT	36964	CAAATCAGCCAACCAAAAATC
8319	QISTLTF	22642	CAGATTTCTACGTTGACTTTT	36965	CAAATCAGCACACTCACATTC
8320	QIVPQGP	22643	CAGATTGTGCCGCAGGGTCCT	36966	CAAATCGTCCCACAAGGACCA
8321	QIVTGLS	22644	CAGATTGTTACTGGGCTTAGT	36967	CAAATCGTCACAGGACTCAGC
8322	QIYGSES	22645	CAGATTTATGGGTCTGAGTCG	36968	CAAATCTACGGAAGCGAAAGC
8323	QKAASAD	22646	CAGAAGGCGGCTTCGGCTGAT	36969	CAAAAAGCAGCAAGCGCAGAC
8324	QKAIDSL	22647	CAGAAGGCGATTGATTCGTTG	36970	CAAAAAGCAATCGACAGCCTC
8325	QKELIVD	22648	CAGAAGGAGCTGATTGTTGAT	36971	CAAAAAGAACTCATCGTCGAC
8326	QKEPGPS	22649	CAGAAGGAGCCGGGTCCTTCT	36972	CAAAAAGAACCAGGACCAAGC
8327	QKFADKG	22650	CAGAAGTTTGCTGATAAGGGT	36973	CAAAAATTCGCAGACAAAGGA
8328	QKHDIRS	22651	CAGAAGCATGATATTAGGAGT	36974	CAAAAACACGACATCAGAAGC
8329	QKHNCPV	22652	CAGAAGCATAATTGTCCTGTG	36975	CAAAAACACAACTGCCCAGTC
8330	QKKDPIP	22653	CAGAAGAAGGATCCGATTCCT	36976	CAAAAAAAAGACCCAATCCCA
8331	QKMQHYD	22654	CAGAAGATGCAGCATTATGAT	36977	CAAAAAATGCAACACTACGAC
8332	QKPATRD	22655	CAGAAGCCTGCTACGCGGGAT	36978	CAAAAACCAGCAACAAGAGAC
8333	QKSNNAL	22656	CAGAAGTCGAATAATGCGCTT	36979	CAAAAAAGCAACAACGCACTC
8334	QKVIAEV	22657	CAGAAGGTTATTGCGGAGGTG	36980	CAAAAAGTCATCGCAGAAGTC
8335	QKVMQPG	22658	CAGAAGGTTATGCAGCCGGGG	36981	CAAAAAGTCATGCAACCAGGA
8336	QLANHVG	22659	CAGTTGGCGAATCATGTGGGT	36982	CAACTCGCAAACCACGTCGGA
8337	QLAPPKT	22660	CAGTTGGCGCCGCCGAAGACT	36983	CAACTCGCACCACCAAAAACA
8338	QLASNAF	22661	CAGCTGGCGTCTAATGCGTTT	36984	CAACTCGCAAGCAACGCATTC
8339	QLASVRI	22662	CAGCTTGCGAGTGTGAGGATT	36985	CAACTCGCAAGCGTCAGAATC
8340	QLDFDLV	22663	CAGCTGGATTTTGATTTGGTG	36986	CAACTCGACTTCGACCTCGTC
8341	QLDSLSV	22664	CAGCTGGATTCTCTTTCGGTT	36987	CAACTCGACAGCCTCAGCGTC
8342	QLGPSVP	22665	CAGCTGGGGCCTTCGGTTCCG	36988	CAACTCGGACCAAGCGTCCCA
8343	QLGSLDG	22666	CAGCTGGGGTCGTTGGATGGT	36989	CAACTCGGAAGCCTCGACGGA
8344	QLGVRSQ	22667	CAGCTGGGGGTGCGTTCGCAG	36990	CAACTCGGAGTCAGAAGCCAA
8345	QLHYANE	22668	CAGCTGCATTATGCTAATGAG	36991	CAACTCCACTACGCAAACGAA
8346	QLIKTPG	22669	CAGCTTATTAAGACTCCTGGT	36992	CAACTCATCAAAACACCAGGA
8347	QLKAVEF	22670	CAGCTGAAGGCTGTTGAGTTT	36993	CAACTCAAAGCAGTCGAATTC
8348	QLKPLYF	22671	CAGTTGAAGCCTCTGTATTTT	36994	CAACTCAAACCACTCTACTTC
8349	QLKTEML	22672	CAGTTGAAGACTGAGATGCTG	36995	CAACTCAAAACAGAAATGCTC
8350	QLKTSLS	22673	CAGTTGAAGACGTCGCTGTCG	36996	CAACTCAAAACAAGCCTCAGC
8351	QLLRTGD	22674	CAGCTGCTTCGGACGGGTGAT	36997	CAACTCCTCAGAACAGGAGAC
8352	QLLRVTG	22675	CAGCTTTTGCGTGTGACGGGT	36998	CAACTCCTCAGAGTCACAGGA
8353	QLMRLGV	22676	CAGTTGATGAGGCTGGGGGTG	36999	CAACTCATGAGACTCGGAGTC
8354	QLNDLAR	22677	CAGTTGAATGATCTTGCGCGG	37000	CAACTCAACGACCTCGCAAGA
8355	QLNRPPS	22678	CAGCTGAATCGTCCGCCTTCT	37001	CAACTCAACAGACCACCAAGC
8356	QLPADNA	22679	CAGCTTCCGGCGGATAATGCT	37002	CAACTCCCAGCAGACAACGCA
8357	QLPHDSA	22680	CAGTTGCCGCATGATTCTGCT	37003	CAACTCCCACACGACAGCGCA
8358	QLPHVKV	22681	CAGTTGCCTCATGTGAAGGTT	37004	CAACTCCCACACGTCAAAGTC
8359	QLPHVSM	22682	CAGCTGCCGCATGTTTCTATG	37005	CAACTCCCACACGTCAGCATG

8360	QLPLTPH	22683	CAGCTGCCGTTGACTCCGCAT	37006	CAACTCCCACTCACACCACAC
8361	QLPSTRS	22684	CAGCTTCCTAGTACGCGGTCT	37007	CAACTCCCAAGCACAAGAAGC
8362	QLPTKLD	22685	CAGCTTCCTACTAAGCTGGAT	37008	CAACTCCCAACAAAACTCGAC
8363	QLPVNSS	22686	CAGTTGCCGGTTAATTCTAGT	37009	CAACTCCCAGTCAACAGCAGC
8364	QLQITTG	22687	CAGCTGCAGATTACTACTGGT	37010	CAACTCCAAATCACAACAGGA
8365	QLQLKTA	22688	CAGCTTCAGCTTAAGACTGCT	37011	CAACTCCAACTCAAAACAGCA
8366	QLQTDKT	22689	CAGTTGCAGACTGATAAGACG	37012	CAACTCCAAACAGACAAAACA
8367	QLRGSYP	22690	CAGTTGCGTGGGTCTTATCCG	37013	CAACTCAGAGGAAGCTACCCA
8368	QLRHTDF	22691	CAGTTGCGTCATACTGATTTT	37014	CAACTCAGACACACAGACTTC
8369	QLRPANS	22692	CAGCTGAGGCCGGCTAATTCT	37015	CAACTCAGACCAGCAAACAGC
8370	QLRPEGL	22693	CAGCTGAGGCCTGAGGGTCTG	37016	CAACTCAGACCAGAAGGACTC
8371	QLSAPAA	22694	CAGCTGTCTGCTCCTGCGGCT	37017	CAACTCAGCGCACCAGCAGCA
8372	QLSASTR	22695	CAGCTTTCTGCTTCGACGCGT	37018	CAACTCAGCGCAAGCACAAGA
8373	QLSKDVS	22696	CAGCTTTCGAAGGATGTTTCT	37019	CAACTCAGCAAAGACGTCAGC
8374	QLSLEPF	22697	CAGCTTTCTCTGGAGCCTTTT	37020	CAACTCAGCCTCGAACCATTC
8375	QLSREEP	22698	CAGTTGAGTCGGGAGGAGCCT	37021	CAACTCAGCAGAGAAGAACCA
8376	QLSRPVP	22699	CAGTTGTCGCGGCCTGTTCCG	37022	CAACTCAGCAGACCAGTCCCA
8377	QLSSAPT	22700	CAGCTGTCTTCGGCTCCTACT	37023	CAACTCAGCAGCGCACCAACA
8378	QLSTTQG	22701	CAGTTGTCGACGACTCAGGGT	37024	CAACTCAGCACAACACAAGGA
8379	QLTAGVP	22702	CAGTTGACTGCGGGTGTGCCG	37025	CAACTCACAGCAGGAGTCCCA
8380	QLTPVHH	22703	CAGCTTACGCCGGTTCATCAT	37026	CAACTCACACCAGTCCACCAC
8381	QLTRGNY	22704	CAGCTTACTCGGGGTAATTAT	37027	CAACTCACAAGAGGAAACTAC
8382	QLTVHTL	22705	CAGTTGACTGTGCATACGCTT	37028	CAACTCACAGTCCACACACTC
8383	QLVQQHL	22706	CAGCTGGTGCAGCAGCATTTG	37029	CAACTCGTCCAACAACACCTC
8384	QMAETSR	22707	CAGATGGCGGAGACTAGTAGG	37030	CAAATGGCAGAAACAAGCAGA
8385	QMARTMS	22708	CAGATGGCTCGTACTATGTCT	37031	CAAATGGCAAGAACAATGAGC
8386	QMASIPS	22709	CAGATGGCGTCGATTCCGTCG	37032	CAAATGGCAAGCATCCCAAGC
8387	QMDDAPS	22710	CAGATGGATGATGCTCCGTCG	37033	CAAATGGACGACGCACCAAGC
8388	QMDNRNP	22711	CAGATGGATAATCGGAATCCT	37034	CAAATGGACAACAGAAACCCA
8389	QMDRSRV	22712	CAGATGGATCGTTCGCGTGTG	37035	CAAATGGACAGAAGCAGAGTC
8390	QMEAALY	22713	CAGATGGAGGCGGCGCTTTAT	37036	CAAATGGAAGCAGCACTCTAC
8391	QMHSSLH	22714	CAGATGCATAGTTCTCTTCAT	37037	CAAATGCACAGCAGCCTCCAC
8392	QMKNQAT	22715	CAGATGAAGAATCAGGCGACT	37038	CAAATGAAAAACCAAGCAACA
8393	QMLDKNH	22716	CAGATGCTTGATAAGAATCAT	37039	CAAATGCTCGACAAAAACCAC
8394	QMNALPM	22717	CAGATGAATGCTCTTCCTATG	37040	CAAATGAACGCACTCCCAATG
8395	QMNMPND	22718	CAGATGAATATGCCGAATGAT	37041	CAAATGAACATGCCAAACGAC
8396	QMPATAK	22719	CAGATGCCTGCTACGGCGAAG	37042	CAAATGCCAGCAACAGCAAAA
8397	QMPEGTS	22720	CAGATGCCTGAGGGGACTAGT	37043	CAAATGCCAGAAGGAACAAGC
8398	QMPPNSN	22721	CAGATGCCGCCTAATTCTAAT	37044	CAAATGCCACCAAACAGCAAC
8399	QMPSFGE	22722	CAGATGCCTTCTTTTGGTGAG	37045	CAAATGCCAAGCTTCGGAGAA
8400	QMPSMSG	22723	CAGATGCCGTCGATGTCGGGT	37046	CAAATGCCAAGCATGAGCGGA
8401	QMPSSRS	22724	CAGATGCCGTCGAGTCGTTCT	37047	CAAATGCCAAGCAGCAGAAGC
8402	QMPTRTT	22725	CAGATGCCTACGAGGACTACT	37048	CAAATGCCAACAAGAACAACA
8403	QMQRPLI	22726	CAGATGCAGCGTCCTCTGATT	37049	CAAATGCAAAGACCACTCATC
8404	QMSIVVP	22727	CAGATGAGTATTGTTGTGCCT	37050	CAAATGAGCATCGTCGTCCCA

8405	QMTILKQ	22728	CAGATGACGATTTTGAAGCAG	37051	CAAATGACAATCCTCAAACAA
8406	QNEALVG	22729	CAGAATGAGGCGTTGGTGGGG	37052	CAAAACGAAGCACTCGTCGGA
8407	QNELFRA	22730	CAGAATGAGCTGTTTCGGGCG	37053	CAAAACGAACTCTTCAGAGCA
8408	QNGLPQT	22731	CAGAATGGGCTGCCTCAGACG	37054	CAAAACGGACTCCCACAAACA
8409	QNHPVTK	22732	CAGAATCATCCGGTGACGAAG	37055	CAAAACCACCCAGTCACAAAA
8410	QNILAHW	22733	CAGAATATTCTTGCGCATTGG	37056	CAAAACATCCTCGCACACTGG
8411	QNKSNSY	22734	CAGAATAAGTCGAATTCGTAT	37057	CAAAACAAAAGCAACAGCTAC
8412	QNLPSAY	22735	CAGAATCTGCCTAGTGCTTAT	37058	CAAAACCTCCCAAGCGCATAC
8413	QNLTFGM	22736	CAGAATCTGACTTTTGGGATG	37059	CAAAACCTCACATTCGGAATG
8414	QNLTGKS	22737	CAGAATCTGACGGGTAAGTCG	37060	CAAAACCTCACAGGAAAAAGC
8415	QNMVCVA	22738	CAGAATATGGTTTGTGTTGCT	37061	CAAAACATGGTCTGCGTCGCA
8416	QNPNISG	22739	CAGAATCCGAATATTTCGGGG	37062	CAAAACCCAAACATCAGCGGA
8417	QNPPHIQ	22740	CAGAATCCTCCTCATATTCAG	37063	CAAAACCCACCACACATCCAA
8418	QNPRLPL	22741	CAGAATCCTCGGCTTCCGCTT	37064	CAAAACCCAAGACTCCCACTC
8419	QNPRTGQ	22742	CAGAATCCTCGGACTGGTCAG	37065	CAAAACCCAAGAACAGGACAA
8420	QNPTYKL	22743	CAGAATCCGACGTATAAGCTT	37066	CAAAACCCAACATACAAACTC
8421	QNRIVEP	22744	CAGAATCGGATTGTGGAGCCG	37067	CAAAACAGAATCGTCGAACCA
8422	QNSAPAI	22745	CAGAATTCTGCTCCTGCGATT	37068	CAAAACAGCGCACCAGCAATC
8423	QNTSSGL	22746	CAGAATACTTCTAGTGGTCTT	37069	CAAAACACAAGCAGCGGACTC
8424	QNVMHMS	22747	CAGAATGTTATGCATATGAGT	37070	CAAAACGTCATGCACATGAGC
8425	QNVQRYP	22748	CAGAATGTTCAGCGTTATCCG	37071	CAAAACGTCCAAAGATACCCA
8426	QNVRSQT	22749	CAGAATGTTCGGTCGCAGACG	37072	CAAAACGTCAGAAGCCAAACA
8427	QNYLKTE	22750	CAGAATTATTTGAAGACTGAG	37073	CAAAACTACCTCAAAACAGAA
8428	QPAAGHF	22751	CAGCCTGCGGCGGGTCATTTT	37074	CAACCAGCAGCAGGACACTTC
8429	QPAHCSD	22752	CAGCCTGCGCATTGTTCTGAT	37075	CAACCAGCACACTGCAGCGAC
8430	QPAKGYP	22753	CAGCCGGCGAAGGGTTATCCT	37076	CAACCAGCAAAAGGATACCCA
8431	QPAPTLR	22754	CAGCCTGCTCCGACGCTGAGG	37077	CAACCAGCACCAACACTCAGA
8432	QPATEVL	22755	CAGCCTGCTACTGAGGTTCTT	37078	CAACCAGCAACAGAAGTCCTC
8433	QPAVMES	22756	CAGCCTGCTGTGATGGAGTCG	37079	CAACCAGCAGTCATGGAAAGC
8434	QPDPSPP	22757	CAGCCGGATCCTTCTCCGCCG	37080	CAACCAGACCCAAGCCCACCA
8435	QPFYSDE	22758	CAGCCTTTTTATTCTGATGAG	37081	CAACCATTCTACAGCGACGAA
8436	QPGVSHT	22759	CAGCCGGGGGTGAGTCATACT	37082	CAACCAGGAGTCAGCCACACA
8437	QPHGDPM	22760	CAGCCGCATGGGGATCCTATG	37083	CAACCACACGGAGACCCAATG
8438	QPIAHTD	22761	CAGCCGATTGCTCATACGGAT	37084	CAACCAATCGCACACACAGAC
8439	QPIQTRA	22762	CAGCCGATTCAGACTCGTGCG	37085	CAACCAATCCAAACAAGAGCA
8440	QPISATL	22763	CAGCCTATTTCGGCTACGCTG	37086	CAACCAATCAGCGCAACACTC
8441	QPKFCGA	22764	CAGCCTAAGTTTTGTGGGGCT	37087	CAACCAAAATTCTGCGGAGCA
8442	QPKLSAS	22765	CAGCCTAAGCTGAGTGCGTCG	37088	CAACCAAAACTCAGCGCAAGC
8443	QPKSSGV	22766	CAGCCGAAGTCTTCGGGGGTG	37089	CAACCAAAAAGCAGCGGAGTC
8444	QPLARAS	22767	CAGCCGCTGGCGCGGGCGAGT	37090	CAACCACTCGCAAGAGCAAGC
8445	QPLASKT	22768	CAGCCTCTGGCTTCGAAGACG	37091	CAACCACTCGCAAGCAAAACA
8446	QPLLSAS	22769	CAGCCTCTGTTGAGTGCTTCG	37092	CAACCACTCCTCAGCGCAAGC
8447	QPLTMRS	22770	CAGCCGTTGACTATGCGTAGT	37093	CAACCACTCACAATGAGAAGC
8448	QPLTSDT	22771	CAGCCGCTGACTTCTGATACG	37094	CAACCACTCACAAGCGACACA
8449	QPMLVVS	22772	CAGCCTATGCTTGTTGTGAGT	37095	CAACCAATGCTCGTCGTCAGC

8450	QPNPVAH	22773	CAGCCGAATCCGGTTGCGCAT	37096	CAACCAAACCCAGTCGCACAC
8451	QPNYPCA	22774	CAGCCTAATTATCCGTGTGCT	37097	CAACCAAACTACCCATGCGCA
8452	QPPGMSS	22775	CAGCCTCCTGGTATGTCTAGT	37098	CAACCACCAGGAATGAGCAGC
8453	QPPNTED	22776	CAGCCTCCTAATACTGAGGAT	37099	CAACCACCAAACACAGAAGAC
8454	QPPRSQL	22777	CAGCCTCCGCGTAGTCAGCTG	37100	CAACCACCAAGAAGCCAACTC
8455	QPPSPIS	22778	CAGCCGCCTTCGCCGATTAGT	37101	CAACCACCAAGCCCAATCAGC
8456	QPPYLSG	22779	CAGCCGCCGTATCTTAGTGGT	37102	CAACCACCATACCTCAGCGGA
8457	QPQGREP	22780	CAGCCGCAGGGTCGGGAGCCG	37103	CAACCACAAGGAAGAGAACCA
8458	QPRAEVP	22781	CAGCCGCGTGCGGAGGTGCCT	37104	CAACCAAGAGCAGAAGTCCCA
8459	QPRDAGS	22782	CAGCCGCGGGATGCTGGGAGT	37105	CAACCAAGAGACGCAGGAAGC
8460	QPRLLDN	22783	CAGCCTCGGCTTTTGGATAAT	37106	CAACCAAGACTCCTCGACAAC
8461	QPRTLST	22784	CAGCCTAGGACTCTGTCGACT	37107	CAACCAAGAACACTCAGCACA
8462	QPSAAAR	22785	CAGCCGTCGGCTGCTGCTCGG	37108	CAACCAAGCGCAGCAGCAAGA
8463	QPSHGTP	22786	CAGCCTAGTCATGGGACGCCT	37109	CAACCAAGCCACGGAACACCA
8464	QPSLVTL	22787	CAGCCGAGTCTTGTGACGCTT	37110	CAACCAAGCCTCGTCACACTC
8465	QPSMEPQ	22788	CAGCCGAGTATGGAGCCTCAG	37111	CAACCAAGCATGGAACCACAA
8466	QPSMQSE	22789	CAGCCTTCTATGCAGTCTGAG	37112	CAACCAAGCATGCAAAGCGAA
8467	QPSNMGH	22790	CAGCCTTCGAATATGGGGCAT	37113	CAACCAAGCAACATGGGACAC
8468	QPSPGFH	22791	CAGCCTTCTCCTGGGTTTCAT	37114	CAACCAAGCCCAGGATTCCAC
8469	QPSSHPV	22792	CAGCCTAGTTCTCATCCTGTG	37115	CAACCAAGCAGCCACCCAGTC
8470	QPTDTLS	22793	CAGCCTACTGATACTCTGTCG	37116	CAACCAACAGACACACTCAGC
8471	QPTPTPH	22794	CAGCCTACGCCTACTCCTCAT	37117	CAACCAACACCAACACCACAC
8472	QPVNPMH	22795	CAGCCTGTGAATCCGATGCAT	37118	CAACCAGTCAACCCAATGCAC
8473	QPVNPRV	22796	CAGCCTGTGAATCCTCGGGTG	37119	CAACCAGTCAACCCAAGAGTC
8474	QPVVTPK	22797	CAGCCGGTTGTGACGCCGAAG	37120	CAACCAGTCGTCACACCAAAA
8475	QPYSSSL	22798	CAGCCTTATTCGAGTAGTCTT	37121	CAACCATACAGCAGCAGCCTC
8476	QQADATI	22799	CAGCAGGCTGATGCGACTATT	37122	CAACAAGCAGACGCAACAATC
8477	QQALSMA	22800	CAGCAGGCGCTTAGTATGGCT	37123	CAACAAGCACTCAGCATGGCA
8478	QQAPYRP	22801	CAGCAGGCTCCTTATCGGCCT	37124	CAACAAGCACCATACAGACCA
8479	QQEVARL	22802	CAGCAGGAGGTGGCTCGTTTG	37125	CAACAAGAAGTCGCAAGACTC
8480	QQGRCPD	22803	CAGCAGGGTCGTTGTCCTGAT	37126	CAACAAGGAAGATGCCCAGAC
8481	QQIIESL	22804	CAGCAGATTATTGAGTCGTTG	37127	CAACAAATCATCGAAAGCCTC
8482	QQKMSYD	22805	CAGCAGAAGATGAGTTATGAT	37128	CAACAAAAAATGAGCTACGAC
8483	QQRLMGE	22806	CAGCAGCGTTTGATGGGGGAG	37129	CAACAAAGACTCATGGGAGAA
8484	QQRLQMM	22807	CAGCAGAGGCTTCAGATGATG	37130	CAACAAAGACTCCAAATGATG
8485	QQRSSLL	22808	CAGCAGCGTAGTTCTCTGCTG	37131	CAACAAAGAAGCAGCCTCCTC
8486	QQRVNPE	22809	CAGCAGCGTGTTAATCCTGAG	37132	CAACAAAGAGTCAACCCAGAA
8487	QQSNQTK	22810	CAGCAGTCTAATCAGACGAAG	37133	CAACAAAGCAACCAAACAAAA
8488	QQTAGSD	22811	CAGCAGACGGCTGGTTCGGAT	37134	CAACAAACAGCAGGAAGCGAC
8489	QQTGYLP	22812	CAGCAGACTGGTTATTTGCCT	37135	CAACAAACAGGATACCTCCCA
8490	QQTHMGS	22813	CAGCAGACTCATATGGGTTCT	37136	CAACAAACACACATGGGAAGC
8491	QQTKQLQ	22814	CAGCAGACGAAGCAGCTGCAG	37137	CAACAAACAAAACAACTCCAA
8492	QQTKSTA	22815	CAGCAGACGAAGTCTACGGCT	37138	CAACAAACAAAAAGCACAGCA
8493	QQTNDRN	22816	CAGCAGACGAATGATCGGAAT	37139	CAACAAACAAACGACAGAAAC
8494	QQTRTSL	22817	CAGCAGACGCGTACGTCGTTG	37140	CAACAAACAAGAACAAGCCTC

8495	QQTSARE	22818	CAGCAGACTTCGGCTCGGGAG	37141	CAACAAACAAGCGCAAGAGAA
8496	QQVKSGD	22819	CAGCAGGTGAAGTCTGGGGAT	37142	CAACAAGTCAAAAGCGGAGAC
8497	QRAPDGW	22820	CAGCGTGCTCCGGATGGGTGG	37143	CAAAGAGCACCAGACGGATGG
8498	QRAPESM	22821	CAGCGTGCGCCTGAGTCGATG	37144	CAAAGAGCACCAGAAAGCATG
8499	QRAQLNS	22822	CAGAGGGCTCAGCTTAATTCG	37145	CAAAGAGCACAACTCAACAGC
8500	QRAVAPT	22823	CAGCGTGCTGTTGCGCCTACG	37146	CAAAGAGCAGTCGCACCAACA
8501	QRAVQVY	22824	CAGCGTGCTGTTCAGGTGTAT	37147	CAAAGAGCAGTCCAAGTCTAC
8502	QRDARLD	22825	CAGAGGGATGCTCGTTTGGAT	37148	CAAAGAGACGCAAGACTCGAC
8503	QRGKEAH	22826	CAGCGGGGTAAGGAGGCTCAT	37149	CAAAGAGGAAAAGAAGCACAC
8504	QRGPGNQ	22827	CAGCGGGGGCCTGGGAATCAG	37150	CAAAGAGGACCAGGAAACCAA
8505	QRGPMEL	22828	CAGAGGGGGCCGATGGAGCTT	37151	CAAAGAGGACCAATGGAACTC
8506	QRIGPAL	22829	CAGCGGATTGGGCCGGCGTTG	37152	CAAAGAATCGGACCAGCACTC
8507	QRIPVDV	22830	CAGCGGATTCCGGTTGATGTT	37153	CAAAGAATCCCAGTCGACGTC
8508	QRLASPS	22831	CAGCGTTTGGCTTCGCCTTCT	37154	CAAAGACTCGCAAGCCCAAGC
8509	QRLTAQE	22832	CAGCGTTTGACTGCTCAGGAG	37155	CAAAGACTCACAGCACAAGAA
8510	QRMANMS	22833	CAGAGGATGGCTAATATGTCG	37156	CAAAGAATGGCAAACATGAGC
8511	QRMTQDM	22834	CAGAGGATGACGCAGGATATG	37157	CAAAGAATGACACAAGACATG
8512	QRNSNTF	22835	CAGCGTAATTCGAATACGTTT	37158	CAAAGAAACAGCAACACATTC
8513	QRPGLHM	22836	CAGCGGCCGGGGCTGCATATG	37159	CAAAGACCAGGACTCCACATG
8514	QRPLGGL	22837	CAGCGTCCGTTGGGGGGTTTG	37160	CAAAGACCACTCGGAGGACTC
8515	QRPPSVD	22838	CAGCGTCCTCCTAGTGTTGAT	37161	CAAAGACCACCAAGCGTCGAC
8516	QRPTDRT	22839	CAGCGTCCGACTGATCGGACG	37162	CAAAGACCAACAGACAGAACA
8517	QRQPVLD	22840	CAGCGTCAGCCTGTTTTGGAT	37163	CAAAGACAACCAGTCCTCGAC
8518	QRQRDLP	22841	CAGAGGCAGAGGGATCTTCCT	37164	CAAAGACAAAGAGACCTCCCA
8519	QRSANVA	22842	CAGAGGTCGGCGAATGTGGCG	37165	CAAAGAAGCGCAAACGTCGCA
8520	QRSHMNP	22843	CAGCGTTCGCATATGAATCCG	37166	CAAAGAAGCCACATGAACCCA
8521	QRSSGTP	22844	CAGCGGTCTTCTGGTACGCCT	37167	CAAAGAAGCAGCGGAACACCA
8522	QRSTNLN	22845	CAGCGGTCGACTAATTTGAAT	37168	CAAAGAAGCACAAACCTCAAC
8523	QRTVHQG	22846	CAGCGGACTGTGCATCAGGGT	37169	CAAAGAACAGTCCACCAAGGA
8524	QRTVRGE	22847	CAGAGGACTGTTCGGGGTGAG	37170	CAAAGAACAGTCAGAGGAGAA
8525	QRVNSSG	22848	CAGCGTGTGAATTCTAGTGGT	37171	CAAAGAGTCAACAGCAGCGGA
8526	QSADLDY	22849	CAGTCGGCTGATCTTGATTAT	37172	CAAAGCGCAGACCTCGACTAC
8527	QSAEAEA	22850	CAGTCGGCGGAGGCGGAGGCG	37173	CAAAGCGCAGAAGCAGAAGCA
8528	QSAHPAT	22851	CAGAGTGCTCATCCGGCTACG	37174	CAAAGCGCACACCCAGCAACA
8529	QSAPVRV	22852	CAGTCTGCTCCGGTTCGTGTT	37175	CAAAGCGCACCAGTCAGAGTC
8530	QSASALQ	22853	CAGAGTGCTTCGGCTCTTCAG	37176	CAAAGCGCAAGCGCACTCCAA
8531	QSASVMN	22854	CAGTCGGCGTCTGTGATGAAT	37177	CAAAGCGCAAGCGTCATGAAC
8532	QSAVLEY	22855	CAGTCGGCTGTTTTGGAGTAT	37178	CAAAGCGCAGTCCTCGAATAC
8533	QSDDWPV	22856	CAGTCTGATGATTGGCCGGTG	37179	CAAAGCGACGACTGGCCAGTC
8534	QSDIRNP	22857	CAGAGTGATATTCGTAATCCG	37180	CAAAGCGACATCAGAAACCCA
8535	QSDWVPV	22858	CAGTCTGATTGGGTGCCGGTT	37181	CAAAGCGACTGGGTCCCAGTC
8536	QSEKGTY	22859	CAGTCTGAGAAGGGGACTTAT	37182	CAAAGCGAAAAAGGAACATAC
8537	QSEMMDA	22860	CAGTCTGAGATGATGGATGCG	37183	CAAAGCGAAATGATGGACGCA
8538	QSERATV	22861	CAGTCTGAGCGTGCGACTGTG	37184	CAAAGCGAAAGAGCAACAGTC
8539	QSFHHER	22862	CAGTCGTTTCATCATGAGCGG	37185	CAAAGCTTCCACCACGAAAGA

8540	QSFPLQA	22863	CAGTCGTTTCCGCTGCAGGCG	37186	CAAAGCTTCCCACTCCAAGCA
8541	QSGQGMY	22864	CAGTCGGGGCAGGGGATGTAT	37187	CAAAGCGGACAAGGAATGTAC
8542	QSGRWHW	22865	CAGAGTGGGCGGTGGCATTGG	37188	CAAAGCGGAAGATGGCACTGG
8543	QSGSSAR	22866	CAGTCTGGTTCGTCTGCGCGT	37189	CAAAGCGGAAGCAGCGCAAGA
8544	QSHPFND	22867	CAGAGTCATCCTTTTAATGAT	37190	CAAAGCCACCCATTCAACGAC
8545	QSHTQGS	22868	CAGAGTCATACGCAGGGTAGT	37191	CAAAGCCACACACAAGGAAGC
8546	QSIAVTI	22869	CAGTCTATTGCGGTTACGATT	37192	CAAAGCATCGCAGTCACAATC
8547	QSIVIAH	22870	CAGTCTATTGTGATTGCGCAT	37193	CAAAGCATCGTCATCGCACAC
8548	QSKLASL	22871	CAGAGTAAGCTGGCGAGTCTT	37194	CAAAGCAAACTCGCAAGCCTC
8549	QSKLYLE	22872	CAGAGTAAGCTTTATTTGGAG	37195	CAAAGCAAACTCTACCTCGAA
8550	QSKMPNW	22873	CAGTCGAAGATGCCGAATTGG	37196	CAAAGCAAAATGCCAAACTGG
8551	QSLNDLK	22874	CAGAGTCTGAATGATCTGAAG	37197	CAAAGCCTCAACGACCTCAAA
8552	QSMSSTL	22875	CAGAGTATGTCGTCTACGTTG	37198	CAAAGCATGAGCAGCACACTC
8553	QSNQDRQ	22876	CAGTCTAATCAGGATCGTCAG	37199	CAAAGCAACCAAGACAGACAA
8554	QSNSSNT	22877	CAGAGTAATTCGAGTAATACT	37200	CAAAGCAACAGCAGCAACACA
8555	QSPGHPS	22878	CAGTCTCCTGGTCATCCGAGT	37201	CAAAGCCCAGGACACCCAAGC
8556	QSPKECY	22879	CAGAGTCCTAAGGAGTGTTAT	37202	CAAAGCCCAAAAGAATGCTAC
8557	QSPLYAS	22880	CAGTCGCCGCTTTATGCGTCG	37203	CAAAGCCCACTCTACGCAAGC
8558	QSPNLPL	22881	CAGTCTCCGAATTTGCCGCTG	37204	CAAAGCCCAAACCTCCCACTC
8559	QSPPSTD	22882	CAGAGTCCGCCTAGTACTGAT	37205	CAAAGCCCACCAAGCACAGAC
8560	QSPRNYV	22883	CAGTCGCCGCGGAATTATGTT	37206	CAAAGCCCAAGAAACTACGTC
8561	QSPTNDM	22884	CAGTCTCCTACTAATGATATG	37207	CAAAGCCCAACAAACGACATG
8562	QSQAPHG	22885	CAGAGTCAGGCGCCGCATGGT	37208	CAAAGCCAAGCACCACACGGA
8563	QSRDIPT	22886	CAGTCTCGTGATATTCCTACG	37209	CAAAGCAGAGACATCCCAACA
8564	QSRGALP	22887	CAGAGTCGTGGGGCGTTGCCT	37210	CAAAGCAGAGGAGCACTCCCA
8565	QSRLGSF	22888	CAGAGTCGGCTTGGGAGTTTT	37211	CAAAGCAGACTCGGAAGCTTC
8566	QSRTMTP	22889	CAGAGTCGTACGATGACGCCG	37212	CAAAGCAGAACAATGACACCA
8567	QSRTPSP	22890	CAGTCTCGTACTCCTTCTCCT	37213	CAAAGCAGAACACCAAGCCCA
8568	QSSAISY	22891	CAGTCGTCTGCGATTTCTTAT	37214	CAAAGCAGCGCAATCAGCTAC
8569	QSSARGM	22892	CAGTCGAGTGCGCGTGGTATG	37215	CAAAGCAGCGCAAGAGGAATG
8570	QSSATRN	22893	CAGTCGAGTGCGACTCGTAAT	37216	CAAAGCAGCGCAACAAGAAAC
8571	QSSAVLT	22894	CAGTCTAGTGCTGTTTTGACT	37217	CAAAGCAGCGCAGTCCTCACA
8572	QSSDTGE	22895	CAGTCGTCGGATACGGGGGAG	37218	CAAAGCAGCGACACAGGAGAA
8573	QSSGQTV	22896	CAGAGTTCTGGTCAGACGGTT	37219	CAAAGCAGCGGACAAACAGTC
8574	QSSKIVY	22897	CAGAGTAGTAAGATTGTGTAT	37220	CAAAGCAGCAAAATCGTCTAC
8575	QSSLSLS	22898	CAGTCTTCTCTTTCGTTGTCG	37221	CAAAGCAGCCTCAGCCTCAGC
8576	QSSMPQT	22899	CAGTCGTCTATGCCGCAGACT	37222	CAAAGCAGCATGCCACAAACA
8577	QSSNFQS	22900	CAGTCTTCGAATTTTCAGTCG	37223	CAAAGCAGCAACTTCCAAAGC
8578	QSSRAMG	22901	CAGTCTTCTAGGGCTATGGGT	37224	CAAAGCAGCAGAGCAATGGGA
8579	QSSRPSP	22902	CAGTCGAGTAGGCCGTCGCCT	37225	CAAAGCAGCAGACCAAGCCCA
8580	QSSTLQS	22903	CAGTCGAGTACTTTGCAGTCG	37226	CAAAGCAGCACACTCCAAAGC
8581	QSTDQKD	22904	CAGAGTACGGATCAGAAGGAT	37227	CAAAGCACAGACCAAAAAGAC
8582	QSTGALR	22905	CAGTCTACGGGTGCTTTGCGT	37228	CAAAGCACAGGAGCACTCAGA
8583	QSTNESS	22906	CAGTCTACTAATGAGAGTTCG	37229	CAAAGCACAAACGAAAGCAGC
8584	QSTQLDH	22907	CAGAGTACGCAGCTGGATCAT	37230	CAAAGCACACAACTCGACCAC

8585	QSTQSDK	22908	CAGAGTACGCAGAGTGATAAG	37231	CAAAGCACACAAAGCGACAAA
8586	QSTTRHP	22909	CAGTCTACTACTAGGCATCCT	37232	CAAAGCACAACAAGACACCCA
8587	QSTVTVR	22910	CAGTCGACTGTGACGGTTCGG	37233	CAAAGCACAGTCACAGTCAGA
8588	QSVHSPL	22911	CAGAGTGTGCATAGTCCTCTT	37234	CAAAGCGTCCACAGCCCACTC
8589	QSVKYDR	22912	CAGTCGGTGAAGTATGATCGT	37235	CAAAGCGTCAAATACGACAGA
8590	QSVMTAP	22913	CAGTCTGTGATGACGGCTCCG	37236	CAAAGCGTCATGACAGCACCA
8591	QSVNAEL	22914	CAGAGTGTTAATGCGGAGCTT	37237	CAAAGCGTCAACGCAGAACTC
8592	QSVPLAS	22915	CAGTCGGTTCCGCTGGCTAGT	37238	CAAAGCGTCCCACTCGCAAGC
8593	QSYEARG	22916	CAGTCTTATGAGGCGCGGGGG	37239	CAAAGCTACGAAGCAAGAGGA
8594	QSYNGLG	22917	CAGAGTTATAATGGGCTGGGT	37240	CAAAGCTACAACGGACTCGGA
8595	QTAGRLA	22918	CAGACGGCGGGGAGGCTTGCT	37241	CAAACAGCAGGAAGACTCGCA
8596	QTANKPV	22919	CAGACTGCTAATAAGCCGGTG	37242	CAAACAGCAAACAAACCAGTC
8597	QTDGAKD	22920	CAGACGGATGGTGCTAAGGAT	37243	CAAACAGACGGAGCAAAAGAC
8598	QTDRAYV	22921	CAGACGGATAGGGCGTATGTT	37244	CAAACAGACAGAGCATACGTC
8599	QTDVDDM	22922	CAGACTGATGTGGATGATATG	37245	CAAACAGACGTCGACGACATG
8600	QTFGGPG	22923	CAGACTTTTGGGGGTCCGGGT	37246	CAAACATTCGGAGGACCAGGA
8601	QTGGRSP	22924	CAGACGGGTGGGCGTTCGCCT	37247	CAAACAGGAGGAAGAAGCCCA
8602	QTGLNQD	22925	CAGACGGGTCTTAATCAGGAT	37248	CAAACAGGACTCAACCAAGAC
8603	QTGPTRD	22926	CAGACGGGTCCTACTCGTGAT	37249	CAAACAGGACCAACAAGAGAC
8604	QTGREPM	22927	CAGACGGGGCGTGAGCCTATG	37250	CAAACAGGAAGAGAACCAATG
8605	QTGSSYS	22928	CAGACTGGTTCTTCTTATAGT	37251	CAAACAGGAAGCAGCTACAGC
8606	QTIRTED	22929	CAGACGATTCGGACGGAGGAT	37252	CAAACAATCAGAACAGAAGAC
8607	QTISKDP	22930	CAGACGATTTCTAAGGATCCG	37253	CAAACAATCAGCAAAGACCCA
8608	QTKHGES	22931	CAGACGAAGCATGGTGAGAGT	37254	CAAACAAAACACGGAGAAAGC
8609	QTKNTHP	22932	CAGACGAAGAATACGCATCCT	37255	CAAACAAAAAACACACACCCA
8610	QTKSLIP	22933	CAGACTAAGTCTCTGATTCCT	37256	CAAACAAAAAGCCTCATCCCA
8611	QTLQHAT	22934	CAGACGCTGCAGCATGCGACT	37257	CAAACACTCCAACACGCAACA
8612	QTLSGMR	22935	CAGACGCTTTCGGGGATGCGT	37258	CAAACACTCAGCGGAATGAGA
8613	QTMMPVP	22936	CAGACTATGATGCCTGTGCCG	37259	CAAACAATGATGCCAGTCCCA
8614	QTMRSAG	22937	CAGACTATGCGGTCTGCTGGT	37260	CAAACAATGAGAAGCGCAGGA
8615	QTNMQSP	22938	CAGACTAATATGCAGTCTCCT	37261	CAAACAAACATGCAAAGCCCA
8616	QTNPNMV	22939	CAGACTAATCCTAATATGGTT	37262	CAAACAAACCCAAACATGGTC
8617	QTNTATK	22940	CAGACGAATACTGCGACGAAG	37263	CAAACAAACACAGCAACAAAA
8618	QTPPSAA	22941	CAGACTCCTCCTTCGGCGGCG	37264	CAAACACCACCAAGCGCAGCA
8619	QTPPTNR	22942	CAGACTCCTCCTACGAATCGT	37265	CAAACACCACCAACAAACAGA
8620	QTPRVIQ	22943	CAGACGCCGCGTGTTATTCAG	37266	CAAACACCAAGAGTCATCCAA
8621	QTPSMTR	22944	CAGACGCCTTCGATGACTCGT	37267	CAAACACCAAGCATGACAAGA
8622	QTPSYLG	22945	CAGACTCCGTCTTATCTTGGT	37268	CAAACACCAAGCTACCTCGGA
8623	QTQIRVG	22946	CAGACTCAGATTAGGGTGGGT	37269	CAAACACAAATCAGAGTCGGA
8624	QTQPQSS	22947	CAGACTCAGCCTCAGTCGTCT	37270	CAAACACAACCACAAAGCAGC
8625	QTQSLYP	22948	CAGACGCAGAGTTTGTATCCT	37271	CAAACACAAAGCCTCTACCCA
8626	QTQSPVP	22949	CAGACTCAGTCGCCTGTTCCT	37272	CAAACACAAAGCCCAGTCCCA
8627	QTQVSYG	22950	CAGACTCAGGTTAGTTATGGT	37273	CAAACACAAGTCAGCTACGGA
8628	QTRHDLL	22951	CAGACTAGGCATGATCTGCTT	37274	CAAACAAGACACGACCTCCTC
8629	QTRLAQH	22952	CAGACGAGGTTGGCTCAGCAT	37275	CAAACAAGACTCGCACAACAC

8630	QTRLPAS	22953	CAGACGCGGCTGCCGGCTTCG	37276	CAAACAAGACTCCCAGCAAGC
8631	QTSAARV	22954	CAGACTTCGGCTGCGCGGGTG	37277	CAAACAAGCGCAGCAAGAGTC
8632	QTSPGVM	22955	CAGACTTCTCCTGGGGTTATG	37278	CAAACAAGCCCAGGAGTCATG
8633	QTSTDNA	22956	CAGACGAGTACGGATAATGCT	37279	CAAACAAGCACAGACAACGCA
8634	QTSVHLK	22957	CAGACTAGTGTTCATCTTAAG	37280	CAAACAAGCGTCCACCTCAAA
8635	QTTARAQ	22958	CAGACTACGGCTAGGGCGCAG	37281	CAAACAACAGCAAGAGCACAA
8636	QTVHAFG	22959	CAGACTGTGCATGCGTTTGGT	37282	CAAACAGTCCACGCATTCGGA
8637	QTVRLTS	22960	CAGACTGTGCGGCTTACTTCG	37283	CAAACAGTCAGACTCACAAGC
8638	QTVSALG	22961	CAGACTGTTTCTGCGCTTGGT	37284	CAAACAGTCAGCGCACTCGGA
8639	QTYDPAS	22962	CAGACTTATGATCCTGCTAGT	37285	CAAACATACGACCCAGCAAGC
8640	QTYHTLE	22963	CAGACTTATCATACGCTGGAG	37286	CAAACATACCACACACTCGAA
8641	QTYPTME	22964	CAGACTTATCCGACGATGGAG	37287	CAAACATACCCAACAATGGAA
8642	QVAGMKF	22965	CAGGTTGCTGGTATGAAGTTT	37288	CAAGTCGCAGGAATGAAATTC
8643	QVASPYR	22966	CAGGTTGCTTCTCCTTATCGG	37289	CAAGTCGCAAGCCCATACAGA
8644	QVDRSPH	22967	CAGGTTGATCGTTCTCCTCAT	37290	CAAGTCGACAGAAGCCCACAC
8645	QVEHGQT	22968	CAGGTTGAGCATGGGCAGACT	37291	CAAGTCGAACACGGACAAACA
8646	QVEREAW	22969	CAGGTGGAGCGTGAGGCTTGG	37292	CAAGTCGAAAGAGAAGCATGG
8647	QVGGRAF	22970	CAGGTTGGTGGTCGTGCTTTT	37293	CAAGTCGGAGGAAGAGCATTC
8648	QVGKVTL	22971	CAGGTGGGTAAGGTTACGTTG	37294	CAAGTCGGAAAAGTCACACTC
8649	QVGVKNG	22972	CAGGTGGGTGTGAAGAATGGG	37295	CAAGTCGGAGTCAAAAACGGA
8650	QVLNGRE	22973	CAGGTTCTGAATGGGAGGGAG	37296	CAAGTCCTCAACGGAAGAGAA
8651	QVMPNVS	22974	CAGGTGATGCCGAATGTGTCG	37297	CAAGTCATGCCAAACGTCAGC
8652	QVPFPAD	22975	CAGGTTCCGTTTCCGGCGGAT	37298	CAAGTCCCATTCCCAGCAGAC
8653	QVPLSLE	22976	CAGGTTCCTCTGTCTTTGGAG	37299	CAAGTCCCACTCAGCCTCGAA
8654	QVPYAPA	22977	CAGGTTCCGTATGCTCCGGCG	37300	CAAGTCCCATACGCACCAGCA
8655	QVQPVHI	22978	CAGGTGCAGCCTGTGCATATT	37301	CAAGTCCAACCAGTCCACATC
8656	QVRAAVT	22979	CAGGTTCGTGCTGCTGTGACT	37302	CAAGTCAGAGCAGCAGTCACA
8657	QVRDSYS	22980	CAGGTGAGGGATTCTTATTCG	37303	CAAGTCAGAGACAGCTACAGC
8658	QVREPAI	22981	CAGGTGCGTGAGCCTGCTATT	37304	CAAGTCAGAGAACCAGCAATC
8659	QVRESSS	22982	CAGGTGCGTGAGTCGTCTTCG	37305	CAAGTCAGAGAAAGCAGCAGC
8660	QVRLEPS	22983	CAGGTTCGTCTGGAGCCGAGT	37306	CAAGTCAGACTCGAACCAAGC
8661	QVRPGLL	22984	CAGGTTCGGCCGGGGCTTCTT	37307	CAAGTCAGACCAGGACTCCTC
8662	QVSHRDS	22985	CAGGTGTCTCATCGGGATAGT	37308	CAAGTCAGCCACAGAGACAGC
8663	QVSLGSV	22986	CAGGTGTCGCTTGGTAGTGTT	37309	CAAGTCAGCCTCGGAAGCGTC
8664	QVSPSLN	22987	CAGGTGTCTCCGAGTCTTAAT	37310	CAAGTCAGCCCAAGCCTCAAC
8665	QVSSPVP	22988	CAGGTGTCTTCTCCTGTTCCT	37311	CAAGTCAGCAGCCCAGTCCCA
8666	QVTKSHT	22989	CAGGTGACTAAGTCTCATACT	37312	CAAGTCACAAAAAGCCACACA
8667	QVVASLG	22990	CAGGTTGTGGCGTCGTTGGGG	37313	CAAGTCGTCGCAAGCCTCGGA
8668	QVVPHQE	22991	CAGGTTGTTCCTCATCAGGAG	37314	CAAGTCGTCCCACACCAAGAA
8669	QVVRSSS	22992	CAGGTTGTGCGGTCGAGTTCG	37315	CAAGTCGTCAGAAGCAGCAGC
8670	QVYTNQY	22993	CAGGTTTATACTAATCAGTAT	37316	CAAGTCTACACAAACCAATAC
8671	QWANTGE	22994	CAGTGGGCGAATACTGGTGAG	37317	CAATGGGCAAACACAGGAGAA
8672	QWEDHST	22995	CAGTGGGAGGATCATTCGACG	37318	CAATGGGAAGACCACAGCACA
8673	QYGDGPK	22996	CAGTATGGGGATGGGCCTAAG	37319	CAATACGGAGACGGACCAAAA
8674	QYGQQHS	22997	CAGTATGGTCAGCAGCATTCT	37320	CAATACGGACAACAACACAGC

8675	QYGSVHG	22998	CAGTATGGTAGTGTTCATGGG	37321	CAATACGGAAGCGTCCACGGA
8676	QYHASGK	22999	CAGTATCATGCTAGTGGGAAG	37322	CAATACCACGCAAGCGGAAAA
8677	QYKRAEL	23000	CAGTATAAGCGGGCGGAGCTT	37323	CAATACAAAAGAGCAGAACTC
8678	QYKTDMT	23001	CAGTATAAGACTGATATGACT	37324	CAATACAAAACAGACATGACA
8679	QYKTGAQ	23002	CAGTATAAGACTGGGGCGCAG	37325	CAATACAAAACAGGAGCACAA
8680	QYLATHG	23003	CAGTATCTGGCGACTCATGGG	37326	CAATACCTCGCAACACACGGA
8681	QYPNSDT	23004	CAGTATCCTAATTCTGATACG	37327	CAATACCCAAACAGCGACACA
8682	QYPVSPS	23005	CAGTATCCGGTTTCGCCGTCG	37328	CAATACCCAGTCAGCCCAAGC
8683	QYTASNS	23006	CAGTATACTGCTTCGAATTCT	37329	CAATACACAGCAAGCAACAGC
8684	QYTGTQK	23007	CAGTATACTGGGACTCAGAAG	37330	CAATACACAGGAACACAAAAA
8685	QYTVLTE	23008	CAGTATACTGTTCTGACGGAG	37331	CAATACACAGTCCTCACAGAA
8686	QYVGIGT	23009	CAGTATGTTGGTATTGGGACT	37332	CAATACGTCGGAATCGGAACA
8687	RAAAYGA	23010	AGGGCTGCGGCTTATGGGGCT	37333	AGAGCAGCAGCATACGGAGCA
8688	RAAMMNP	23011	CGTGCGGCTATGATGAATCCT	37334	AGAGCAGCAATGATGAACCCA
8689	RAAMVAV	23012	AGGGCTGCTATGGTTGCGGTT	37335	AGAGCAGCAATGGTCGCAGTC
8690	RAANDFP	23013	CGGGCGGCGAATGATTTTCCG	37336	AGAGCAGCAAACGACTTCCCA
8691	RAAPTSS	23014	AGGGCTGCGCCTACGTCGAGT	37337	AGAGCAGCACCAACAAGCAGC
8692	RAATVPN	23015	CGTGCTGCTACTGTGCCTAAT	37338	AGAGCAGCAACAGTCCCAAAC
8693	RADKGPS	23016	CGGGCGGATAAGGGTCCGTCT	37339	AGAGCAGACAAAGGACCAAGC
8694	RADPRPG	23017	AGGGCGGATCCGAGGCCTGGG	37340	AGAGCAGACCCAAGACCAGGA
8695	RADRATY	23018	CGGGCTGATAGGGCGACGTAT	37341	AGAGCAGACAGAGCAACATAC
8696	RADVPPV	23019	CGTGCTGATGTTCCTCCTGTT	37342	AGAGCAGACGTCCCACCAGTC
8697	RADYHHN	23020	AGGGCTGATTATCATCATAAT	37343	AGAGCAGACTACCACCACAAC
8698	RAEAVWD	23021	CGTGCTGAGGCGGTTTGGGAT	37344	AGAGCAGAAGCAGTCTGGGAC
8699	RAENISR	23022	CGGGCGGAGAATATTTCGAGG	37345	AGAGCAGAAAACATCAGCAGA
8700	RAESLLG	23023	AGGGCTGAGAGTTTGCTTGGT	37346	AGAGCAGAAAGCCTCCTCGGA
8701	RAEVLYT	23024	CGTGCTGAGGTGTTGTATACG	37347	AGAGCAGAAGTCCTCTACACA
8702	RAEYQSP	23025	CGTGCGGAGTATCAGTCTCCG	37348	AGAGCAGAATACCAAAGCCCA
8703	RAFGQSP	23026	CGTGCTTTTGGTCAGTCGCCT	37349	AGAGCATTCGGACAAAGCCCA
8704	RAFPNDS	23027	CGGGCGTTTCCGAATGATAGT	37350	AGAGCATTCCCAAACGACAGC
8705	RAFSQAE	23028	CGTGCTTTTTCTCAGGCGGAG	37351	AGAGCATTCAGCCAAGCAGAA
8706	RAGLSPN	23029	CGTGCTGGGCTGTCTCCGAAT	37352	AGAGCAGGACTCAGCCCAAAC
8707	RAGPVST	23030	AGGGCTGGGCCTGTGAGTACT	37353	AGAGCAGGACCAGTCAGCACA
8708	RAGSYES	23031	CGGGCTGGTTCTTATGAGTCT	37354	AGAGCAGGAAGCTACGAAAGC
8709	RAGVQCI	23032	AGGGCTGGTGTTCAGTGTATT	37355	AGAGCAGGAGTCCAATGCATC
8710	RAHGSGA	23033	AGGGCGCATGGGAGTGGTGCT	37356	AGAGCACACGGAAGCGGAGCA
8711	RAIAQAV	23034	AGGGCGATTGCGCAGGCGGTG	37357	AGAGCAATCGCACAAGCAGTC
8712	RAIDLPK	23035	CGTGCTATTGATTTGCCTAAG	37358	AGAGCAATCGACCTCCCAAAA
8713	RAIDSVP	23036	CGTGCGATTGATTCTGTGCCT	37359	AGAGCAATCGACAGCGTCCCA
8714	RAIKSDP	23037	CGGGCTATTAAGAGTGATCCT	37360	AGAGCAATCAAAAGCGACCCA
8715	RAIPTPG	23038	AGGGCTATTCCTACGCCGGGT	37361	AGAGCAATCCCAACACCAGGA
8716	RALDVNA	23039	CGTGCGTTGGATGTTAATGCG	37362	AGAGCACTCGACGTCAACGCA
8717	RALLNLQ	23040	CGTGCTCTGCTTAATTTGCAG	37363	AGAGCACTCCTCAACCTCCAA
8718	RALQTTS	23041	CGTGCTCTGCAGACTACGAGT	37364	AGAGCACTCCAAACAACAAGC
8719	RALSANV	23042	AGGGCGCTTTCTGCGAATGTT	37365	AGAGCACTCAGCGCAAACGTC

8720	RALSSLP	23043	CGTGCTCTGTCTTCGCTTCCG	37366	AGAGCACTCAGCAGCCTCCCA
8721	RALTDLV	23044	CGTGCTCTTACGGATCTTGTT	37367	AGAGCACTCACAGACCTCGTC
8722	RAMGNVL	23045	CGGGCGATGGGTAATGTTTTG	37368	AGAGCAATGGGAAACGTCCTC
8723	RAMLDRA	23046	CGTGCGATGCTTGATCGTGCT	37369	AGAGCAATGCTCGACAGAGCA
8724	RAMPGEV	23047	AGGGCGATGCCGGGTGAGGTT	37370	AGAGCAATGCCAGGAGAAGTC
8725	RAMPPSS	23048	CGGGCGATGCCTCCTTCTTCG	37371	AGAGCAATGCCACCAAGCAGC
8726	RANDPPP	23049	AGGGCTAATGATCCTCCTCCG	37372	AGAGCAAACGACCCACCACCA
8727	RANLNIP	23050	CGTGCTAATCTGAATATTCCT	37373	AGAGCAAACCTCAACATCCCA
8728	RAPETEL	23051	AGGGCGCCGGAGACGGAGTTG	37374	AGAGCACCAGAAACAGAACTC
8729	RAPPSPK	23052	CGTGCGCCTCCTAGTCCTAAG	37375	AGAGCACCACCAAGCCCAAAA
8730	RAPQGST	23053	CGTGCTCCGCAGGGGTCTACG	37376	AGAGCACCACAAGGAAGCACA
8731	RAPQGYG	23054	CGTGCTCCGCAGGGTTATGGT	37377	AGAGCACCACAAGGATACGGA
8732	RAPRPIE	23055	CGGGCTCCGCGTCCTATTGAG	37378	AGAGCACCAAGACCAATCGAA
8733	RAPVSPM	23056	CGTGCTCCTGTTAGTCCTATG	37379	AGAGCACCAGTCAGCCCAATG
8734	RAQPSLH	23057	CGGGCGCAGCCGTCTCTGCAT	37380	AGAGCACAACCAAGCCTCCAC
8735	RAQSPLS	23058	AGGGCGCAGTCGCCGTTGTCG	37381	AGAGCACAAAGCCCACTCAGC
8736	RAQTTLS	23059	CGTGCTCAGACTACTCTTTCT	37382	AGAGCACAAACAACACTCAGC
8737	RAQYSQD	23060	CGTGCGCAGTATTCGCAGGAT	37383	AGAGCACAATACAGCCAAGAC
8738	RAQYTGN	23061	CGTGCGCAGTATACGGGTAAT	37384	AGAGCACAATACACAGGAAAC
8739	RASFPPD	23062	CGGGCTTCGTTTCCGCCTGAT	37385	AGAGCAAGCTTCCCACCAGAC
8740	RASHDTN	23063	CGGGCGAGTCATGATACGAAT	37386	AGAGCAAGCCACGACACAAAC
8741	RASLRVE	23064	CGTGCTTCGCTTCGTGTGGAG	37387	AGAGCAAGCCTCAGAGTCGAA
8742	RASNRPD	23065	AGGGCGTCTAATCGGCCGGAT	37388	AGAGCAAGCAACAGACCAGAC
8743	RASPTTS	23066	CGTGCGAGTCCGACGACTAGT	37389	AGAGCAAGCCCAACAACAAGC
8744	RASSELP	23067	CGGGCTTCTTCGGAGTTGCCG	37390	AGAGCAAGCAGCGAACTCCCA
8745	RASSSED	23068	AGGGCTTCTTCTAGTGAGGAT	37391	AGAGCAAGCAGCAGCGAAGAC
8746	RASSVDM	23069	CGGGCGAGTTCTGTTGATATG	37392	AGAGCAAGCAGCGTCGACATG
8747	RASTGMA	23070	CGGGCTTCTACGGGTATGGCT	37393	AGAGCAAGCACAGGAATGGCA
8748	RASTHTL	23071	AGGGCTAGTACGCATACGCTT	37394	AGAGCAAGCACACACACACTC
8749	RATEHSF	23072	AGGGCTACGGAGCATTCGTTT	37395	AGAGCAACAGAACACAGCTTC
8750	RATEPAF	23073	AGGGCTACGGAGCCGGCGTTT	37396	AGAGCAACAGAACCAGCATTC
8751	RATLPKT	23074	CGTGCGACTCTGCCGAAGACT	37397	AGAGCAACACTCCCAAAAACA
8752	RATNDRA	23075	CGTGCGACGAATGATCGTGCT	37398	AGAGCAACAAACGACAGAGCA
8753	RATNDST	23076	CGGGCTACTAATGATAGTACT	37399	AGAGCAACAAACGACAGCACA
8754	RATNTIL	23077	CGGGCTACGAATACTATTCTT	37400	AGAGCAACAAACACAATCCTC
8755	RATTSTF	23078	CGTGCTACGACGTCGACGTTT	37401	AGAGCAACAACAAGCACATTC
8756	RAVEDRH	23079	CGTGCTGTGGAGGATAGGCAT	37402	AGAGCAGTCGAAGACAGACAC
8757	RAVLNIG	23080	CGGGCGGTGCTTAATATTGGT	37403	AGAGCAGTCCTCAACATCGGA
8758	RAVQPML	23081	CGGGCGGTTCAGCCTATGCTT	37404	AGAGCAGTCCAACCAATGCTC
8759	RAVSLQA	23082	AGGGCTGTGAGTCTTCAGGCT	37405	AGAGCAGTCAGCCTCCAAGCA
8760	RAVYQTQ	23083	CGGGCTGTGTATCAGACGCAG	37406	AGAGCAGTCTACCAAACACAA
8761	RAYGPTN	23084	AGGGCGTATGGGCCGACGAAT	37407	AGAGCATACGGACCAACAAAC
8762	RAYMTDP	23085	CGGGCGTATATGACTGATCCT	37408	AGAGCATACATGACAGACCCA
8763	RAYNAVV	23086	AGGGCGTATAATGCTGTTGTT	37409	AGAGCATACAACGCAGTCGTC
8764	RAYPVDD	23087	CGGGCTTATCCTGTGGATGAT	37410	AGAGCATACCCAGTCGACGAC

8765	RDAASSC	23088	CGGGATGCTGCGTCTTCTTGT	37411	AGAGACGCAGCAAGCAGCTGC
8766	RDDSSLL	23089	CGTGATGATTCTTCGCTTCTG	37412	AGAGACGACAGCAGCCTCCTC
8767	RDDVRTY	23090	CGGGATGATGTGCGTACTTAT	37413	AGAGACGACGTCAGAACATAC
8768	RDGEMDP	23091	CGGGATGGGGAGATGGATCCG	37414	AGAGACGGAGAAATGGACCCA
8769	RDGKWVA	23092	CGGGATGGGAAGTGGGTGGCT	37415	AGAGACGGAAAATGGGTCGCA
8770	RDGQHTS	23093	CGGGATGGGCAGCATACGTCG	37416	AGAGACGGACAACACACAAGC
8771	RDHLTVA	23094	AGGGATCATTTGACTGTTGCT	37417	AGAGACCACCTCACAGTCGCA
8772	RDIAAKT	23095	AGGGATATTGCGGCTAAGACT	37418	AGAGACATCGCAGCAAAAACA
8773	RDKSDHA	23096	CGTGATAAGTCTGATCATGCT	37419	AGAGACAAAAGCGACCACGCA
8774	RDLKTQS	23097	CGTGATCTGAAGACGCAGTCG	37420	AGAGACCTCAAAACACAAAGC
8775	RDLQHLS	23098	AGGGATCTGCAGCATCTTTCT	37421	AGAGACCTCCAACACCTCAGC
8776	RDLSSES	23099	CGTGATCTGTCTAGTGAGTCT	37422	AGAGACCTCAGCAGCGAAAGC
8777	RDNKANI	23100	AGGGATAATAAGGCGAATATT	37423	AGAGACAACAAAGCAAACATC
8778	RDNSSVV	23101	CGTGATAATTCGAGTGTGGTG	37424	AGAGACAACAGCAGCGTCGTC
8779	RDPNINP	23102	CGTGATCCTAATATTAATCCT	37425	AGAGACCCAAACATCAACCCA
8780	RDPRAGF	23103	CGTGATCCTCGGGCGGGGTTT	37426	AGAGACCCAAGAGCAGGATTC
8781	RDPRAHL	23104	CGTGATCCTAGGGCTCATCTT	37427	AGAGACCCAAGAGCACACCTC
8782	RDPRGQG	23105	AGGGATCCGCGGGGTCAGGGG	37428	AGAGACCCAAGAGGACAAGGA
8783	RDQASKN	23106	CGGGATCAGGCTAGTAAGAAT	37429	AGAGACCAAGCAAGCAAAAAC
8784	RDQGLES	23107	CGTGATCAGGGTCTTGAGTCG	37430	AGAGACCAAGGACTCGAAAGC
8785	RDQVATP	23108	AGGGATCAGGTTGCTACGCCT	37431	AGAGACCAAGTCGCAACACCA
8786	RDRDPTS	23109	CGGGATCGGGATCCGACGTCG	37432	AGAGACAGAGACCCAACAAGC
8787	RDREPAL	23110	CGTGATCGGGAGCCGGCGCTT	37433	AGAGACAGAGAACCAGCACTC
8788	RDREVSW	23111	CGGGATCGTGAGGTGTCGTGG	37434	AGAGACAGAGAAGTCAGCTGG
8789	RDSAFAV	23112	CGTGATTCGGCGTTTGCTGTG	37435	AGAGACAGCGCATTCGCAGTC
8790	RDSKSNS	23113	AGGGATAGTAAGAGTAATTCT	37436	AGAGACAGCAAAAGCAACAGC
8791	RDSKVSH	23114	CGGGATTCTAAGGTTTCTCAT	37437	AGAGACAGCAAAGTCAGCCAC
8792	RDSLETQ	23115	CGGGATTCTCTTGAGACTCAG	37438	AGAGACAGCCTCGAAACACAA
8793	RDSMLVA	23116	CGTGATAGTATGTTGGTTGCG	37439	AGAGACAGCATGCTCGTCGCA
8794	RDSMPAA	23117	CGTGATAGTATGCCTGCTGCT	37440	AGAGACAGCATGCCAGCAGCA
8795	RDSRMLS	23118	AGGGATAGTCGTATGCTGTCT	37441	AGAGACAGCAGAATGCTCAGC
8796	RDSSHFP	23119	AGGGATAGTTCTCATTTTCCG	37442	AGAGACAGCAGCCACTTCCCA
8797	RDSSLYL	23120	AGGGATTCTAGTCTGTATTTG	37443	AGAGACAGCAGCCTCTACCTC
8798	RDSSYTD	23121	CGGGATAGTTCGTATACTGAT	37444	AGAGACAGCAGCTACACAGAC
8799	RDTIISA	23122	AGGGATACGATTATTTCTGCT	37445	AGAGACACAATCATCAGCGCA
8800	RDTSLPV	23123	AGGGATACGTCGTTGCCTGTT	37446	AGAGACACAAGCCTCCCAGTC
8801	RDTSSIG	23124	AGGGATACGAGTTCTATTGGG	37447	AGAGACACAAGCAGCATCGGA
8802	RDVAARS	23125	CGGGATGTGGCTGCGCGTTCT	37448	AGAGACGTCGCAGCAAGAAGC
8803	RDVAMQD	23126	AGGGATGTTGCTATGCAGGAT	37449	AGAGACGTCGCAATGCAAGAC
8804	RDVPQAV	23127	CGTGATGTGCCGCAGGCTGTG	37450	AGAGACGTCCCACAAGCAGTC
8805	RDVSGPV	23128	CGGGATGTGAGTGGTCCGGTT	37451	AGAGACGTCAGCGGACCAGTC
8806	RDVSIPS	23129	CGTGATGTTAGTATTCCTTCT	37452	AGAGACGTCAGCATCCCAAGC
8807	RDVSRLP	23130	CGGGATGTTTCTAGGCTTCCT	37453	AGAGACGTCAGCAGACTCCCA
8808	RDVTRLP	23131	CGGGATGTTACTCGTCTTCCT	37454	AGAGACGTCACAAGACTCCCA
8809	REAAFAD	23132	CGTGAGGCGGCGTTTGCTGAT	37455	AGAGAAGCAGCATTCGCAGAC

8810	REAGGAS	23133	CGTGAGGCGGGGGGTGCTAGT	37456	AGAGAAGCAGGAGGAGCAAGC
8811	REAGGLA	23134	CGTGAGGCGGGGGGGCTTGCG	37457	AGAGAAGCAGGAGGACTCGCA
8812	REAKPAW	23135	AGGGAGGCTAAGCCTGCGTGG	37458	AGAGAAGCAAAACCAGCATGG
8813	REAVTKA	23136	CGTGAGGCTGTGACGAAGGCG	37459	AGAGAAGCAGTCACAAAAGCA
8814	REAYETP	23137	CGGGAGGCTTATGAGACGCCG	37460	AGAGAAGCATACGAAACACCA
8815	REDNSND	23138	CGGGAGGATAATAGTAATGAT	37461	AGAGAAGACAACAGCAACGAC
8816	REGGQSR	23139	AGGGAGGGGGGTCAGTCGCGG	37462	AGAGAAGGAGGACAAAGCAGA
8817	REGLYSH	23140	CGTGAGGGGCTGTATTCTCAT	37463	AGAGAAGGACTCTACAGCCAC
8818	REIGCTG	23141	CGTGAGATTGGGTGTACGGGT	37464	AGAGAAATCGGATGCACAGGA
8819	REKTDRF	23142	CGGGAGAAGACGGATAGGTTT	37465	AGAGAAAAAACAGACAGATTC
8820	RELEGFT	23143	CGGGAGCTGGAGGGTTTTACT	37466	AGAGAACTCGAAGGATTCACA
8821	RELSPMY	23144	CGTGAGTTGTCTCCTATGTAT	37467	AGAGAACTCAGCCCAATGTAC
8822	RELSYAS	23145	CGTGAGCTGTCGTATGCGTCT	37468	AGAGAACTCAGCTACGCAAGC
8823	REMLPSS	23146	CGTGAGATGCTGCCTAGTTCG	37469	AGAGAAATGCTCCCAAGCAGC
8824	RENGLSL	23147	AGGGAGAATGGGCTGAGTCTT	37470	AGAGAAAACGGACTCAGCCTC
8825	RENLAAG	23148	AGGGAGAATCTGGCTGCTGGG	37471	AGAGAAAACCTCGCAGCAGGA
8826	RENNTVK	23149	CGGGAGAATAATACGGTTAAG	37472	AGAGAAAACAACACAGTCAAA
8827	REPHTSN	23150	CGGGAGCCTCATACTTCGAAT	37473	AGAGAACCACACACAAGCAAC
8828	REPPTLS	23151	CGTGAGCCTCCGACGTTGTCG	37474	AGAGAACCACCAACACTCAGC
8829	REQFRNL	23152	CGGGAGCAGTTTCGTAATCTG	37475	AGAGAACAATTCAGAAACCTC
8830	RERSALT	23153	CGTGAGCGTTCTGCGTTGACT	37476	AGAGAAAGAAGCGCACTCACA
8831	RERSPMP	23154	CGGGAGCGGAGTCCGATGCCG	37477	AGAGAAAGAAGCCCAATGCCA
8832	RESCPDA	23155	CGTGAGTCGTGTCCTGATGCT	37478	AGAGAAAGCTGCCCAGACGCA
8833	RESHKGP	23156	CGTGAGTCTCATAAGGGGCCT	37479	AGAGAAAGCCACAAAGGACCA
8834	RESLNNM	23157	CGTGAGAGTCTTAATAATATG	37480	AGAGAAAGCCTCAACAACATG
8835	RESTTHG	23158	AGGGAGTCGACGACGCATGGT	37481	AGAGAAAGCACAACACACGGA
8836	RESVSIN	23159	CGGGAGTCGGTTTCGATTAAT	37482	AGAGAAAGCGTCAGCATCAAC
8837	RESYESG	23160	CGGGAGTCGTATGAGAGTGGT	37483	AGAGAAAGCTACGAAAGCGGA
8838	RETLGSP	23161	CGGGAGACGCTTGGGAGTCCT	37484	AGAGAAACACTCGGAAGCCCA
8839	RETMAST	23162	CGGGAGACTATGGCTTCGACT	37485	AGAGAAACAATGGCAAGCACA
8840	RETPNIP	23163	CGGGAGACGCCTAATATTCCT	37486	AGAGAAACACCAAACATCCCA
8841	RETSSSQ	23164	CGGGAGACGAGTTCTAGTCAG	37487	AGAGAAACAAGCAGCAGCCAA
8842	RETVRNV	23165	CGGGAGACTGTTCGGAATGTG	37488	AGAGAAACAGTCAGAAACGTC
8843	REVLSTC	23166	CGTGAGGTGCTGTCTACTTGT	37489	AGAGAAGTCCTCAGCACATGC
8844	REVSASP	23167	CGGGAGGTGAGTGCTTCTCCT	37490	AGAGAAGTCAGCGCAAGCCCA
8845	REVSFDW	23168	CGGGAGGTGTCGTTTGATTGG	37491	AGAGAAGTCAGCTTCGACTGG
8846	REYPSGS	23169	CGGGAGTATCCTAGTGGGTCG	37492	AGAGAATACCCAAGCGGAAGC
8847	RFAETRP	23170	AGGTTTGCGGAGACTCGGCCT	37493	AGATTCGCAGAAACAAGACCA
8848	RFAGAGV	23171	AGGTTTGCTGGTGCGGGTGTG	37494	AGATTCGCAGGAGCAGGAGTC
8849	RFAGSLI	23172	CGTTTTGCTGGGTCTCTGATT	37495	AGATTCGCAGGAAGCCTCATC
8850	RFANSGV	23173	CGTTTTGCGAATTCGGGTGTG	37496	AGATTCGCAAACAGCGGAGTC
8851	RFELAHN	23174	CGGTTTGAGCTTGCTCATAAT	37497	AGATTCGAACTCGCACACAAC
8852	RFESSVP	23175	CGTTTTGAGTCTTCTGTGCCG	37498	AGATTCGAAAGCAGCGTCCCA
8853	RFHAATS	23176	AGGTTTCATGCTGCTACTTCT	37499	AGATTCCACGCAGCAACAAGC
8854	RFKEMPM	23177	CGTTTTAAGGAGATGCCGATG	37500	AGATTCAAAGAAATGCCAATG

8855	RFKTTGE	23178	CGGTTTAAGACTACGGGTGAG	37501	AGATTCAAAACAACAGGAGAA
8856	RFPQPDP	23179	AGGTTTCCTCAGCCTGATCCT	37502	AGATTCCCACAACCAGACCCA
8857	RFPVDGV	23180	CGTTTTCCGGTTGATGGTGTG	37503	AGATTCCCAGTCGACGGAGTC
8858	RFSDSRM	23181	CGTTTTTCGGATTCGAGGATG	37504	AGATTCAGCGACAGCAGAATG
8859	RFSGMVE	23182	CGTTTTTCTGGTATGGTGGAG	37505	AGATTCAGCGGAATGGTCGAA
8860	RFSQSPA	23183	AGGTTTTCGCAGTCTCCTGCG	37506	AGATTCAGCCAAAGCCCAGCA
8861	RFSTGPS	23184	CGTTTTTCTACGGGTCCTTCT	37507	AGATTCAGCACAGGACCAAGC
8862	RFSTQQS	23185	CGTTTTTCTACTCAGCAGAGT	37508	AGATTCAGCACACAACAAAGC
8863	RFVPDRP	23186	CGGTTTGTGCCGGATAGGCCT	37509	AGATTCGTCCCAGACAGACCA
8864	RGAAPVT	23187	AGGGGTGCTGCGCCGGTGACG	37510	AGAGGAGCAGCACCAGTCACA
8865	RGAELGG	23188	CGTGGGGCTGAGTTGGGGGGG	37511	AGAGGAGCAGAACTCGGAGGA
8866	RGAGDAH	23189	AGGGGTGCGGGGGATGCGCAT	37512	AGAGGAGCAGGAGACGCACAC
8867	RGAGPST	23190	AGGGGGGCGGGGCCTTCGACT	37513	AGAGGAGCAGGACCAAGCACA
8868	RGAIATS	23191	CGTGGTGCTATTGCTACGTCG	37514	AGAGGAGCAATCGCAACAAGC
8869	RGAIGNG	23192	CGTGGGGCTATTGGGAATGGT	37515	AGAGGAGCAATCGGAAACGGA
8870	RGAIPLP	23193	CGTGGGGCGATTCCGTTGCCG	37516	AGAGGAGCAATCCCACTCCCA
8871	RGATVAP	23194	CGTGGGGCTACTGTGGCGCCT	37517	AGAGGAGCAACAGTCGCACCA
8872	RGDGVSL	23195	CGTGGTGATGGTGTTTCTTTG	37518	AGAGGAGACGGAGTCAGCCTC
8873	RGDPGLG	23196	CGTGGGGATCCTGGTCTGGGT	37519	AGAGGAGACCCAGGACTCGGA
8874	RGENSNP	23197	CGGGGTGAGAATTCTAATCCT	37520	AGAGGAGAAAACAGCAACCCA
8875	RGERSVF	23198	AGGGGTGAGCGTAGTGTGTTT	37521	AGAGGAGAAAGAAGCGTCTTC
8876	RGESAST	23199	CGTGGTGAGTCGGCTTCTACT	37522	AGAGGAGAAAGCGCAAGCACA
8877	RGGGLSM	23200	CGGGGTGGTGGGCTGTCTATG	37523	AGAGGAGGAGGACTCAGCATG
8878	RGGTMTI	23201	CGGGGTGGGACTATGACGATT	37524	AGAGGAGGAACAATGACAATC
8879	RGGTNVE	23202	CGTGGTGGTACGAATGTTGAG	37525	AGAGGAGGAACAAACGTCGAA
8880	RGHHDNE	23203	CGTGGGCATCATGATAATGAG	37526	AGAGGACACCACGACAACGAA
8881	RGHLSDP	23204	CGTGGTCATCTTTCTGATCCT	37527	AGAGGACACCTCAGCGACCCA
8882	RGIELRG	23205	AGGGGTATTGAGTTGCGGGGT	37528	AGAGGAATCGAACTCAGAGGA
8883	RGIELTV	23206	CGTGGGATTGAGCTGACTGTT	37529	AGAGGAATCGAACTCACAGTC
8884	RGIPAIA	23207	CGTGGTATTCCGGCGATTGCT	37530	AGAGGAATCCCAGCAATCGCA
8885	RGKEPFP	23208	CGGGGTAAGGAGCCTTTTCCG	37531	AGAGGAAAAGAACCATTCCCA
8886	RGLGNGT	23209	CGTGGTCTTGGTAATGGTACT	37532	AGAGGACTCGGAAACGGAACA
8887	RGMAVPG	23210	CGTGGGATGGCGGTTCCGGGG	37533	AGAGGAATGGCAGTCCCAGGA
8888	RGNEWSL	23211	CGGGGTAATGAGTGGTCGTTG	37534	AGAGGAAACGAATGGAGCCTC
8889	RGPATAS	23212	AGGGGGCCGGCTACGGCGAGT	37535	AGAGGACCAGCAACAGCAAGC
8890	RGPDTGA	23213	CGGGGTCCGGATACGGGGGCT	37536	AGAGGACCAGACACAGGAGCA
8891	RGPGEPN	23214	CGTGGGCCGGGGGAGCCTAAT	37537	AGAGGACCAGGAGAACCAAAC
8892	RGPLTSE	23215	CGTGGGCCTTTGACGAGTGAG	37538	AGAGGACCACTCACAAGCGAA
8893	RGPPPAT	23216	CGTGGGCCGCCGCCTGCGACT	37539	AGAGGACCACCACCAGCAACA
8894	RGPSTSD	23217	AGGGGTCCTAGTACTTCGGAT	37540	AGAGGACCAAGCACAAGCGAC
8895	RGPVTRD	23218	CGTGGGCCTGTTACGCGTGAT	37541	AGAGGACCAGTCACAAGAGAC
8896	RGQHNLS	23219	CGTGGTCAGCATAATCTTTCG	37542	AGAGGACAACACAACCTCAGC
8897	RGQTIRE	23220	CGGGGTCAGACGATTCGTGAG	37543	AGAGGACAAACAATCAGAGAA
8898	RGSAGVA	23221	CGGGGGAGTGCGGGTGTGGCG	37544	AGAGGAAGCGCAGGAGTCGCA
8899	RGSDASA	23222	CGTGGTTCGGATGCTTCTGCG	37545	AGAGGAAGCGACGCAAGCGCA

8900	RGSGTLT	23223	CGTGGGTCGGGTACGTTGACT	37546	AGAGGAAGCGGAACACTCACA
8901	RGSMLGD	23224	CGGGGTAGTATGCTGGGTGAT	37547	AGAGGAAGCATGCTCGGAGAC
8902	RGSNASG	23225	CGTGGTTCGAATGCGTCTGGG	37548	AGAGGAAGCAACGCAAGCGGA
8903	RGSPAAT	23226	AGGGGTTCTCCTGCTGCGACT	37549	AGAGGAAGCCCAGCAGCAACA
8904	RGSPQSS	23227	CGTGGGTCGCCGCAGTCTTCG	37550	AGAGGAAGCCCACAAAGCAGC
8905	RGSQTGN	23228	CGGGGTTCGCAGACTGGGAAT	37551	AGAGGAAGCCAAACAGGAAAC
8906	RGSQTSF	23229	CGGGGGTCTCAGACTTCTTTT	37552	AGAGGAAGCCAAACAAGCTTC
8907	RGSSTIE	23230	AGGGGTAGTTCGACGATTGAG	37553	AGAGGAAGCAGCACAATCGAA
8908	RGSTANA	23231	CGTGGTTCTACTGCGAATGCG	37554	AGAGGAAGCACAGCAAACGCA
8909	RGSTVMF	23232	CGGGGTTCTACGGTGATGTTT	37555	AGAGGAAGCACAGTCATGTTC
8910	RGTAHLL	23233	AGGGGTACGGCGCATCTTTTG	37556	AGAGGAACAGCACACCTCCTC
8911	RGTESPS	23234	AGGGGGACTGAGTCGCCGTCG	37557	AGAGGAACAGAAAGCCCAAGC
8912	RGTGNLN	23235	CGGGGTACTGGGAATCTTAAT	37558	AGAGGAACAGGAAACCTCAAC
8913	RGTGTAW	23236	AGGGGGACGGGTACGGCGTGG	37559	AGAGGAACAGGAACAGCATGG
8914	RGTMMAA	23237	CGGGGTACTATGATGGCGGCT	37560	AGAGGAACAATGATGGCAGCA
8915	RGTNTLQ	23238	AGGGGTACTAATACTCTGCAG	37561	AGAGGAACAAACACACTCCAA
8916	RGVAVPP	23239	CGTGGTGTTGCTGTGCCGCCT	37562	AGAGGAGTCGCAGTCCCACCA
8917	RGVHSPD	23240	AGGGGTGTTCATTCGCCTGAT	37563	AGAGGAGTCCACAGCCCAGAC
8918	RGVMYGD	23241	AGGGGGGTGATGTATGGTGAT	37564	AGAGGAGTCATGTACGGAGAC
8919	RHAGQDN	23242	AGGCATGCGGGTCAGGATAAT	37565	AGACACGCAGGACAAGACAAC
8920	RHAPVAS	23243	CGTCATGCTCCGGTGGCGTCT	37566	AGACACGCACCAGTCGCAAGC
8921	RHAVSNF	23244	CGGCATGCGGTTTCGAATTTT	37567	AGACACGCAGTCAGCAACTTC
8922	RHDRMDN	23245	CGGCATGATCGGATGGATAAT	37568	AGACACGACAGAATGGACAAC
8923	RHELHST	23246	CGTCATGAGTTGCATTCTACG	37569	AGACACGAACTCCACAGCACA
8924	RHENIRD	23247	CGGCATGAGAATATTCGGGAT	37570	AGACACGAAAACATCAGAGAC
8925	RHERPMA	23248	CGTCATGAGAGGCCTATGGCG	37571	AGACACGAAAGACCAATGGCA
8926	RHGSSMT	23249	CGGCATGGTAGTTCGATGACG	37572	AGACACGGAAGCAGCATGACA
8927	RHGTHPS	23250	CGGCATGGGACGCATCCTTCG	37573	AGACACGGAACACACCCAAGC
8928	RHHSAPN	23251	AGGCATCATTCTGCGCCGAAT	37574	AGACACCACAGCGCACCAAAC
8929	RHLGSLP	23252	CGTCATTTGGGGTCGCTGCCG	37575	AGACACCTCGGAAGCCTCCCA
8930	RHPAAHA	23253	CGGCATCCTGCTGCTCATGCT	37576	AGACACCCAGCAGCACACGCA
8931	RHPATIS	23254	CGGCATCCTGCTACTATTTCT	37577	AGACACCCAGCAACAATCAGC
8932	RHPMLTG	23255	AGGCATCCGATGCTTACTGGG	37578	AGACACCCAATGCTCACAGGA
8933	RHPPNSF	23256	CGTCATCCTCCGAATTCTTTT	37579	AGACACCCACCAAACAGCTTC
8934	RHPSTPN	23257	CGGCATCCGAGTACTCCGAAT	37580	AGACACCCAAGCACACCAAAC
8935	RHPVTEP	23258	CGGCATCCGGTGACTGAGCCG	37581	AGACACCCAGTCACAGAACCA
8936	RHQTIIA	23259	AGGCATCAGACGATTATTGCT	37582	AGACACCAAACAATCATCGCA
8937	RHRPAPE	23260	AGGCATAGGCCTGCGCCGGAG	37583	AGACACAGACCAGCACCAGAA
8938	RHSEVTF	23261	CGTCATAGTGAGGTGACGTTT	37584	AGACACAGCGAAGTCACATTC
8939	RHSHTIS	23262	AGGCATTCTCATACTATTTCG	37585	AGACACAGCCACACAATCAGC
8940	RHSLSLD	23263	CGGCATTCTCTGAGTTTGGAT	37586	AGACACAGCCTCAGCCTCGAC
8941	RHSNQTL	23264	AGGCATTCTAATCAGACGTTG	37587	AGACACAGCAACCAAACACTC
8942	RHSPLTG	23265	CGTCATTCTCCTTTGACTGGT	37588	AGACACAGCCCACTCACAGGA
8943	RHSQGPF	23266	AGGCATAGTCAGGGTCCTTTT	37589	AGACACAGCCAAGGACCATTC
8944	RHTMETS	23267	CGTCATACGATGGAGACTTCG	37590	AGACACACAATGGAAACAAGC

8945	RHTPDQG	23268	CGTCATACGCCTGATCAGGGT	37591	AGACACACACCAGACCAAGGA
8946	RIAPTGN	23269	CGGATTGCGCCGACTGGTAAT	37592	AGAATCGCACCAACAGGAAAC
8947	RIDAELE	23270	CGTATTGATGCTGAGCTTGAG	37593	AGAATCGACGCAGAACTCGAA
8948	RIDGILS	23271	CGTATTGATGGGATTCTGTCT	37594	AGAATCGACGGAATCCTCAGC
8949	RIENEVV	23272	CGTATTGAGAATGAGGTTGTG	37595	AGAATCGAAAACGAAGTCGTC
8950	RIGDHIR	23273	CGGATTGGTGATCATATTCGT	37596	AGAATCGGAGACCACATCAGA
8951	RIGKNDS	23274	CGTATTGGTAAGAATGATTCT	37597	AGAATCGGAAAAAACGACAGC
8952	RIGQNLA	23275	CGGATTGGTCAGAATTTGGCT	37598	AGAATCGGACAAAACCTCGCA
8953	RIGQTFA	23276	CGGATTGGGCAGACGTTTGCG	37599	AGAATCGGACAAACATTCGCA
8954	RIGSGTG	23277	AGGATTGGTTCGGGTACTGGT	37600	AGAATCGGAAGCGGAACAGGA
8955	RIGWTID	23278	CGTATTGGTTGGACGATTGAT	37601	AGAATCGGATGGACAATCGAC
8956	RIHYEGM	23279	CGTATTCATTATGAGGGGATG	37602	AGAATCCACTACGAAGGAATG
8957	RINIAET	23280	CGTATTAATATTGCTGAGACT	37603	AGAATCAACATCGCAGAAACA
8958	RIPALSG	23281	CGTATTCCGGCTTTGTCTGGT	37604	AGAATCCCAGCACTCAGCGGA
8959	RIPTSPP	23282	CGGATTCCTACGAGTCCTCCG	37605	AGAATCCCAACAAGCCCACCA
8960	RIPVRVD	23283	CGTATTCCTGTTCGGGTTGAT	37606	AGAATCCCAGTCAGAGTCGAC
8961	RIRYPEG	23284	CGGATTAGGTATCCGGAGGGT	37607	AGAATCAGATACCCAGAAGGA
8962	RISALQP	23285	CGTATTTCTGCTTTGCAGCCT	37608	AGAATCAGCGCACTCCAACCA
8963	RISDYPP	23286	CGGATTAGTGATTATCCTCCT	37609	AGAATCAGCGACTACCCACCA
8964	RISGHAS	23287	AGGATTAGTGGGCATGCTAGT	37610	AGAATCAGCGGACACGCAAGC
8965	RISPTPI	23288	CGGATTTCTCCGACTCCGATT	37611	AGAATCAGCCCAACACCAATC
8966	RISSGID	23289	CGGATTTCGAGTGGGATTGAT	37612	AGAATCAGCAGCGGAATCGAC
8967	RISSSPD	23290	CGTATTTCTAGTTCTCCTGAT	37613	AGAATCAGCAGCAGCCCAGAC
8968	RIYDQSI	23291	CGTATTTATGATCAGTCTATT	37614	AGAATCTACGACCAAAGCATC
8969	RIYSPDG	23292	AGGATTTATAGTCCGGATGGG	37615	AGAATCTACAGCCCAGACGGA
8970	RIYTTSP	23293	AGGATTTATACTACGTCGCCT	37616	AGAATCTACACAACAAGCCCA
8971	RKDDTTW	23294	CGGAAGGATGATACTACGTGG	37617	AGAAAAGACGACACAACATGG
8972	RKDLSWD	23295	CGTAAGGATCTTTCGTGGGAT	37618	AGAAAAGACCTCAGCTGGGAC
8973	RKDRSPE	23296	AGGAAGGATCGTAGTCCTGAG	37619	AGAAAAGACAGAAGCCCAGAA
8974	RKDTPMH	23297	CGGAAGGATACGCCGATGCAT	37620	AGAAAAGACACACCAATGCAC
8975	RKDTVPN	23298	CGTAAGGATACTGTTCCGAAT	37621	AGAAAAGACACAGTCCCAAAC
8976	RKGLDDA	23299	CGTAAGGGTTTGGATGATGCG	37622	AGAAAAGGACTCGACGACGCA
8977	RKLPLVD	23300	CGTAAGCTTCCTCTTGTTGAT	37623	AGAAAACTCCCACTCGTCGAC
8978	RKMNQDQ	23301	AGGAAGATGAATCAGGATCAG	37624	AGAAAAATGAACCAAGACCAA
8979	RKNYQLD	23302	CGTAAGAATTATCAGCTGGAT	37625	AGAAAAAACTACCAACTCGAC
8980	RKPLTAP	23303	AGGAAGCCTTTGACGGCTCCT	37626	AGAAAACCACTCACAGCACCA
8981	RKSPQEA	23304	CGTAAGTCGCCGCAGGAGGCG	37627	AGAAAAAGCCCACAAGAAGCA
8982	RKSTLDT	23305	CGTAAGTCTACGTTGGATACT	37628	AGAAAAAGCACACTCGACACA
8983	RKVESRR	23306	CGTAAGGTGGAGTCGAGGAGG	37629	AGAAAAGTCGAAAGCAGAAGA
8984	RKVTPDT	23307	CGTAAGGTTACTCCTGATACT	37630	AGAAAAGTCACACCAGACACA
8985	RLAAETL	23308	AGGCTTGCTGCGGAGACTCTG	37631	AGACTCGCAGCAGAAACACTC
8986	RLAANHL	23309	CGTTTGGCGGCGAATCATCTT	37632	AGACTCGCAGCAAACCACCTC
8987	RLAETSH	23310	AGGTTGGCGGAGACGTCTCAT	37633	AGACTCGCAGAAACAAGCCAC
8988	RLALESN	23311	CGGTTGGCGCTTGAGTCTAAT	37634	AGACTCGCACTCGAAAGCAAC
8989	RLAMQAA	23312	AGGCTGGCTATGCAGGCGGCT	37635	AGACTCGCAATGCAAGCAGCA

8990	RLAQINS	23313	CGGCTTGCTCAGATTAATTCG	37636	AGACTCGCACAAATCAACAGC
8991	RLATEDP	23314	CGGCTTGCTACTGAGGATCCT	37637	AGACTCGCAACAGAAGACCCA
8992	RLDANSR	23315	CGGCTTGATGCGAATAGTCGG	37638	AGACTCGACGCAAACAGCAGA
8993	RLDDVGL	23316	CGTCTTGATGATGTTGGGCTT	37639	AGACTCGACGACGTCGGACTC
8994	RLDFDTP	23317	CGGTTGGATTTTGATACGCCG	37640	AGACTCGACTTCGACACACCA
8995	RLDMRIE	23318	CGGTTGGATATGCGTATTGAG	37641	AGACTCGACATGAGAATCGAA
8996	RLDPGEP	23319	CGTCTGGATCCTGGGGAGCCG	37642	AGACTCGACCCAGGAGAACCA
8997	RLDPHSS	23320	AGGCTTGATCCTCATTCTTCT	37643	AGACTCGACCCACACAGCAGC
8998	RLDSLAL	23321	CGGTTGGATTCGTTGGCTCTG	37644	AGACTCGACAGCCTCGCACTC
8999	RLDSMFS	23322	CGGCTTGATAGTATGTTTTCT	37645	AGACTCGACAGCATGTTCAGC
9000	RLDTTMQ	23323	CGGCTTGATACTACGATGCAG	37646	AGACTCGACACAACAATGCAA
9001	RLDTVSS	23324	AGGCTTGATACGGTTTCGTCT	37647	AGACTCGACACAGTCAGCAGC
9002	RLEAQVA	23325	CGTCTTGAGGCTCAGGTGGCG	37648	AGACTCGAAGCACAAGTCGCA
9003	RLEPMQN	23326	AGGCTTGAGCCTATGCAGAAT	37649	AGACTCGAACCAATGCAAAAC
9004	RLESSRP	23327	CGTCTTGAGTCTTCTCGGCCG	37650	AGACTCGAAAGCAGCAGACCA
9005	RLFGDDY	23328	CGTCTTTTTGGTGATGATTAT	37651	AGACTCTTCGGAGACGACTAC
9006	RLGDGAD	23329	CGGCTGGGGGATGGGGCGGAT	37652	AGACTCGGAGACGGAGCAGAC
9007	RLGDVWA	23330	CGTCTGGGGGATGTTTGGGCT	37653	AGACTCGGAGACGTCTGGGCA
9008	RLGMVSE	23331	CGGTTGGGTATGGTTTCTGAG	37654	AGACTCGGAATGGTCAGCGAA
9009	RLGPGYP	23332	AGGTTGGGGCCTGGGTATCCT	37655	AGACTCGGACCAGGATACCCA
9010	RLGPVSG	23333	CGGCTGGGTCCGGTTAGTGGT	37656	AGACTCGGACCAGTCAGCGGA
9011	RLGSQTS	23334	AGGCTGGGTTCGCAGACTTCT	37657	AGACTCGGAAGCCAAACAAGC
9012	RLGTHSE	23335	CGGCTGGGGACTCATTCGGAG	37658	AGACTCGGAACACACAGCGAA
9013	RLGTWAE	23336	CGTCTTGGGACTTGGGCTGAG	37659	AGACTCGGAACATGGGCAGAA
9014	RLGVCPS	23337	AGGCTTGGGGTGTGTCCGTCT	37660	AGACTCGGAGTCTGCCCAAGC
9015	RLHIGSG	23338	CGTCTGCATATTGGGTCTGGG	37661	AGACTCCACATCGGAAGCGGA
9016	RLHINSE	23339	CGTCTGCATATTAATAGTGAG	37662	AGACTCCACATCAACAGCGAA
9017	RLHTDLG	23340	CGGCTTCATACGGATTTGGGT	37663	AGACTCCACACAGACCTCGGA
9018	RLIHSGF	23341	CGGCTGATTCATTCGGGTTTT	37664	AGACTCATCCACAGCGGATTC
9019	RLINNSA	23342	AGGCTGATTAATAATTCTGCT	37665	AGACTCATCAACAACAGCGCA
9020	RLLKTPS	23343	CGGTTGTTGAAGACTCCGAGT	37666	AGACTCCTCAAAACACCAAGC
9021	RLLSATG	23344	CGTCTTCTGTCGGCGACTGGT	37667	AGACTCCTCAGCGCAACAGGA
9022	RLMDRAG	23345	CGTTTGATGGATCGTGCGGGT	37668	AGACTCATGGACAGAGCAGGA
9023	RLMNPKG	23346	CGGTTGATGAATCCGAAGGGT	37669	AGACTCATGAACCCAAAAGGA
9024	RLNDLTL	23347	AGGCTGAATGATCTGACTCTT	37670	AGACTCAACGACCTCACACTC
9025	RLNLSTT	23348	CGGTTGAATTTGTCGACTACT	37671	AGACTCAACCTCAGCACAACA
9026	RLNNNTL	23349	AGGCTGAATAATAATACTCTG	37672	AGACTCAACAACAACACACTC
9027	RLNQVPA	23350	CGTCTGAATCAGGTTCCGGCG	37673	AGACTCAACCAAGTCCCAGCA
9028	RLNTSMM	23351	AGGCTTAATACTTCGATGATG	37674	AGACTCAACACAAGCATGATG
9029	RLPDPSS	23352	AGGTTGCCTGATCCTAGTTCG	37675	AGACTCCCAGACCCAAGCAGC
9030	RLPGPER	23353	AGGCTGCCGGGGCCTGAGCGT	37676	AGACTCCCAGGACCAGAAAGA
9031	RLPLENL	23354	CGTCTGCCGTTGGAGAATTTG	37677	AGACTCCCACTCGAAAACCTC
9032	RLPLSAH	23355	CGTTTGCCGCTGTCGGCTCAT	37678	AGACTCCCACTCAGCGCACAC
9033	RLPPSGI	23356	CGTCTTCCTCCGTCGGGGATT	37679	AGACTCCCACCAAGCGGAATC
9034	RLPPTDV	23357	AGGCTGCCGCCTACGGATGTG	37680	AGACTCCCACCAACAGACGTC

9035	RLPQRDI	23358	CGGTTGCCTCAGAGGGATATT	37681	AGACTCCCACAAAGAGACATC
9036	RLPSEKQ	23359	CGTCTGCCGTCTGAGAAGCAG	37682	AGACTCCCAAGCGAAAAACAA
9037	RLPSLVD	23360	CGGCTTCCTTCTTTGGTTGAT	37683	AGACTCCCAAGCCTCGTCGAC
9038	RLPTRLD	23361	AGGCTGCCTACGCGGCTTGAT	37684	AGACTCCCAACAAGACTCGAC
9039	RLPTSHF	23362	CGTCTTCCTACTTCTCATTTT	37685	AGACTCCCAACAAGCCACTTC
9040	RLPTVTG	23363	AGGCTGCCGACTGTTACTGGG	37686	AGACTCCCAACAGTCACAGGA
9041	RLPVQPS	23364	CGGCTTCCGGTGCAGCCGTCG	37687	AGACTCCCAGTCCAACCAAGC
9042	RLQDNGS	23365	AGGCTGCAGGATAATGGTTCG	37688	AGACTCCAAGACAACGGAAGC
9043	RLQGFPN	23366	CGTCTTCAGGGGTTTCCGAAT	37689	AGACTCCAAGGATTCCCAAAC
9044	RLQLQDH	23367	CGTCTGCAGCTTCAGGATCAT	37690	AGACTCCAACTCCAAGACCAC
9045	RLQNTGT	23368	CGTTTGCAGAATACGGGGACG	37691	AGACTCCAAAACACAGGAACA
9046	RLQPAEE	23369	CGTCTTCAGCCTGCTGAGGAG	37692	AGACTCCAACCAGCAGAAGAA
9047	RLQQVGV	23370	CGGCTTCAGCAGGTTGGGGTG	37693	AGACTCCAACAAGTCGGAGTC
9048	RLQSSIE	23371	CGTCTGCAGTCTTCTATTGAG	37694	AGACTCCAAAGCAGCATCGAA
9049	RLRPGLD	23372	CGGCTTCGTCCGGGTCTTGAT	37695	AGACTCAGACCAGGACTCGAC
9050	RLSADTH	23373	AGGCTGAGTGCGGATACGCAT	37696	AGACTCAGCGCAGACACACAC
9051	RLSHAGV	23374	CGTCTTTCTCATGCTGGGGTG	37697	AGACTCAGCCACGCAGGAGTC
9052	RLSIGSV	23375	AGGCTGAGTATTGGTAGTGTT	37698	AGACTCAGCATCGGAAGCGTC
9053	RLSLDRF	23376	CGTCTGTCTTTGGATAGGTTT	37699	AGACTCAGCCTCGACAGATTC
9054	RLSLPST	23377	AGGTTGTCGTTGCCTTCTACG	37700	AGACTCAGCCTCCCAAGCACA
9055	RLSNSEP	23378	AGGCTTTCGAATTCGGAGCCT	37701	AGACTCAGCAACAGCGAACCA
9056	RLSPPPS	23379	CGTCTGTCTCCGCCGCCTAGT	37702	AGACTCAGCCCACCACCAAGC
9057	RLSPQPA	23380	AGGTTGTCGCCTCAGCCGGCT	37703	AGACTCAGCCCACAACCAGCA
9058	RLSQSNN	23381	CGTCTGAGTCAGTCGAATAAT	37704	AGACTCAGCCAAAGCAACAAC
9059	RLSSGPI	23382	CGGCTGTCGTCTGGTCCTATT	37705	AGACTCAGCAGCGGACCAATC
9060	RLSSNLE	23383	CGGCTTTCTAGTAATCTGGAG	37706	AGACTCAGCAGCAACCTCGAA
9061	RLTATSN	23384	AGGCTTACGGCTACGTCTAAT	37707	AGACTCACAGCAACAAGCAAC
9062	RLTDRST	23385	CGGCTGACTGATAGGTCTACG	37708	AGACTCACAGACAGAAGCACA
9063	RLTEPHR	23386	CGTTTGACGGAGCCTCATCGT	37709	AGACTCACAGAACCACACAGA
9064	RLTHESP	23387	CGGCTGACGCATGAGTCTCCG	37710	AGACTCACACACGAAAGCCCA
9065	RLTHTGH	23388	CGGCTTACTCATACTGGTCAT	37711	AGACTCACACACACAGGACAC
9066	RLTMVRD	23389	AGGCTTACTATGGTTCGGGAT	37712	AGACTCACAATGGTCAGAGAC
9067	RLTPEGQ	23390	CGTCTGACTCCGGAGGGTCAG	37713	AGACTCACACCAGAAGGACAA
9068	RLVDNLP	23391	AGGCTTGTTGATAATTTGCCG	37714	AGACTCGTCGACAACCTCCCA
9069	RLVNQMS	23392	CGTCTGGTTAATCAGATGTCG	37715	AGACTCGTCAACCAAATGAGC
9070	RLVQAFA	23393	CGGCTGGTGCAGGCGTTTGCG	37716	AGACTCGTCCAAGCATTCGCA
9071	RLYSGIE	23394	AGGCTTTATTCTGGGATTGAG	37717	AGACTCTACAGCGGAATCGAA
9072	RLYSNSP	23395	CGTCTGTATTCGAATTCGCCT	37718	AGACTCTACAGCAACAGCCCA
9073	RMAKETS	23396	CGGATGGCTAAGGAGACTTCT	37719	AGAATGGCAAAAGAAACAAGC
9074	RMEPPIS	23397	CGGATGGAGCCTCCTATTTCG	37720	AGAATGGAACCACCAATCAGC
9075	RMEPSAV	23398	AGGATGGAGCCTTCTGCTGTT	37721	AGAATGGAACCAAGCGCAGTC
9076	RMGAAVY	23399	AGGATGGGGGCTGCTGTGTAT	37722	AGAATGGGAGCAGCAGTCTAC
9077	RMGVHPT	23400	CGGATGGGTGTTCATCCGACT	37723	AGAATGGGAGTCCACCCAACA
9078	RMGYVEA	23401	AGGATGGGTTATGTTGAGGCT	37724	AGAATGGGATACGTCGAAGCA
9079	RMHVTEA	23402	AGGATGCATGTGACTGAGGCT	37725	AGAATGCACGTCACAGAAGCA

9080	RMIQSGH	23403	CGGATGATTCAGTCGGGTCAT	37726	AGAATGATCCAAAGCGGACAC
9081	RMLAPSG	23404	CGTATGTTGGCGCCGTCTGGG	37727	AGAATGCTCGCACCAAGCGGA
9082	RMLDQLN	23405	AGGATGCTGGATCAGTTGAAT	37728	AGAATGCTCGACCAACTCAAC
9083	RMLPDVY	23406	AGGATGTTGCCGGATGTGTAT	37729	AGAATGCTCCCAGACGTCTAC
9084	RMMPDLP	23407	CGGATGATGCCTGATCTTCCT	37730	AGAATGATGCCAGACCTCCCA
9085	RMNEALG	23408	AGGATGAATGAGGCGCTGGGG	37731	AGAATGAACGAAGCACTCGGA
9086	RMNIQVG	23409	CGTATGAATATTCAGGTTGGT	37732	AGAATGAACATCCAAGTCGGA
9087	RMNYGTE	23410	CGGATGAATTATGGGACTGAG	37733	AGAATGAACTACGGAACAGAA
9088	RMPAMAV	23411	AGGATGCCGGCTATGGCTGTT	37734	AGAATGCCAGCAATGGCAGTC
9089	RMPASNA	23412	AGGATGCCGGCGTCGAATGCG	37735	AGAATGCCAGCAAGCAACGCA
9090	RMPREQS	23413	CGTATGCCTAGGGAGCAGTCG	37736	AGAATGCCAAGAGAACAAAGC
9091	RMQSAYV	23414	CGGATGCAGTCGGCGTATGTG	37737	AGAATGCAAAGCGCATACGTC
9092	RMQSQGF	23415	CGTATGCAGTCGCAGGGTTTT	37738	AGAATGCAAAGCCAAGGATTC
9093	RMSDSFV	23416	CGTATGTCTGATTCGTTTGTG	37739	AGAATGAGCGACAGCTTCGTC
9094	RMSEVTI	23417	AGGATGTCTGAGGTTACGATT	37740	AGAATGAGCGAAGTCACAATC
9095	RMSIPND	23418	CGTATGAGTATTCCTAATGAT	37741	AGAATGAGCATCCCAAACGAC
9096	RMSLASE	23419	CGGATGTCGTTGGCTAGTGAG	37742	AGAATGAGCCTCGCAAGCGAA
9097	RMSNSPQ	23420	CGGATGTCTAATAGTCCTCAG	37743	AGAATGAGCAACAGCCCACAA
9098	RMSSDLP	23421	CGTATGTCTAGTGATCTTCCT	37744	AGAATGAGCAGCGACCTCCCA
9099	RMTAAIC	23422	CGGATGACGGCGGCTATTTGT	37745	AGAATGACAGCAGCAATCTGC
9100	RMTHTAP	23423	CGTATGACTCATACTGCGCCT	37746	AGAATGACACACACAGCACCA
9101	RMTIGTT	23424	CGGATGACTATTGGTACTACG	37747	AGAATGACAATCGGAACAACA
9102	RMVGGGD	23425	CGTATGGTTGGTGGTGGTGAT	37748	AGAATGGTCGGAGGAGGAGAC
9103	RMVNLGH	23426	AGGATGGTTAATCTTGGGCAT	37749	AGAATGGTCAACCTCGGACAC
9104	RMVSSSA	23427	CGTATGGTTTCTAGTTCGGCG	37750	AGAATGGTCAGCAGCAGCGCA
9105	RMYGSSS	23428	CGTATGTATGGTTCGTCTTCT	37751	AGAATGTACGGAAGCAGCAGC
9106	RNAAVDP	23429	AGGAATGCGGCTGTGGATCCG	37752	AGAAACGCAGCAGTCGACCCA
9107	RNAGETH	23430	AGGAATGCGGGGGAGACTCAT	37753	AGAAACGCAGGAGAAACACAC
9108	RNAGTDR	23431	CGTAATGCTGGGACGGATCGG	37754	AGAAACGCAGGAACAGACAGA
9109	RNANMPT	23432	AGGAATGCTAATATGCCTACG	37755	AGAAACGCAAACATGCCAACA
9110	RNAPSAD	23433	CGTAATGCGCCTTCTGCGGAT	37756	AGAAACGCACCAAGCGCAGAC
9111	RNATAMV	23434	AGGAATGCTACTGCGATGGTT	37757	AGAAACGCAACAGCAATGGTC
9112	RNDLTGV	23435	AGGAATGATTTGACGGGTGTT	37758	AGAAACGACCTCACAGGAGTC
9113	RNDMVQS	23436	CGGAATGATATGGTGCAGTCT	37759	AGAAACGACATGGTCCAAAGC
9114	RNDNRVT	23437	CGGAATGATAATAGGGTTACT	37760	AGAAACGACAACAGAGTCACA
9115	RNDRSFA	23438	CGTAATGATAGGTCGTTTGCT	37761	AGAAACGACAGAAGCTTCGCA
9116	RNDTSDL	23439	CGTAATGATACTAGTGATTTG	37762	AGAAACGACACAAGCGACCTC
9117	RNDVSDI	23440	CGTAATGATGTTTCGGATATT	37763	AGAAACGACGTCAGCGACATC
9118	RNEHHLP	23441	CGTAATGAGCATCATTTGCCT	37764	AGAAACGAACACCACCTCCCA
9119	RNEPNGG	23442	CGTAATGAGCCGAATGGTGGG	37765	AGAAACGAACCAAACGGAGGA
9120	RNFADSM	23443	CGGAATTTTGCTGATTCTATG	37766	AGAAACTTCGCAGACAGCATG
9121	RNFTGPE	23444	CGGAATTTTACTGGTCCTGAG	37767	AGAAACTTCACAGGACCAGAA
9122	RNGAIQA	23445	CGTAATGGTGCTATTCAGGCT	37768	AGAAACGGAGCAATCCAAGCA
9123	RNGRDAG	23446	CGGAATGGTCGTGATGCGGGG	37769	AGAAACGGAAGAGACGCAGGA
9124	RNGVTAA	23447	CGTAATGGTGTGACGGCGGCG	37770	AGAAACGGAGTCACAGCAGCA

9125	RNHGFAE	23448	CGGAATCATGGTTTTGCTGAG	37771	AGAAACCACGGATTCGCAGAA
9126	RNIDDAN	23449	CGGAATATTGATGATGCGAAT	37772	AGAAACATCGACGACGCAAAC
9127	RNKENVG	23450	CGTAATAAGGAGAATGTTGGG	37773	AGAAACAAAGAAAACGTCGGA
9128	RNLPPRD	23451	CGTAATCTTCCGCCTCGTGAT	37774	AGAAACCTCCCACCAAGAGAC
9129	RNLTIPE	23452	CGGAATCTGACTATTCCTGAG	37775	AGAAACCTCACAATCCCAGAA
9130	RNMALTS	23453	AGGAATATGGCGCTGACTAGT	37776	AGAAACATGGCACTCACAAGC
9131	RNNALPD	23454	AGGAATAATGCTCTGCCGGAT	37777	AGAAACAACGCACTCCCAGAC
9132	RNNSHGF	23455	CGTAATAATTCTCATGGGTTT	37778	AGAAACAACAGCCACGGATTC
9133	RNPDMHH	23456	AGGAATCCTGATATGCATCAT	37779	AGAAACCCAGACATGCACCAC
9134	RNPLSAQ	23457	AGGAATCCGCTTAGTGCTCAG	37780	AGAAACCCACTCAGCGCACAA
9135	RNQGLLA	23458	AGGAATCAGGGGCTTTTGGCT	37781	AGAAACCAAGGACTCCTCGCA
9136	RNQTSTS	23459	CGGAATCAGACTAGTACGTCT	37782	AGAAACCAAACAAGCACAAGC
9137	RNRDPQF	23460	AGGAATCGGGATCCGCAGTTT	37783	AGAAACAGAGACCCACAATTC
9138	RNSAALQ	23461	AGGAATAGTGCTGCTTTGCAG	37784	AGAAACAGCGCAGCACTCCAA
9139	RNSDYSV	23462	CGGAATTCGGATTATTCGGTT	37785	AGAAACAGCGACTACAGCGTC
9140	RNSLGFG	23463	AGGAATTCTCTTGGTTTTGGG	37786	AGAAACAGCCTCGGATTCGGA
9141	RNSQVPI	23464	CGTAATAGTCAGGTTCCTATT	37787	AGAAACAGCCAAGTCCCAATC
9142	RNSSSLG	23465	CGTAATTCTTCTTCGTTGGGG	37788	AGAAACAGCAGCAGCCTCGGA
9143	RNSTSMT	23466	CGTAATTCTACGTCTATGACG	37789	AGAAACAGCACAAGCATGACA
9144	RNSVTTP	23467	CGGAATTCGGTGACTACTCCT	37790	AGAAACAGCGTCACAACACCA
9145	RNSYPSD	23468	CGGAATAGTTATCCTAGTGAT	37791	AGAAACAGCTACCCAAGCGAC
9146	RNTDVDS	23469	CGTAATACGGATGTTGATTCG	37792	AGAAACACAGACGTCGACAGC
9147	RNTLLMD	23470	AGGAATACTCTTCTGATGGAT	37793	AGAAACACACTCCTCATGGAC
9148	RNTLVIP	23471	CGTAATACGCTGGTTATTCCT	37794	AGAAACACACTCGTCATCCCA
9149	RNTPNRD	23472	AGGAATACTCCTAATCGGGAT	37795	AGAAACACACCAAACAGAGAC
9150	RNTSQLD	23473	CGGAATACTTCGCAGCTGGAT	37796	AGAAACACAAGCCAACTCGAC
9151	RNVETAG	23474	CGTAATGTGGAGACTGCTGGT	37797	AGAAACGTCGAAACAGCAGGA
9152	RNVGHGD	23475	CGTAATGTTGGTCATGGTGAT	37798	AGAAACGTCGGACACGGAGAC
9153	RNVGPPT	23476	CGTAATGTTGGTCCTCCTACT	37799	AGAAACGTCGGACCACCAACA
9154	RNVPEHR	23477	AGGAATGTTCCTGAGCATCGG	37800	AGAAACGTCCCAGAACACAGA
9155	RNVQFSP	23478	CGGAATGTTCAGTTTTCGCCG	37801	AGAAACGTCCAATTCAGCCCA
9156	RNVRDTP	23479	CGGAATGTGCGTGATACTCCG	37802	AGAAACGTCAGAGACACACCA
9157	RNVSDSS	23480	CGTAATGTGTCTGATAGTTCT	37803	AGAAACGTCAGCGACAGCAGC
9158	RNYAGKD	23481	CGTAATTATGCGGGTAAGGAT	37804	AGAAACTACGCAGGAAAAGAC
9159	RPAAVSN	23482	CGGCCTGCTGCGGTTTCTAAT	37805	AGACCAGCAGCAGTCAGCAAC
9160	RPADKCT	23483	CGTCCGGCTGATAAGTGTACG	37806	AGACCAGCAGACAAATGCACA
9161	RPAKLEL	23484	CGGCCTGCGAAGCTGGAGTTG	37807	AGACCAGCAAAACTCGAACTC
9162	RPAMLAT	23485	CGGCCGGCTATGCTGGCTACT	37808	AGACCAGCAATGCTCGCAACA
9163	RPASGHV	23486	CGGCCGGCGTCGGGTCATGTG	37809	AGACCAGCAAGCGGACACGTC
9164	RPATVGA	23487	CGGCCTGCGACGGTGGGTGCT	37810	AGACCAGCAACAGTCGGAGCA
9165	RPAVMKG	23488	CGTCCTGCTGTGATGAAGGGG	37811	AGACCAGCAGTCATGAAAGGA
9166	RPDASES	23489	CGTCCTGATGCTTCTGAGTCT	37812	AGACCAGACGCAAGCGAAAGC
9167	RPDDPAN	23490	AGGCCTGATGATCCTGCGAAT	37813	AGACCAGACGACCCAGCAAAC
9168	RPDGMAS	23491	CGTCCTGATGGTATGGCTTCT	37814	AGACCAGACGGAATGGCAAGC
9169	RPDHSNV	23492	CGTCCTGATCATTCTAATGTT	37815	AGACCAGACCACAGCAACGTC

9170	RPDNSKA	23493	AGGCCGGATAATTCTAAGGCG	37816	AGACCAGACAACAGCAAAGCA
9171	RPDSLKL	23494	AGGCCGGATTCGCTGAAGCTT	37817	AGACCAGACAGCCTCAAACTC
9172	RPDSPFT	23495	CGGCCGGATTCGCCTTTTACT	37818	AGACCAGACAGCCCATTCACA
9173	RPDTRAA	23496	CGGCCGGATACTCGGGCTGCT	37819	AGACCAGACACAAGAGCAGCA
9174	RPEEATS	23497	AGGCCTGAGGAGGCTACGTCG	37820	AGACCAGAAGAAGCAACAAGC
9175	RPEGSMG	23498	CGTCCTGAGGGGTCTATGGGT	37821	AGACCAGAAGGAAGCATGGGA
9176	RPELGLL	23499	AGGCCTGAGCTTGGTCTTCTG	37822	AGACCAGAACTCGGACTCCTC
9177	RPELKQS	23500	CGTCCTGAGTTGAAGCAGAGT	37823	AGACCAGAACTCAAACAAAGC
9178	RPELSSR	23501	AGGCCTGAGCTGTCTTCGAGG	37824	AGACCAGAACTCAGCAGCAGA
9179	RPESVYG	23502	CGGCCTGAGTCGGTGTATGGG	37825	AGACCAGAAAGCGTCTACGGA
9180	RPFAPQE	23503	AGGCCGTTTGCTCCTCAGGAG	37826	AGACCATTCGCACCACAAGAA
9181	RPFSPTP	23504	CGTCCGTTTAGTCCGACGCCG	37827	AGACCATTCAGCCCAACACCA
9182	RPGADAR	23505	AGGCCTGGTGCTGATGCTAGG	37828	AGACCAGGAGCAGACGCAAGA
9183	RPGGGTE	23506	AGGCCGGGGGGTGGTACGGAG	37829	AGACCAGGAGGAGGAACAGAA
9184	RPGLSTL	23507	CGGCCGGGGTTGTCGACGCTT	37830	AGACCAGGACTCAGCACACTC
9185	RPGNTLP	23508	AGGCCTGGGAATACGTTGCCT	37831	AGACCAGGAAACACACTCCCA
9186	RPGREPL	23509	CGGCCGGGGAGGGAGCCGCTT	37832	AGACCAGGAAGAGAACCACTC
9187	RPGSSTE	23510	AGGCCGGGTTCGAGTACTGAG	37833	AGACCAGGAAGCAGCACAGAA
9188	RPGTSTV	23511	CGTCCGGGTACGTCGACGGTT	37834	AGACCAGGAACAAGCACAGTC
9189	RPHSDKF	23512	CGTCCGCATAGTGATAAGTTT	37835	AGACCACACAGCGACAAATTC
9190	RPIASTN	23513	CGGCCTATTGCTTCTACGAAT	37836	AGACCAATCGCAAGCACAAAC
9191	RPKESSV	23514	CGGCCTAAGGAGTCGTCTGTT	37837	AGACCAAAAGAAAGCAGCGTC
9192	RPLDAPD	23515	AGGCCTCTTGATGCGCCTGAT	37838	AGACCACTCGACGCACCAGAC
9193	RPLDQES	23516	CGTCCTCTTGATCAGGAGAGT	37839	AGACCACTCGACCAAGAAAGC
9194	RPLESRD	23517	CGGCCGCTGGAGTCTCGGGAT	37840	AGACCACTCGAAAGCAGAGAC
9195	RPLGPHI	23518	CGTCCTCTTGGTCCGCATATT	37841	AGACCACTCGGACCACACATC
9196	RPLGPND	23519	CGTCCTCTGGGTCCTAATGAT	37842	AGACCACTCGGACCAAACGAC
9197	RPLGSDT	23520	CGTCCGCTGGGGTCTGATACT	37843	AGACCACTCGGAAGCGACACA
9198	RPLIPNN	23521	CGGCCTCTGATTCCTAATAAT	37844	AGACCACTCATCCCAAACAAC
9199	RPLKHDP	23522	AGGCCGTTGAAGCATGATCCT	37845	AGACCACTCAAACACGACCCA
9200	RPLTEYV	23523	CGTCCGCTGACTGAGTATGTG	37846	AGACCACTCACAGAATACGTC
9201	RPLVMGV	23524	AGGCCGCTTGTTATGGGGGTT	37847	AGACCACTCGTCATGGGAGTC
9202	RPMATLS	23525	AGGCCGATGGCTACTTTGTCT	37848	AGACCAATGGCAACACTCAGC
9203	RPMITSA	23526	AGGCCGATGATTACGTCTGCG	37849	AGACCAATGATCACAAGCGCA
9204	RPMNLKE	23527	CGGCCGATGAATCTTAAGGAG	37850	AGACCAATGAACCTCAAAGAA
9205	RPMPNSP	23528	CGTCCGATGCCGAATTCGCCT	37851	AGACCAATGCCAAACAGCCCA
9206	RPMSLES	23529	CGTCCGATGTCTCTTGAGTCG	37852	AGACCAATGAGCCTCGAAAGC
9207	RPMTPQL	23530	AGGCCGATGACTCCGCAGCTT	37853	AGACCAATGACACCACAACTC
9208	RPNAVTV	23531	AGGCCGAATGCTGTTACTGTG	37854	AGACCAAACGCAGTCACAGTC
9209	RPPEIHF	23532	CGTCCGCCTGAGATTCATTTT	37855	AGACCACCAGAAATCCACTTC
9210	RPPGPMS	23533	CGTCCTCCGGGTCCTATGTCT	37856	AGACCACCAGGACCAATGAGC
9211	RPPLGEG	23534	CGGCCGCCTTTGGGTGAGGGT	37857	AGACCACCACTCGGAGAAGGA
9212	RPPNATP	23535	CGGCCTCCGAATGCTACTCCT	37858	AGACCACCAAACGCAACACCA
9213	RPPNGDM	23536	AGGCCTCCTAATGGGGATATG	37859	AGACCACCAAACGGAGACATG
9214	RPPSTVN	23537	CGGCCGCCTTCGACGGTTAAT	37860	AGACCACCAAGCACAGTCAAC

9215	RPPSVQP	23538	AGGCCGCCTAGTGTTCAGCCT	37861	AGACCACCAAGCGTCCAACCA
9216	RPPVQTG	23539	CGTCCGCCTGTTCAGACGGGG	37862	AGACCACCAGTCCAAACAGGA
9217	RPQHIMP	23540	CGTCCGCAGCATATTATGCCT	37863	AGACCACAACACATCATGCCA
9218	RPQKASE	23541	CGTCCGCAGAAGGCGTCTGAG	37864	AGACCACAAAAAGCAAGCGAA
9219	RPQPTPC	23542	CGTCCTCAGCCTACGCCGTGT	37865	AGACCACAACCAACACCATGC
9220	RPREISP	23543	CGTCCGCGGGAGATTTCGCCG	37866	AGACCAAGAGAAATCAGCCCA
9221	RPRFASD	23544	CGGCCGCGTTTTGCTAGTGAT	37867	AGACCAAGATTCGCAAGCGAC
9222	RPSAATP	23545	CGGCCGTCGGCGGCTACTCCG	37868	AGACCAAGCGCAGCAACACCA
9223	RPSDLKN	23546	CGTCCGAGTGATCTGAAGAAT	37869	AGACCAAGCGACCTCAAAAAC
9224	RPSGMAH	23547	AGGCCTTCTGGTATGGCTCAT	37870	AGACCAAGCGGAATGGCACAC
9225	RPSLAVG	23548	CGGCCGTCGCTTGCGGTGGGT	37871	AGACCAAGCCTCGCAGTCGGA
9226	RPSLPDF	23549	CGTCCGAGTTTGCCGGATTTT	37872	AGACCAAGCCTCCCAGACTTC
9227	RPSLSGT	23550	CGTCCTTCTCTTAGTGGTACG	37873	AGACCAAGCCTCAGCGGAACA
9228	RPSLSPT	23551	CGTCCGTCGCTTTCTCCGACT	37874	AGACCAAGCCTCAGCCCAACA
9229	RPSNAMA	23552	AGGCCTTCGAATGCTATGGCG	37875	AGACCAAGCAACGCAATGGCA
9230	RPSNQSS	23553	CGTCCTAGTAATCAGAGTTCT	37876	AGACCAAGCAACCAAAGCAGC
9231	RPSTDSY	23554	AGGCCTTCGACTGATTCTTAT	37877	AGACCAAGCACAGACAGCTAC
9232	RPSTYPS	23555	CGTCCGTCGACGTATCCGTCT	37878	AGACCAAGCACATACCCAAGC
9233	RPSVNEH	23556	AGGCCGTCTGTGAATGAGCAT	37879	AGACCAAGCGTCAACGAACAC
9234	RPTLPMA	23557	CGTCCTACGCTGCCGATGGCT	37880	AGACCAACACTCCCAATGGCA
9235	RPTQILG	23558	AGGCCTACTCAGATTCTTGGT	37881	AGACCAACACAAATCCTCGGA
9236	RPTSPPA	23559	CGGCCTACTTCTCCGCCGGCG	37882	AGACCAACAAGCCCACCAGCA
9237	RPTSTTS	23560	CGGCCGACTTCTACTACTTCT	37883	AGACCAACAAGCACAACAAGC
9238	RPTTSNG	23561	AGGCCGACTACGTCTAATGGT	37884	AGACCAACAACAAGCAACGGA
9239	RPTTTQE	23562	AGGCCTACTACGACGCAGGAG	37885	AGACCAACAACAACACAAGAA
9240	RPTTTSV	23563	AGGCCGACTACTACGTCTGTT	37886	AGACCAACAACAACAAGCGTC
9241	RPVCDGT	23564	CGTCCTGTTTGTGATGGTACT	37887	AGACCAGTCTGCGACGGAACA
9242	RPVDWDL	23565	CGTCCTGTTGATTGGGATCTT	37888	AGACCAGTCGACTGGGACCTC
9243	RPVKEYV	23566	CGGCCTGTGAAGGAGTATGTG	37889	AGACCAGTCAAAGAATACGTC
9244	RPVLSTG	23567	CGTCCTGTGTTGTCTACTGGG	37890	AGACCAGTCCTCAGCACAGGA
9245	RPVPDQI	23568	CGGCCTGTTCCGGATCAGATT	37891	AGACCAGTCCCAGACCAAATC
9246	RPYPPPI	23569	CGTCCTTATCCGCCGCCTATT	37892	AGACCATACCCACCACCAATC
9247	RQALISG	23570	AGGCAGGCTCTGATTAGTGGT	37893	AGACAAGCACTCATCAGCGGA
9248	RQDAAIS	23571	AGGCAGGATGCTGCTATTTCT	37894	AGACAAGACGCAGCAATCAGC
9249	RQDDHKI	23572	CGGCAGGATGATCATAAGATT	37895	AGACAAGACGACCACAAAATC
9250	RQFTENA	23573	AGGCAGTTTACGGAGAATGCT	37896	AGACAATTCACAGAAAACGCA
9251	RQGVTPT	23574	CGTCAGGGTGTTACTCCTACT	37897	AGACAAGGAGTCACACCAACA
9252	RQHQLPH	23575	CGGCAGCATCAGCTTCCGCAT	37898	AGACAACACCAACTCCCACAC
9253	RQIPHTE	23576	CGTCAGATTCCGCATACGGAG	37899	AGACAAATCCCACACACAGAA
9254	RQKEHNL	23577	CGTCAGAAGGAGCATAATCTT	37900	AGACAAAAAGAACACAACCTC
9255	RQLEADP	23578	CGGCAGCTGGAGGCGGATCCT	37901	AGACAACTCGAAGCAGACCCA
9256	RQNDVCS	23579	AGGCAGAATGATGTTTGTTCT	37902	AGACAAAACGACGTCTGCAGC
9257	RQNHMPA	23580	AGGCAGAATCATATGCCTGCT	37903	AGACAAAACCACATGCCAGCA
9258	RQNRCID	23581	CGTCAGAATAGGTGTATTGAT	37904	AGACAAAACAGATGCATCGAC
9259	RQPLYTD	23582	CGTCAGCCTTTGTATACGGAT	37905	AGACAACCACTCTACACAGAC

9260	RQPPKLA	23583	AGGCAGCCTCCGAAGCTTGCT	37906	AGACAACCACCAAAACTCGCA
9261	RQQAHLV	23584	CGGCAGCAGGCGCATTTGGTT	37907	AGACAACAAGCACACCTCGTC
9262	RQSDLYS	23585	CGTCAGTCGGATCTTTATAGT	37908	AGACAAAGCGACCTCTACAGC
9263	RQSNFAT	23586	AGGCAGTCTAATTTTGCGACT	37909	AGACAAAGCAACTTCGCAACA
9264	RQSNTLN	23587	CGTCAGTCTAATACTTTGAAT	37910	AGACAAAGCAACACACTCAAC
9265	RQSQCPM	23588	AGGCAGTCTCAGTGTCCTATG	37911	AGACAAAGCCAATGCCCAATG
9266	RQSSYDV	23589	AGGCAGAGTTCGTATGATGTG	37912	AGACAAAGCAGCTACGACGTC
9267	RQSTQLL	23590	CGGCAGTCGACGCAGCTGCTT	37913	AGACAAAGCACACAACTCCTC
9268	RQSVPTS	23591	CGTCAGTCGGTTCCGACGTCG	37914	AGACAAAGCGTCCCAACAAGC
9269	RQSVSNL	23592	CGTCAGTCGGTGTCTAATTTG	37915	AGACAAAGCGTCAGCAACCTC
9270	RQTHTLQ	23593	CGGCAGACTCATACTCTGCAG	37916	AGACAAACACACACACTCCAA
9271	RQTQQMY	23594	AGGCAGACGCAGCAGATGTAT	37917	AGACAAACACAACAAATGTAC
9272	RQVETMS	23595	AGGCAGGTTGAGACTATGAGT	37918	AGACAAGTCGAAACAATGAGC
9273	RQVGMLS	23596	CGGCAGGTGGGGATGCTGTCG	37919	AGACAAGTCGGAATGCTCAGC
9274	RQVPSAE	23597	AGGCAGGTTCCGTCTGCGGAG	37920	AGACAAGTCCCAAGCGCAGAA
9275	RRDDGSS	23598	CGGCGGGATGATGGTAGTTCT	37921	AGAAGAGACGACGGAAGCAGC
9276	RRDELTL	23599	CGTCGGGATGAGTTGACTTTG	37922	AGAAGAGACGAACTCACACTC
9277	RRDGMLM	23600	AGGAGGGATGGGATGCTTATG	37923	AGAAGAGACGGAATGCTCATG
9278	RRDHAPI	23601	CGGCGTGATCATGCTCCTATT	37924	AGAAGAGACCACGCACCAATC
9279	RRDPSTV	23602	CGGCGTGATCCTTCGACGGTT	37925	AGAAGAGACCCAAGCACAGTC
9280	RRDQPVP	23603	CGGCGTGATCAGCCTGTGCCT	37926	AGAAGAGACCAACCAGTCCCA
9281	RRDVSGP	23604	CGGAGGGATGTGTCTGGTCCG	37927	AGAAGAGACGTCAGCGGACCA
9282	RRESGIG	23605	AGGCGGGAGTCGGGTATTGGT	37928	AGAAGAGAAAGCGGAATCGGA
9283	RRGTSEP	23606	AGGCGTGGGACTTCTGAGCCT	37929	AGAAGAGGAACAAGCGAACCA
9284	RRLPGDV	23607	AGGCGTCTGCCTGGTGATGTT	37930	AGAAGACTCCCAGGAGACGTC
9285	RRNDALP	23608	AGGCGGAATGATGCTCTTCCT	37931	AGAAGAAACGACGCACTCCCA
9286	RRPEIER	23609	CGTAGGCCGGAGATTGAGAGG	37932	AGAAGACCAGAAATCGAAAGA
9287	RRPSLSD	23610	AGGCGGCCTTCGTTGAGTGAT	37933	AGAAGACCAAGCCTCAGCGAC
9288	RRPSPDV	23611	AGGCGGCCGTCTCCTGATGTT	37934	AGAAGACCAAGCCCAGACGTC
9289	RRSDLYV	23612	CGGCGGAGTGATCTGTATGTG	37935	AGAAGAAGCGACCTCTACGTC
9290	RRTDTLY	23613	CGTCGTACGGATACGCTGTAT	37936	AGAAGAACAGACACACTCTAC
9291	RRVGTGD	23614	AGGCGTGTTGGTACTGGTGAT	37937	AGAAGAGTCGGAACAGGAGAC
9292	RSAAAVY	23615	AGGTCTGCGGCGGCGGTGTAT	37938	AGAAGCGCAGCAGCAGTCTAC
9293	RSAAMSE	23616	CGGAGTGCGGCGATGAGTGAG	37939	AGAAGCGCAGCAATGAGCGAA
9294	RSAATST	23617	AGGAGTGCGGCGACGTCGACT	37940	AGAAGCGCAGCAACAAGCACA
9295	RSAAVTY	23618	AGGAGTGCTGCGGTTACGTAT	37941	AGAAGCGCAGCAGTCACATAC
9296	RSAGPNE	23619	AGGTCTGCGGGTCCTAATGAG	37942	AGAAGCGCAGGACCAAACGAA
9297	RSALNTS	23620	CGTTCTGCTTTGAATACGAGT	37943	AGAAGCGCACTCAACACAAGC
9298	RSALPNL	23621	CGTTCTGCGTTGCCTAATTTG	37944	AGAAGCGCACTCCCAAACCTC
9299	RSAMAGP	23622	AGGTCTGCTATGGCGGGGCCG	37945	AGAAGCGCAATGGCAGGACCA
9300	RSANQSV	23623	CGTAGTGCTAATCAGAGTGTG	37946	AGAAGCGCAAACCAAAGCGTC
9301	RSAPAVI	23624	CGTAGTGCTCCTGCGGTGATT	37947	AGAAGCGCACCAGCAGTCATC
9302	RSAPELT	23625	CGTTCGGCTCCGGAGCTGACT	37948	AGAAGCGCACCAGAACTCACA
9303	RSAQLTA	23626	CGTAGTGCTCAGCTGACGGCG	37949	AGAAGCGCACAACTCACAGCA
9304	RSAQNSL	23627	CGTAGTGCTCAGAATTCGTTG	37950	AGAAGCGCACAAAACAGCCTC

9305	RSASLQS	23628	AGGTCTGCTAGTTTGCAGTCT	37951	AGAAGCGCAAGCCTCCAAAGC
9306	RSAVPDS	23629	CGTTCTGCTGTTCCTGATTCG	37952	AGAAGCGCAGTCCCAGACAGC
9307	RSDELRT	23630	CGTTCGGATGAGCTTAGGACT	37953	AGAAGCGACGAACTCAGAACA
9308	RSDGRSI	23631	CGTTCTGATGGGCGTAGTATT	37954	AGAAGCGACGGAAGAAGCATC
9309	RSDPART	23632	CGGAGTGATCCGGCGCGTACG	37955	AGAAGCGACCCAGCAAGAACA
9310	RSDSRPL	23633	AGGTCGGATTCTAGGCCTCTT	37956	AGAAGCGACAGCAGACCACTC
9311	RSDSVTH	23634	AGGAGTGATAGTGTTACGCAT	37957	AGAAGCGACAGCGTCACACAC
9312	RSDVRLA	23635	AGGTCGGATGTGAGGCTTGCT	37958	AGAAGCGACGTCAGACTCGCA
9313	RSEEIRD	23636	CGGAGTGAGGAGATTCGGGAT	37959	AGAAGCGAAGAAATCAGAGAC
9314	RSEILVT	23637	AGGTCTGAGATTCTTGTTACT	37960	AGAAGCGAAATCCTCGTCACA
9315	RSEKVAP	23638	CGTTCGGAGAAGGTGGCTCCT	37961	AGAAGCGAAAAAGTCGCACCA
9316	RSEPDEY	23639	AGGTCGGAGCCGGATGAGTAT	37962	AGAAGCGAACCAGACGAATAC
9317	RSEYAPQ	23640	CGGTCTGAGTATGCGCCTCAG	37963	AGAAGCGAATACGCACCACAA
9318	RSGHSGY	23641	CGTTCTGGGCATAGTGGGTAT	37964	AGAAGCGGACACAGCGGATAC
9319	RSGLASG	23642	CGTTCTGGGCTGGCTTCGGGG	37965	AGAAGCGGACTCGCAAGCGGA
9320	RSGLDKT	23643	CGGTCTGGGCTTGATAAGACT	37966	AGAAGCGGACTCGACAAAACA
9321	RSGLKEL	23644	CGGTCTGGTCTGAAGGAGCTG	37967	AGAAGCGGACTCAAAGAACTC
9322	RSGMVSA	23645	CGTTCTGGTATGGTGTCTGCT	37968	AGAAGCGGAATGGTCAGCGCA
9323	RSGQDAL	23646	CGTTCGGGTCAGGATGCGCTG	37969	AGAAGCGGACAAGACGCACTC
9324	RSGSGLE	23647	CGGTCTGGTTCTGGTCTTGAG	37970	AGAAGCGGAAGCGGACTCGAA
9325	RSHNEEE	23648	CGGAGTCATAATGAGGAGGAG	37971	AGAAGCCACAACGAAGAAGAA
9326	RSHSTDS	23649	CGGTCTCATAGTACGGATTCG	37972	AGAAGCCACAGCACAGACAGC
9327	RSIAADA	23650	CGGTCGATTGCGGCGGATGCG	37973	AGAAGCATCGCAGCAGACGCA
9328	RSIAWSE	23651	CGGAGTATTGCTTGGAGTGAG	37974	AGAAGCATCGCATGGAGCGAA
9329	RSIENAD	23652	CGGTCGATTGAGAATGCGGAT	37975	AGAAGCATCGAAAACGCAGAC
9330	RSIPDPT	23653	CGTTCTATTCCTGATCCTACT	37976	AGAAGCATCCCAGACCCAACA
9331	RSIQPTN	23654	CGGAGTATTCAGCCTACGAAT	37977	AGAAGCATCCAACCAACAAAC
9332	RSIQTNP	23655	CGTTCGATTCAGACGAATCCG	37978	AGAAGCATCCAAACAAACCCA
9333	RSKEATS	23656	CGTTCGAAGGAGGCTACTAGT	37979	AGAAGCAAAGAAGCAACAAGC
9334	RSKQASE	23657	CGGAGTAAGCAGGCTTCGGAG	37980	AGAAGCAAACAAGCAAGCGAA
9335	RSKSSDP	23658	CGGAGTAAGAGTAGTGATCCG	37981	AGAAGCAAAAGCAGCGACCCA
9336	RSLDFPD	23659	AGGTCGTTGGATTTTCCTGAT	37982	AGAAGCCTCGACTTCCCAGAC
9337	RSLEHSN	23660	CGTAGTCTGGAGCATTCTAAT	37983	AGAAGCCTCGAACACAGCAAC
9338	RSLHGSQ	23661	AGGTCGCTTCATGGGAGTCAG	37984	AGAAGCCTCCACGGAAGCCAA
9339	RSLNALP	23662	AGGAGTTTGAATGCGCTGCCT	37985	AGAAGCCTCAACGCACTCCCA
9340	RSLNSTA	23663	AGGAGTCTGAATTCTACGGCT	37986	AGAAGCCTCAACAGCACAGCA
9341	RSLPAET	23664	CGTTCTCTTCCTGCTGAGACT	37987	AGAAGCCTCCCAGCAGAAACA
9342	RSLPSPH	23665	CGGTCGTTGCCGAGTCCGCAT	37988	AGAAGCCTCCCAAGCCCACAC
9343	RSLQLSD	23666	CGTTCTCTTCAGCTTAGTGAT	37989	AGAAGCCTCCAACTCAGCGAC
9344	RSLSFAA	23667	CGTTCTCTTTCTTTTGCTGCT	37990	AGAAGCCTCAGCTTCGCAGCA
9345	RSLSLLG	23668	AGGTCGTTGTCGTTGCTTGGG	37991	AGAAGCCTCAGCCTCCTCGGA
9346	RSLSLPP	23669	CGTAGTCTTAGTCTTCCGCCG	37992	AGAAGCCTCAGCCTCCCACCA
9347	RSLSPTR	23670	CGTTCTTTGTCGCCTACGAGG	37993	AGAAGCCTCAGCCCAACAAGA
9348	RSLTVTA	23671	AGGTCTTTGACGGTTACTGCG	37994	AGAAGCCTCACAGTCACAGCA
9349	RSMAESV	23672	AGGTCGATGGCTGAGTCGGTG	37995	AGAAGCATGGCAGAAAGCGTC

9350	RSMHAGA	23673	CGGAGTATGCATGCTGGTGCG	37996	AGAAGCATGCACGCAGGAGCA
9351	RSMMLSP	23674	CGTTCGATGATGCTGAGTCCG	37997	AGAAGCATGATGCTCAGCCCA
9352	RSMPSGA	23675	AGGAGTATGCCGTCTGGGGCG	37998	AGAAGCATGCCAAGCGGAGCA
9353	RSMPTTT	23676	CGTAGTATGCCGACTACTACT	37999	AGAAGCATGCCAACAACAACA
9354	RSMTGAL	23677	CGTAGTATGACTGGTGCGCTT	38000	AGAAGCATGACAGGAGCACTC
9355	RSNKETS	23678	CGGTCTAATAAGGAGACTAGT	38001	AGAAGCAACAAAGAAACAAGC
9356	RSNLEGL	23679	AGGTCGAATCTGGAGGGGCTG	38002	AGAAGCAACCTCGAAGGACTC
9357	RSNMPMG	23680	AGGTCGAATATGCCTATGGGG	38003	AGAAGCAACATGCCAATGGGA
9358	RSNPAPF	23681	CGTTCTAATCCTGCGCCGTTT	38004	AGAAGCAACCCAGCACCATTC
9359	RSNPVGT	23682	CGGAGTAATCCTGTGGGTACG	38005	AGAAGCAACCCAGTCGGAACA
9360	RSNSDAV	23683	AGGAGTAATTCGGATGCTGTT	38006	AGAAGCAACAGCGACGCAGTC
9361	RSNVESK	23684	AGGAGTAATGTTGAGTCGAAG	38007	AGAAGCAACGTCGAAAGCAAA
9362	RSNVLAQ	23685	CGTAGTAATGTTTTGGCTCAG	38008	AGAAGCAACGTCCTCGCACAA
9363	RSPDTTG	23686	CGGTCTCCTGATACTACGGGG	38009	AGAAGCCCAGACACAACAGGA
9364	RSPEKAL	23687	CGGTCTCCTGAGAAGGCTTTG	38010	AGAAGCCCAGAAAAAGCACTC
9365	RSPFGSA	23688	CGTTCTCCGTTTGGTAGTGCG	38011	AGAAGCCCATTCGGAAGCGCA
9366	RSPGNVG	23689	AGGAGTCCGGGTAATGTTGGT	38012	AGAAGCCCAGGAAACGTCGGA
9367	RSPPQDM	23690	CGTTCTCCTCCGCAGGATATG	38013	AGAAGCCCACCACAAGACATG
9368	RSPPTIA	23691	CGTAGTCCTCCTACTATTGCG	38014	AGAAGCCCACCAACAATCGCA
9369	RSPQLYA	23692	CGTTCGCCTCAGCTTTATGCT	38015	AGAAGCCCACAACTCTACGCA
9370	RSPQVML	23693	CGTTCGCCGCAGGTTATGCTT	38016	AGAAGCCCACAAGTCATGCTC
9371	RSPSGTT	23694	AGGTCGCCTTCTGGGACTACT	38017	AGAAGCCCAAGCGGAACAACA
9372	RSPSTSN	23695	CGTTCTCCTTCTACGTCGAAT	38018	AGAAGCCCAAGCACAAGCAAC
9373	RSPSVLP	23696	CGGTCGCCTAGTGTTCTTCCT	38019	AGAAGCCCAAGCGTCCTCCCA
9374	RSPTFAP	23697	CGTTCTCCGACTTTTGCTCCG	38020	AGAAGCCCAACATTCGCACCA
9375	RSPTSVA	23698	AGGTCTCCGACTTCGGTGGCT	38021	AGAAGCCCAACAAGCGTCGCA
9376	RSPVKGL	23699	CGGTCGCCGGTTAAGGGTCTG	38022	AGAAGCCCAGTCAAAGGACTC
9377	RSQAQVI	23700	AGGTCGCAGGCGCAGGTTATT	38023	AGAAGCCAAGCACAAGTCATC
9378	RSQISDS	23701	CGTTCGCAGATTAGTGATAGT	38024	AGAAGCCAAATCAGCGACAGC
9379	RSQLMGA	23702	AGGTCGCAGCTGATGGGTGCG	38025	AGAAGCCAACTCATGGGAGCA
9380	RSQNQGL	23703	CGTAGTCAGAATCAGGGGCTG	38026	AGAAGCCAAAACCAAGGACTC
9381	RSQPLSL	23704	AGGTCTCAGCCGCTTTCTCTT	38027	AGAAGCCAACCACTCAGCCTC
9382	RSQPSTG	23705	CGGTCGCAGCCTAGTACGGGG	38028	AGAAGCCAACCAAGCACAGGA
9383	RSQQPYE	23706	AGGAGTCAGCAGCCTTATGAG	38029	AGAAGCCAACAACCATACGAA
9384	RSQSATL	23707	CGTTCGCAGTCGGCTACGTTG	38030	AGAAGCCAAAGCGCAACACTC
9385	RSQTNMY	23708	CGTTCGCAGACTAATATGTAT	38031	AGAAGCCAAACAAACATGTAC
9386	RSRDSEH	23709	CGTTCGCGTGATTCGGAGCAT	38032	AGAAGCAGAGACAGCGAACAC
9387	RSSAFGP	23710	CGGTCTAGTGCTTTTGGGCCT	38033	AGAAGCAGCGCATTCGGACCA
9388	RSSEYGS	23711	CGGTCGAGTGAGTATGGTAGT	38034	AGAAGCAGCGAATACGGAAGC
9389	RSSFNKD	23712	CGGTCTTCGTTTAATAAGGAT	38035	AGAAGCAGCTTCAACAAAGAC
9390	RSSHGGE	23713	CGTAGTAGTCATGGTGGGGAG	38036	AGAAGCAGCCACGGAGGAGAA
9391	RSSLNLH	23714	CGTAGTTCTTTGAATCTGCAT	38037	AGAAGCAGCCTCAACCTCCAC
9392	RSSNLNA	23715	CGTAGTAGTAATCTTAATGCT	38038	AGAAGCAGCAACCTCAACGCA
9393	RSSPNFQ	23716	CGGTCGAGTCCGAATTTTCAG	38039	AGAAGCAGCCCAAACTTCCAA
9394	RSSPNSP	23717	CGGAGTTCTCCTAATAGTCCT	38040	AGAAGCAGCCCAAACAGCCCA

9395	RSSPSDK	23718	AGGTCTTCTCCGTCGGATAAG	38041	AGAAGCAGCCCAAGCGACAAA
9396	RSSPYLE	23719	CGTAGTTCTCCTTATTTGGAG	38042	AGAAGCAGCCCATACCTCGAA
9397	RSSSAVV	23720	CGTTCTTCGTCGGCTGTTGTT	38043	AGAAGCAGCAGCGCAGTCGTC
9398	RSSSLTP	23721	CGGTCTTCGTCGCTTACGCCG	38044	AGAAGCAGCAGCCTCACACCA
9399	RSSSNPL	23722	CGTTCGTCGAGTAATCCGCTG	38045	AGAAGCAGCAGCAACCCACTC
9400	RSSSPTT	23723	CGGTCGAGTTCGCCTACGACG	38046	AGAAGCAGCAGCCCAACAACA
9401	RSSSTQS	23724	CGGTCGTCTAGTACGCAGTCT	38047	AGAAGCAGCAGCACACAAAGC
9402	RSSTHSG	23725	CGTAGTTCTACGCATTCGGGT	38048	AGAAGCAGCACACACAGCGGA
9403	RSSTQIP	23726	CGTAGTAGTACGCAGATTCCT	38049	AGAAGCAGCACACAAATCCCA
9404	RSSTTLP	23727	AGGAGTTCTACGACGCTTCCG	38050	AGAAGCAGCACAACACTCCCA
9405	RSSYTEH	23728	CGTTCGTCGTATACGGAGCAT	38051	AGAAGCAGCTACACAGAACAC
9406	RSTADRD	23729	AGGAGTACTGCTGATCGGGAT	38052	AGAAGCACAGCAGACAGAGAC
9407	RSTAIDF	23730	CGTTCTACTGCGATTGATTTT	38053	AGAAGCACAGCAATCGACTTC
9408	RSTALPD	23731	AGGAGTACTGCTCTGCCTGAT	38054	AGAAGCACAGCACTCCCAGAC
9409	RSTGPSV	23732	AGGTCGACTGGTCCGTCTGTG	38055	AGAAGCACAGGACCAAGCGTC
9410	RSTLNSP	23733	AGGTCTACTCTGAATTCGCCT	38056	AGAAGCACACTCAACAGCCCA
9411	RSTMSNS	23734	AGGTCTACTATGAGTAATAGT	38057	AGAAGCACAATGAGCAACAGC
9412	RSTNNLT	23735	AGGTCGACTAATAATCTTACG	38058	AGAAGCACAAACAACCTCACA
9413	RSTSPLP	23736	CGGTCTACTAGTCCTCTTCCG	38059	AGAAGCACAAGCCCACTCCCA
9414	RSTTSHP	23737	CGTTCGACTACGAGTCATCCT	38060	AGAAGCACAACAAGCCACCCA
9415	RSVATGV	23738	CGGAGTGTTGCTACTGGTGTG	38061	AGAAGCGTCGCAACAGGAGTC
9416	RSVEPLA	23739	CGTTCGGTTGAGCCTCTTGCT	38062	AGAAGCGTCGAACCACTCGCA
9417	RSVKFPM	23740	AGGAGTGTGAAGTTTCCGATG	38063	AGAAGCGTCAAATTCCCAATG
9418	RSVPESR	23741	CGTAGTGTGCCTGAGAGTCGT	38064	AGAAGCGTCCCAGAAAGCAGA
9419	RSVQTPS	23742	CGGAGTGTTCAGACGCCGTCT	38065	AGAAGCGTCCAAACACCAAGC
9420	RSVRQND	23743	CGTTCTGTTAGGCAGAATGAT	38066	AGAAGCGTCAGACAAAACGAC
9421	RSVTANN	23744	CGGAGTGTTACGGCTAATAAT	38067	AGAAGCGTCACAGCAAACAAC
9422	RSVTPGI	23745	CGGAGTGTTACTCCTGGTATT	38068	AGAAGCGTCACACCAGGAATC
9423	RSVVAQT	23746	AGGTCTGTGGTTGCTCAGACG	38069	AGAAGCGTCGTCGCACAAACA
9424	RSYGLPE	23747	CGGTCGTATGGTCTGCCTGAG	38070	AGAAGCTACGGACTCCCAGAA
9425	RSYNPES	23748	CGTAGTTATAATCCTGAGAGT	38071	AGAAGCTACAACCCAGAAAGC
9426	RSYSPPT	23749	CGTTCGTATTCGCCGCCGACG	38072	AGAAGCTACAGCCCACCAACA
9427	RTAATCA	23750	CGTACGGCGGCTACGTGTGCG	38073	AGAACAGCAGCAACATGCGCA
9428	RTADMSG	23751	CGTACGGCGGATATGAGTGGT	38074	AGAACAGCAGACATGAGCGGA
9429	RTAIGNL	23752	CGTACTGCGATTGGTAATTTG	38075	AGAACAGCAATCGGAAACCTC
9430	RTANPTP	23753	CGGACGGCGAATCCGACTCCG	38076	AGAACAGCAAACCCAACACCA
9431	RTASLVP	23754	CGTACGGCGTCTCTTGTTCCT	38077	AGAACAGCAAGCCTCGTCCCA
9432	RTASVAA	23755	CGGACTGCTTCGGTGGCGGCT	38078	AGAACAGCAAGCGTCGCAGCA
9433	RTAVIDT	23756	CGGACGGCGGTGACTGATACG	38079	AGAACAGCAGTCACAGACACA
9434	RTDGDVK	23757	CGGACTGATGGTGATGTGAAG	38080	AGAACAGACGGAGACGTCAAA
9435	RTEFNMP	23758	CGGACGGAGTTTAATATGCCT	38081	AGAACAGAATTCAACATGCCA
9436	RTEGCAA	23759	AGGACTGAGGGTTGTGCTGCT	38082	AGAACAGAAGGATGCGCAGCA
9437	RTEPGPS	23760	CGTACTGAGCCGGGTCCTTCG	38083	AGAACAGAACCAGGACCAAGC
9438	RTESPPQ	23761	CGTACGGAGAGTCCTCCGCAG	38084	AGAACAGAAAGCCCACCACAA
9439	RTETGKL	23762	CGGACGGAGACTGGGAAGCTT	38085	AGAACAGAAACAGGAAAACTC

9440	RTFSGAD	23763	CGTACGTTTTCTGGTGCTGAT	38086	AGAACATTCAGCGGAGCAGAC
9441	RTGALSE	23764	AGGACGGGTGCGTTGTCGGAG	38087	AGAACAGGAGCACTCAGCGAA
9442	RTGEVTF	23765	CGTACGGGTGAGGTTACGTTT	38088	AGAACAGGAGAAGTCACATTC
9443	RTGNAAS	23766	CGGACGGGTAATGCGGCTTCG	38089	AGAACAGGAAACGCAGCAAGC
9444	RTGPGSE	23767	CGTACGGGGCCGGGTTCTGAG	38090	AGAACAGGACCAGGAAGCGAA
9445	RTGPTPS	23768	CGTACGGGGCCGACTCCGTCT	38091	AGAACAGGACCAACACCAAGC
9446	RTGSYPQ	23769	CGGACTGGGTCTTATCCTCAG	38092	AGAACAGGAAGCTACCCACAA
9447	RTGVCGN	23770	CGGACTGGTGTGTGTGGTAAT	38093	AGAACAGGAGTCTGCGGAAAC
9448	RTHSPAG	23771	AGGACGCATTCGCCTGCTGGG	38094	AGAACACACAGCCCAGCAGGA
9449	RTLGPVG	23772	CGTACTCTTGGTCCTGTGGGG	38095	AGAACACTCGGACCAGTCGGA
9450	RTLMPHP	23773	CGTACTTTGATGCCGCATCCT	38096	AGAACACTCATGCCACACCCA
9451	RTLNSVA	23774	CGTACTCTTAATTCTGTTGCT	38097	AGAACACTCAACAGCGTCGCA
9452	RTMDAPV	23775	CGTACGATGGATGCTCCGGTG	38098	AGAACAATGGACGCACCAGTC
9453	RTNGDVK	23776	CGGACTAATGGTGATGTGAAG	38099	AGAACAAACGGAGACGTCAAA
9454	RTNGLSP	23777	CGTACTAATGGGCTTTCGCCG	38100	AGAACAAACGGACTCAGCCCA
9455	RTNNDVT	23778	CGTACTAATAATGATGTGACG	38101	AGAACAAACAACGACGTCACA
9456	RTNSQLD	23779	CGGACGAATTCTCAGTTGGAT	38102	AGAACAAACAGCCAACTCGAC
9457	RTNSTSM	23780	AGGACTAATAGTACTTCGATG	38103	AGAACAAACAGCACAAGCATG
9458	RTPALSN	23781	AGGACTCCTGCTCTTTCTAAT	38104	AGAACACCAGCACTCAGCAAC
9459	RTPDSLG	23782	CGTACTCCGGATTCTCTGGGG	38105	AGAACACCAGACAGCCTCGGA
9460	RTPEAIS	23783	CGGACGCCTGAGGCGATTTCG	38106	AGAACACCAGAAGCAATCAGC
9461	RTPHSSF	23784	CGGACTCCTCATTCTTCGTTT	38107	AGAACACCACACAGCAGCTTC
9462	RTPKLPM	23785	CGGACTCCGAAGCTGCCTATG	38108	AGAACACCAAAACTCCCAATG
9463	RTPMLEP	23786	AGGACGCCTATGCTGGAGCCT	38109	AGAACACCAATGCTCGAACCA
9464	RTPVSGE	23787	AGGACGCCTGTTTCGGGTGAG	38110	AGAACACCAGTCAGCGGAGAA
9465	RTQIGVN	23788	CGTACGCAGATTGGTGTGAAT	38111	AGAACACAAATCGGAGTCAAC
9466	RTSAVGL	23789	CGTACTAGTGCGGTGGGTCTG	38112	AGAACAAGCGCAGTCGGACTC
9467	RTSCSPG	23790	CGTACGTCGTGTAGTCCTGGT	38113	AGAACAAGCTGCAGCCCAGGA
9468	RTSDASF	23791	AGGACTAGTGATGCTTCTTTT	38114	AGAACAAGCGACGCAAGCTTC
9469	RTSDLSA	23792	AGGACTTCGGATCTGTCTGCG	38115	AGAACAAGCGACCTCAGCGCA
9470	RTSGPTD	23793	CGTACTAGTGGTCCTACTGAT	38116	AGAACAAGCGGACCAACAGAC
9471	RTSMGQA	23794	CGGACGTCGATGGGTCAGGCT	38117	AGAACAAGCATGGGACAAGCA
9472	RTSMVSN	23795	CGTACGAGTATGGTGAGTAAT	38118	AGAACAAGCATGGTCAGCAAC
9473	RTSPESR	23796	AGGACTAGTCCTGAGTCGCGG	38119	AGAACAAGCCCAGAAAGCAGA
9474	RTSPLAV	23797	CGGACTTCGCCTCTTGCTGTT	38120	AGAACAAGCCCACTCGCAGTC
9475	RTSPQSS	23798	CGGACTAGTCCGCAGTCTAGT	38121	AGAACAAGCCCACAAAGCAGC
9476	RTSPSFH	23799	AGGACTTCGCCGAGTTTTCAT	38122	AGAACAAGCCCAAGCTTCCAC
9477	RTSQTEP	23800	CGTACGTCTCAGACTGAGCCG	38123	AGAACAAGCCAAACAGAACCA
9478	RTSTEGS	23801	CGTACGTCGACGGAGGGGTCG	38124	AGAACAAGCACAGAAGGAAGC
9479	RTSTYGG	23802	CGGACGTCTACTTATGGTGGT	38125	AGAACAAGCACATACGGAGGA
9480	RTSVAVA	23803	CGTACGTCTGTTGCTGTTGCG	38126	AGAACAAGCGTCGCAGTCGCA
9481	RTTDKQG	23804	AGGACTACTGATAAGCAGGGT	38127	AGAACAACAGACAAACAAGGA
9482	RTTEHSM	23805	AGGACGACGGAGCATAGTATG	38128	AGAACAACAGAACACAGCATG
9483	RTTQSVM	23806	CGTACTACTCAGAGTGTTATG	38129	AGAACAACACAAAGCGTCATG
9484	RTTSDTF	23807	CGGACGACTTCTGATACGTTT	38130	AGAACAACAAGCGACACATTC

9485	RTTYQSS	23808	AGGACTACGTATCAGTCGAGT	38131	AGAACAACATACCAAAGCAGC
9486	RTVGSLN	23809	AGGACGGTTGGGTCTTTGAAT	38132	AGAACAGTCGGAAGCCTCAAC
9487	RTVKAEA	23810	AGGACTGTGAAGGCGGAGGCG	38133	AGAACAGTCAAAGCAGAAGCA
9488	RTYHVPD	23811	CGTACTTATCATGTGCCGGAT	38134	AGAACATACCACGTCCCAGAC
9489	RVAASSI	23812	CGTGTGGCGGCTAGTTCTATT	38135	AGAGTCGCAGCAAGCAGCATC
9490	RVAGSNG	23813	AGGGTTGCGGGTTCTAATGGG	38136	AGAGTCGCAGGAAGCAACGGA
9491	RVAMGED	23814	CGGGTTGCGATGGGGGAGGAT	38137	AGAGTCGCAATGGGAGAAGAC
9492	RVASPTA	23815	AGGGTTGCTTCTCCGACGGCT	38138	AGAGTCGCAAGCCCAACAGCA
9493	RVDASHR	23816	CGTGTTGATGCTTCGCATAGG	38139	AGAGTCGACGCAAGCCACAGA
9494	RVDSVRS	23817	AGGGTGGATAGTGTTAGGTCT	38140	AGAGTCGACAGCGTCAGAAGC
9495	RVDTRMQ	23818	AGGGTTGATACGCGGATGCAG	38141	AGAGTCGACACAAGAATGCAA
9496	RVEECVI	23819	CGTGTTGAGGAGTGTGTTATT	38142	AGAGTCGAAGAATGCGTCATC
9497	RVGDGKH	23820	CGTGTTGGTGATGGGAAGCAT	38143	AGAGTCGGAGACGGAAAACAC
9498	RVGDKLQ	23821	AGGGTTGGTGATAAGCTGCAG	38144	AGAGTCGGAGACAAACTCCAA
9499	RVGDSAF	23822	CGGGTTGGGGATAGTGCTTTT	38145	AGAGTCGGAGACAGCGCATTC
9500	RVGGSSS	23823	CGTGTTGGGGGTTCTTCTTCT	38146	AGAGTCGGAGGAAGCAGCAGC
9501	RVGHCLG	23824	AGGGTTGGGCATTGTCTGGGT	38147	AGAGTCGGACACTGCCTCGGA
9502	RVGLAST	23825	AGGGTTGGTCTTGCTTCGACT	38148	AGAGTCGGACTCGCAAGCACA
9503	RVGNVDT	23826	CGTGTTGGGAATGTGGATACT	38149	AGAGTCGGAAACGTCGACACA
9504	RVGRPSE	23827	CGGGTTGGTCGTCCTAGTGAG	38150	AGAGTCGGAAGACCAAGCGAA
9505	RVIPACQ	23828	CGGGTTATTCCTGCGTGTCAG	38151	AGAGTCATCCCAGCATGCCAA
9506	RVLDLEN	23829	CGGGTGCTTGATCTGGAGAAT	38152	AGAGTCCTCGACCTCGAAAAC
9507	RVLIEPV	23830	AGGGTTTTGATTGAGCCTGTT	38153	AGAGTCCTCATCGAACCAGTC
9508	RVLNHLG	23831	AGGGTGCTGAATCATCTGGGG	38154	AGAGTCCTCAACCACCTCGGA
9509	RVMDRAA	23832	CGTGTGATGGATCGTGCGGCT	38155	AGAGTCATGGACAGAGCAGCA
9510	RVNAPGV	23833	CGTGTTAATGCGCCTGGTGTT	38156	AGAGTCAACGCACCAGGAGTC
9511	RVNHDET	23834	CGTGTGAATCATGATGAGACG	38157	AGAGTCAACCACGACGAAACA
9512	RVNILAE	23835	CGGGTGAATATTTTGGCGGAG	38158	AGAGTCAACATCCTCGCAGAA
9513	RVNPDRY	23836	CGTGTTAATCCTGATCGTTAT	38159	AGAGTCAACCCAGACAGATAC
9514	RVNSIAS	23837	CGTGTGAATAGTATTGCTAGT	38160	AGAGTCAACAGCATCGCAAGC
9515	RVPDIAR	23838	CGTGTTCCGGATATTGCGCGG	38161	AGAGTCCCAGACATCGCAAGA
9516	RVPDSTR	23839	CGTGTTCCGGATTCGACTAGG	38162	AGAGTCCCAGACAGCACAAGA
9517	RVPGILH	23840	CGTGTGCCGGGGATTCTGCAT	38163	AGAGTCCCAGGAATCCTCCAC
9518	RVPNTLP	23841	CGTGTGCCTAATACGCTTCCT	38164	AGAGTCCCAAACACACTCCCA
9519	RVPNWPG	23842	CGGGTGCCGAATTGGCCTGGG	38165	AGAGTCCCAAACTGGCCAGGA
9520	RVPSQSS	23843	CGGGTGCCTTCTCAGAGTAGT	38166	AGAGTCCCAAGCCAAAGCAGC
9521	RVQNGLN	23844	CGGGTTCAGAATGGGCTGAAT	38167	AGAGTCCAAAACGGACTCAAC
9522	RVQQASL	23845	CGTGTTCAGCAGGCTTCGCTT	38168	AGAGTCCAACAAGCAAGCCTC
9523	RVQSNVP	23846	CGGGTTCAGTCTAATGTGCCT	38169	AGAGTCCAAAGCAACGTCCCA
9524	RVQTIPS	23847	AGGGTGCAGACTATTCCTAGT	38170	AGAGTCCAAACAATCCCAAGC
9525	RVSQPDM	23848	CGTGTTAGTCAGCCTGATATG	38171	AGAGTCAGCCAACCAGACATG
9526	RVSQVTM	23849	AGGGTTTCGCAGGTTACGATG	38172	AGAGTCAGCCAAGTCACAATG
9527	RVSTIST	23850	AGGGTTTCGACTATTTCTACG	38173	AGAGTCAGCACAATCAGCACA
9528	RVSTTSD	23851	CGGGTGTCTACTACGTCTGAT	38174	AGAGTCAGCACAACAAGCGAC
9529	RVSYDTE	23852	CGTGTGTCGTATGATACGGAG	38175	AGAGTCAGCTACGACACAGAA

9530	RVTIGTS	23853	CGTGTGACGATTGGTACGTCG	38176	AGAGTCACAATCGGAACAAGC
9531	RVTPELF	23854	AGGGTTACTCCTGAGCTTTTT	38177	AGAGTCACACCAGAACTCTTC
9532	RVTSTLS	23855	CGTGTTACGAGTACGTTGAGT	38178	AGAGTCACAAGCACACTCAGC
9533	RVTTAEL	23856	AGGGTTACGACGGCGGAGTTG	38179	AGAGTCACAACAGCAGAACTC
9534	RVTTELP	23857	CGTGTTACGACGGAGTTGCCG	38180	AGAGTCACAACAGAACTCCCA
9535	RVVGGST	23858	CGGGTGGTTGGGGGTTCTACT	38181	AGAGTCGTCGGAGGAAGCACA
9536	RVVGPVN	23859	AGGGTGGTGGGGCCGGTGAAT	38182	AGAGTCGTCGGACCAGTCAAC
9537	RVVTVLE	23860	AGGGTTGTTACGGTTTTGGAG	38183	AGAGTCGTCACAGTCCTCGAA
9538	RVYNMDG	23861	CGGGTGTATAATATGGATGGT	38184	AGAGTCTACAACATGGACGGA
9539	RWADTVT	23862	CGGTGGGCGGATACTGTTACT	38185	AGATGGGCAGACACAGTCACA
9540	RWDDGAR	23863	CGGTGGGATGATGGGGCGCGG	38186	AGATGGGACGACGGAGCAAGA
9541	RWDVKAD	23864	CGGTGGGATGTGAAGGCGGAT	38187	AGATGGGACGTCAAAGCAGAC
9542	RWKAEPP	23865	AGGTGGAAGGCTGAGCCTCCG	38188	AGATGGAAAGCAGAACCACCA
9543	RWSEDGG	23866	CGGTGGAGTGAGGATGGGGGG	38189	AGATGGAGCGAAGACGGAGGA
9544	RWSPAVP	23867	AGGTGGTCGCCGGCTGTTCCG	38190	AGATGGAGCCCAGCAGTCCCA
9545	RYAEPYI	23868	CGTTATGCTGAGCCTTATATT	38191	AGATACGCAGAACCATACATC
9546	RYDLTAP	23869	CGTTATGATTTGACTGCGCCG	38192	AGATACGACCTCACAGCACCA
9547	RYESNAH	23870	CGTTATGAGTCGAATGCGCAT	38193	AGATACGAAAGCAACGCACAC
9548	RYGASNP	23871	CGGTATGGGGCTAGTAATCCG	38194	AGATACGGAGCAAGCAACCCA
9549	RYGGSIS	23872	CGGTATGGGGGGTCTATTTCT	38195	AGATACGGAGGAAGCATCAGC
9550	RYHDTGD	23873	AGGTATCATGATACGGGTGAT	38196	AGATACCACGACACAGGAGAC
9551	RYLDRTE	23874	CGTTATCTTGATCGGACTGAG	38197	AGATACCTCGACAGAACAGAA
9552	RYMEPSP	23875	CGGTATATGGAGCCTTCGCCT	38198	AGATACATGGAACCAAGCCCA
9553	RYNEDEA	23876	AGGTATAATGAGGATGAGGCG	38199	AGATACAACGAAGACGAAGCA
9554	RYNETVS	23877	AGGTATAATGAGACTGTGTCT	38200	AGATACAACGAAACAGTCAGC
9555	RYNNQVP	23878	AGGTATAATAATCAGGTTCCG	38201	AGATACAACAACCAAGTCCCA
9556	RYNTAIS	23879	CGTTATAATACGGCGATTAGT	38202	AGATACAACACAGCAATCAGC
9557	RYPSQTS	23880	AGGTATCCGTCGCAGACTAGT	38203	AGATACCCAAGCCAAACAAGC
9558	RYSNNLP	23881	CGTTATTCGAATAATCTTCCG	38204	AGATACAGCAACAACCTCCCA
9559	RYSPGSP	23882	AGGTATTCGCCTGGTTCTCCT	38205	AGATACAGCCCAGGAAGCCCA
9560	RYTVADA	23883	AGGTATACTGTTGCTGATGCT	38206	AGATACACAGTCGCAGACGCA
9561	RYVDPLM	23884	CGGTATGTGGATCCGCTTATG	38207	AGATACGTCGACCCACTCATG
9562	SAAHIDL	23885	TCTGCTGCTCATATTGATCTG	38208	AGCGCAGCACACATCGACCTC
9563	SAALLEP	23886	AGTGCGGCTCTTCTTGAGCCT	38209	AGCGCAGCACTCCTCGAACCA
9564	SAALREG	23887	AGTGCTGCTCTTAGGGAGGGG	38210	AGCGCAGCACTCAGAGAAGGA
9565	SAARDTD	23888	TCTGCTGCTCGTGATACGGAT	38211	AGCGCAGCAAGAGACACAGAC
9566	SAARMTA	23889	TCTGCTGCGAGGATGACTGCG	38212	AGCGCAGCAAGAATGACAGCA
9567	SAASGHH	23890	TCGGCGGCTTCTGGTCATCAT	38213	AGCGCAGCAAGCGGACACCAC
9568	SAASKLL	23891	AGTGCGGCTTCTAAGTTGTTG	38214	AGCGCAGCAAGCAAACTCCTC
9569	SAASSMR	23892	TCGGCTGCGTCTTCTATGCGG	38215	AGCGCAGCAAGCAGCATGAGA
9570	SAASTVF	23893	AGTGCGGCTTCGACGGTTTTT	38216	AGCGCAGCAAGCACAGTCTTC
9571	SAAYDPK	23894	TCTGCGGCTTATGATCCTAAG	38217	AGCGCAGCATACGACCCAAAA
9572	SADFQRG	23895	TCTGCTGATTTTCAGCGTGGT	38218	AGCGCAGACTTCCAAAGAGGA
9573	SADTMLI	23896	AGTGCTGATACGATGTTGATT	38219	AGCGCAGACACAATGCTCATC
9574	SAEAHIT	23897	TCGGCGGAGGCGCATATTACG	38220	AGCGCAGAAGCACACATCACA

9575	SAEIEFL	23898	AGTGCTGAGATTGAGTTTCTT	38221	AGCGCAGAAATCGAATTCCTC
9576	SAESVPH	23899	AGTGCTGAGAGTGTGCCGCAT	38222	AGCGCAGAAAGCGTCCCACAC
9577	SAEYRSV	23900	AGTGCGGAGTATCGGAGTGTT	38223	AGCGCAGAATACAGAAGCGTC
9578	SAFGQHG	23901	TCGGCTTTTGGGCAGCATGGG	38224	AGCGCATTCGGACAACACGGA
9579	SAFLPHA	23902	TCGGCTTTTCTGCCTCATGCT	38225	AGCGCATTCCTCCCACACGCA
9580	SAFLPTP	23903	TCGGCGTTTCTTCCTACGCCG	38226	AGCGCATTCCTCCCAACACCA
9581	SAFSAGA	23904	TCTGCTTTTTCTGCGGGGGCT	38227	AGCGCATTCAGCGCAGGAGCA
9582	SAFTNYP	23905	TCGGCTTTTACGAATTATCCG	38228	AGCGCATTCACAAACTACCCA
9583	SAGERSL	23906	AGTGCTGGGGAGCGTTCGCTG	38229	AGCGCAGGAGAAAGAAGCCTC
9584	SAGGERT	23907	TCTGCGGGTGGTGAGCGTACG	38230	AGCGCAGGAGGAGAAAGAACA
9585	SAGGGMN	23908	TCGGCTGGGGGTGGGATGAAT	38231	AGCGCAGGAGGAGGAATGAAC
9586	SAGKLPM	23909	AGTGCGGGGAAGCTGCCTATG	38232	AGCGCAGGAAAACTCCCAATG
9587	SAGLHAV	23910	TCTGCTGGGCTTCATGCTGTG	38233	AGCGCAGGACTCCACGCAGTC
9588	SAGPAPR	23911	AGTGCTGGTCCGGCTCCTCGT	38234	AGCGCAGGACCAGCACCAAGA
9589	SAGQSQR	23912	TCTGCGGGTCAGTCGCAGCGT	38235	AGCGCAGGACAAAGCCAAAGA
9590	SAGRFET	23913	TCTGCGGGGAGGTTTGAGACT	38236	AGCGCAGGAAGATTCGAAACA
9591	SAGTAMI	23914	TCGGCTGGGACGGCTATGATT	38237	AGCGCAGGAACAGCAATGATC
9592	SAGVHKS	23915	TCGGCTGGGGTTCATAAGAGT	38238	AGCGCAGGAGTCCACAAAAGC
9593	SAHCPTP	23916	TCTGCGCATTGTCCTACGCCG	38239	AGCGCACACTGCCCAACACCA
9594	SAHHSHM	23917	TCTGCTCATCATTCTCATATG	38240	AGCGCACACCACAGCCACATG
9595	SAHMSRA	23918	TCTGCTCATATGTCGCGTGCT	38241	AGCGCACACATGAGCAGAGCA
9596	SAHQLQT	23919	AGTGCTCATCAGTTGCAGACT	38242	AGCGCACACCAACTCCAAACA
9597	SAHSPQM	23920	AGTGCTCATAGTCCGCAGATG	38243	AGCGCACACAGCCCACAAATG
9598	SAHSTPH	23921	AGTGCTCATAGTACTCCGCAT	38244	AGCGCACACAGCACACCACAC
9599	SAICQSV	23922	TCGGCTATTTGTCAGTCTGTT	38245	AGCGCAATCTGCCAAAGCGTC
9600	SAIMPSP	23923	AGTGCTATTATGCCGTCGCCT	38246	AGCGCAATCATGCCAAGCCCA
9601	SAIMSRS	23924	TCTGCTATTATGAGTCGGTCT	38247	AGCGCAATCATGAGCAGAAGC
9602	SAINRLP	23925	TCTGCTATTAATCGTCTGCCG	38248	AGCGCAATCAACAGACTCCCA
9603	SAISSMS	23926	AGTGCTATTTCGTCGATGAGT	38249	AGCGCAATCAGCAGCATGAGC
9604	SAKCVQA	23927	TCTGCGAAGTGTGTTCAGGCG	38250	AGCGCAAAATGCGTCCAAGCA
9605	SAKHSAM	23928	TCGGCTAAGCATTCTGCGATG	38251	AGCGCAAAACACAGCGCAATG
9606	SAKSAFS	23929	TCGGCTAAGTCTGCGTTTTCT	38252	AGCGCAAAAAGCGCATTCAGC
9607	SAKSMVV	23930	AGTGCTAAGAGTATGGTTGTT	38253	AGCGCAAAAAGCATGGTCGTC
9608	SAKTMIP	23931	TCGGCTAAGACTATGATTCCG	38254	AGCGCAAAAACAATGATCCCA
9609	SAKTSES	23932	TCGGCGAAGACGTCTGAGTCG	38255	AGCGCAAAAACAAGCGAAAGC
9610	SALAGLS	23933	TCTGCGCTTGCTGGGCTTAGT	38256	AGCGCACTCGCAGGACTCAGC
9611	SALDLNH	23934	AGTGCTTTGGATCTTAATCAT	38257	AGCGCACTCGACCTCAACCAC
9612	SALDNIR	23935	AGTGCTTTGGATAATATTCGG	38258	AGCGCACTCGACAACATCAGA
9613	SALGLSV	23936	AGTGCGCTTGGGCTGAGTGTT	38259	AGCGCACTCGGACTCAGCGTC
9614	SALGSRV	23937	TCTGCTCTGGGTTCGCGGGTT	38260	AGCGCACTCGGAAGCAGAGTC
9615	SALHLAA	23938	TCGGCTCTGCATCTGGCTGCT	38261	AGCGCACTCCACCTCGCAGCA
9616	SALKTDS	23939	TCGGCTTTGAAGACGGATTCG	38262	AGCGCACTCAAAACAGACAGC
9617	SALNKRI	23940	AGTGCGCTTAATAAGCGGATT	38263	AGCGCACTCAACAAAAGAATC
9618	SALPKPE	23941	TCTGCGTTGCCTAAGCCTGAG	38264	AGCGCACTCCCAAAACCAGAA
9619	SALRLVS	23942	TCGGCGTTGAGGCTGGTGTCT	38265	AGCGCACTCAGACTCGTCAGC

9620	SALRPDS	23943	AGTGCGCTTCGTCCGGATAGT	38266	AGCGCACTCAGACCAGACAGC
9621	SALRSVT	23944	AGTGCTTTGAGGAGTGTTACT	38267	AGCGCACTCAGAAGCGTCACA
9622	SALRVPA	23945	TCTGCGTTGCGTGTGCCTGCG	38268	AGCGCACTCAGAGTCCCAGCA
9623	SALSTTG	23946	TCGGCGCTGTCGACGACGGGT	38269	AGCGCACTCAGCACAACAGGA
9624	SALTDKL	23947	TCTGCGCTTACGGATAAGCTG	38270	AGCGCACTCACAGACAAACTC
9625	SALTHVS	23948	TCGGCTCTTACGCATGTGTCG	38271	AGCGCACTCACACACGTCAGC
9626	SALTSSL	23949	AGTGCTTTGACGTCTTCTCTG	38272	AGCGCACTCACAAGCAGCCTC
9627	SAMHPML	23950	AGTGCGATGCATCCTATGCTG	38273	AGCGCAATGCACCCAATGCTC
9628	SAMKHPS	23951	AGTGCGATGAAGCATCCGTCT	38274	AGCGCAATGAAACACCCAAGC
9629	SAMRPGS	23952	TCGGCGATGAGGCCTGGTTCG	38275	AGCGCAATGAGACCAGGAAGC
9630	SAMTKNL	23953	TCGGCGATGACTAAGAATCTT	38276	AGCGCAATGACAAAAAACCTC
9631	SANGSSS	23954	TCTGCGAATGGGAGTTCGTCG	38277	AGCGCAAACGGAAGCAGCAGC
9632	SANITVK	23955	TCTGCTAATATTACTGTGAAG	38278	AGCGCAAACATCACAGTCAAA
9633	SANPHIT	23956	AGTGCTAATCCGCATATTACT	38279	AGCGCAAACCCACACATCACA
9634	SANSLPA	23957	AGTGCGAATAGTCTGCCTGCG	38280	AGCGCAAACAGCCTCCCAGCA
9635	SANTARS	23958	TCTGCGAATACTGCGAGGTCG	38281	AGCGCAAACACAGCAAGAAGC
9636	SAPEWMP	23959	TCGGCTCCGGAGTGGATGCCT	38282	AGCGCACCAGAATGGATGCCA
9637	SAPFATE	23960	TCTGCTCCTTTTGCTACGGAG	38283	AGCGCACCATTCGCAACAGAA
9638	SAPGASF	23961	TCTGCGCCGGGTGCTTCTTTT	38284	AGCGCACCAGGAGCAAGCTTC
9639	SAPHTHL	23962	AGTGCGCCTCATACTCATCTT	38285	AGCGCACCACACACACACCTC
9640	SAPHTIP	23963	TCTGCTCCTCATACGATTCCT	38286	AGCGCACCACACACAATCCCA
9641	SAPLIGS	23964	AGTGCGCCTTTGATTGGTTCT	38287	AGCGCACCACTCATCGGAAGC
9642	SAPMTCA	23965	TCGGCGCCTATGACTTGTGCG	38288	AGCGCACCAATGACATGCGCA
9643	SAPNSSS	23966	AGTGCGCCGAATTCTTCGTCG	38289	AGCGCACCAAACAGCAGCAGC
9644	SAPVRSP	23967	TCTGCGCCGGTTCGGTCTCCT	38290	AGCGCACCAGTCAGAAGCCCA
9645	SAQGARP	23968	TCGGCGCAGGGTGCGAGGCCT	38291	AGCGCACAAGGAGCAAGACCA
9646	SAQLSLP	23969	TCGGCGCAGCTTTCGTTGCCG	38292	AGCGCACAACTCAGCCTCCCA
9647	SARDAHS	23970	TCTGCTAGGGATGCTCATTCG	38293	AGCGCAAGAGACGCACACAGC
9648	SARDHRP	23971	TCGGCGCGTGATCATCGGCCT	38294	AGCGCAAGAGACCACAGACCA
9649	SARGSDP	23972	AGTGCGAGGGGTTCTGATCCT	38295	AGCGCAAGAGGAAGCGACCCA
9650	SARGVAT	23973	TCGGCGCGTGGTGTGGCTACG	38296	AGCGCAAGAGGAGTCGCAACA
9651	SARIFKD	23974	TCGGCGCGTATTTTTAAGGAT	38297	AGCGCAAGAATCTTCAAAGAC
9652	SARMALG	23975	AGTGCTCGTATGGCGCTGGGT	38298	AGCGCAAGAATGGCACTCGGA
9653	SARQVSG	23976	TCTGCTCGTCAGGTGTCGGGG	38299	AGCGCAAGACAAGTCAGCGGA
9654	SARSDPA	23977	AGTGCGCGGTCTGATCCGGCT	38300	AGCGCAAGAAGCGACCCAGCA
9655	SARTAGP	23978	AGTGCGCGTACGGCTGGTCCT	38301	AGCGCAAGAACAGCAGGACCA
9656	SARTDRT	23979	AGTGCGCGGACGGATAGGACG	38302	AGCGCAAGAACAGACAGAACA
9657	SARTVDM	23980	AGTGCGCGTACTGTTGATATG	38303	AGCGCAAGAACAGTCGACATG
9658	SARVFPA	23981	AGTGCTCGTGTGTTTCCTGCG	38304	AGCGCAAGAGTCTTCCCAGCA
9659	SARVNIG	23982	TCTGCTCGTGTGAATATTGGG	38305	AGCGCAAGAGTCAACATCGGA
9660	SARVSNS	23983	AGTGCTCGTGTTTCTAATTCT	38306	AGCGCAAGAGTCAGCAACAGC
9661	SASALVL	23984	TCTGCGTCGGCGTTGGTGCTG	38307	AGCGCAAGCGCACTCGTCCTC
9662	SASERFR	23985	AGTGCGAGTGAGCGTTTTCGG	38308	AGCGCAAGCGAAAGATTCAGA
9663	SASESSM	23986	TCGGCTTCGGAGTCGTCTATG	38309	AGCGCAAGCGAAAGCAGCATG
9664	SASIQVM	23987	AGTGCTTCGATTCAGGTGATG	38310	AGCGCAAGCATCCAAGTCATG

9665	SASKPTS	23988	AGTGCGTCTAAGCCTACTAGT	38311	AGCGCAAGCAAACCAACAAGC
9666	SASLRLP	23989	AGTGCTTCGCTTCGTTTGCCG	38312	AGCGCAAGCCTCAGACTCCCA
9667	SASMRAL	23990	TCTGCGTCGATGCGTGCGTTG	38313	AGCGCAAGCATGAGAGCACTC
9668	SASNSVG	23991	AGTGCTTCTAATTCTGTTGGT	38314	AGCGCAAGCAACAGCGTCGGA
9669	SASPAGH	23992	AGTGCTTCTCCTGCTGGTCAT	38315	AGCGCAAGCCCAGCAGGACAC
9670	SASPQRT	23993	TCTGCGTCTCCTCAGAGGACG	38316	AGCGCAAGCCCACAAAGAACA
9671	SASRQIP	23994	TCGGCTTCGCGGCAGATTCCG	38317	AGCGCAAGCAGACAAATCCCA
9672	SASSAAQ	23995	TCGGCTTCTTCTGCTGCGCAG	38318	AGCGCAAGCAGCGCAGCACAA
9673	SASSKTG	23996	AGTGCTTCGTCTAAGACGGGG	38319	AGCGCAAGCAGCAAAACAGGA
9674	SASTPKH	23997	AGTGCTTCTACGCCGAAGCAT	38320	AGCGCAAGCACACCAAAACAC
9675	SASTQIS	23998	AGTGCTTCTACGCAGATTTCT	38321	AGCGCAAGCACACAAATCAGC
9676	SASVRGN	23999	TCGGCGTCTGTGCGGGGTAAT	38322	AGCGCAAGCGTCAGAGGAAAC
9677	SASVTYS	24000	AGTGCGAGTGTTACTTATTCG	38323	AGCGCAAGCGTCACATACAGC
9678	SATFDTT	24001	AGTGCTACGTTTGATACGACT	38324	AGCGCAACATTCGACACAACA
9679	SATLSAL	24002	AGTGCTACTCTTTCTGCTCTT	38325	AGCGCAACACTCAGCGCACTC
9680	SATPHRA	24003	AGTGCTACGCCGCATAGGGCT	38326	AGCGCAACACCACACAGAGCA
9681	SATPISR	24004	TCTGCTACTCCTATTTCGCGG	38327	AGCGCAACACCAATCAGCAGA
9682	SATQHTG	24005	TCGGCTACGCAGCATACTGGT	38328	AGCGCAACACAACACACAGGA
9683	SATQRIV	24006	AGTGCTACGCAGCGTATTGTG	38329	AGCGCAACACAAAGAATCGTC
9684	SATSPDR	24007	TCTGCGACTTCTCCGGATCGT	38330	AGCGCAACAAGCCCAGACAGA
9685	SATVPRP	24008	TCGGCGACGGTGCCTCGTCCT	38331	AGCGCAACAGTCCCAAGACCA
9686	SAVAILT	24009	TCGGCTGTGGCGATTTTGACT	38332	AGCGCAGTCGCAATCCTCACA
9687	SAVGAHS	24010	TCGGCTGTGGGGGCGCATAGT	38333	AGCGCAGTCGGAGCACACAGC
9688	SAVGNAR	24011	AGTGCTGTGGGTAATGCGCGT	38334	AGCGCAGTCGGAAACGCAAGA
9689	SAVGRST	24012	AGTGCGGTTGGTCGTAGTACT	38335	AGCGCAGTCGGAAGAAGCACA
9690	SAVGTSY	24013	TCGGCTGTTGGTACGTCGTAT	38336	AGCGCAGTCGGAACAAGCTAC
9691	SAVHRMD	24014	TCTGCGGTTCATAGGATGGAT	38337	AGCGCAGTCCACAGAATGGAC
9692	SAVIRAS	24015	TCTGCGGTGATTCGTGCTTCT	38338	AGCGCAGTCATCAGAGCAAGC
9693	SAVLPQR	24016	TCGGCTGTGTTGCCGCAGCGT	38339	AGCGCAGTCCTCCCACAAAGA
9694	SAVNEAR	24017	AGTGCGGTGAATGAGGCTCGG	38340	AGCGCAGTCAACGAAGCAAGA
9695	SAVNSRM	24018	TCGGCGGTGAATTCTAGGATG	38341	AGCGCAGTCAACAGCAGAATG
9696	SAVRMAT	24019	AGTGCGGTTCGTATGGCTACG	38342	AGCGCAGTCAGAATGGCAACA
9697	SAVRPLP	24020	AGTGCTGTGCGTCCGTTGCCG	38343	AGCGCAGTCAGACCACTCCCA
9698	SAVTGAW	24021	TCGGCTGTTACTGGGGCGTGG	38344	AGCGCAGTCACAGGAGCATGG
9699	SAVTSHM	24022	TCTGCTGTGACGTCTCATATG	38345	AGCGCAGTCACAAGCCACATG
9700	SAVYQGH	24023	TCTGCGGTGTATCAGGGTCAT	38346	AGCGCAGTCTACCAAGGACAC
9701	SAWSSTG	24024	TCGGCTTGGTCGAGTACTGGT	38347	AGCGCATGGAGCAGCACAGGA
9702	SAYASSS	24025	AGTGCTTATGCTTCGTCTAGT	38348	AGCGCATACGCAAGCAGCAGC
9703	SAYQNMA	24026	TCTGCTTATCAGAATATGGCG	38349	AGCGCATACCAAAACATGGCA
9704	SAYVDTR	24027	TCTGCTTATGTGGATACTAGG	38350	AGCGCATACGTCGACACAAGA
9705	SCELLPA	24028	TCTTGTGAGCTGCTTCCGGCT	38351	AGCTGCGAACTCCTCCCAGCA
9706	SCLNGVP	24029	AGTTGTTTGAATGGTGTTCCG	38352	AGCTGCCTCAACGGAGTCCCA
9707	SDAMTIA	24030	TCTGATGCGATGACGATTGCT	38353	AGCGACGCAATGACAATCGCA
9708	SDANGSS	24031	TCGGATGCGAATGGTAGTTCT	38354	AGCGACGCAAACGGAAGCAGC
9709	SDANVGM	24032	AGTGATGCGAATGTTGGGATG	38355	AGCGACGCAAACGTCGGAATG

9710	SDAPPYR	24033	TCTGATGCTCCTCCTTATAGG	38356	AGCGACGCACCACCATACAGA
9711	SDCITHS	24034	TCTGATTGTATTACTCATTCT	38357	AGCGACTGCATCACACACAGC
9712	SDDGPSA	24035	TCGGATGATGGGCCGAGTGCT	38358	AGCGACGACGGACCAAGCGCA
9713	SDDLVPK	24036	TCGGATGATTTGGTTCCGAAG	38359	AGCGACGACCTCGTCCCAAAA
9714	SDDRENC	24037	TCTGATGATCGTGAGAATTGT	38360	AGCGACGACAGAGAAAACTGC
9715	SDDSKNT	24038	AGTGATGATTCTAAGAATACG	38361	AGCGACGACAGCAAAAACACA
9716	SDESGMP	24039	TCTGATGAGTCTGGTATGCCT	38362	AGCGACGAAAGCGGAATGCCA
9717	SDGPRLS	24040	TCGGATGGTCCTCGTTTGAGT	38363	AGCGACGGACCAAGACTCAGC
9718	SDGSSLA	24041	AGTGATGGGTCTTCGCTTGCT	38364	AGCGACGGAAGCAGCCTCGCA
9719	SDHRYLI	24042	AGTGATCATCGTTATCTGATT	38365	AGCGACCACAGATACCTCATC
9720	SDHSSRT	24043	TCGGATCATAGTTCTCGGACG	38366	AGCGACCACAGCAGCAGAACA
9721	SDIPRPS	24044	TCTGATATTCCGCGTCCGAGT	38367	AGCGACATCCCAAGACCAAGC
9722	SDIVASP	24045	TCGGATATTGTTGCGTCTCCG	38368	AGCGACATCGTCGCAAGCCCA
9723	SDKFFPS	24046	TCTGATAAGTTTTTTCCGAGT	38369	AGCGACAAATTCTTCCCAAGC
9724	SDLNKLA	24047	TCTGATCTGAATAAGCTTGCG	38370	AGCGACCTCAACAAACTCGCA
9725	SDLPMLV	24048	TCTGATCTGCCTATGCTGGTT	38371	AGCGACCTCCCAATGCTCGTC
9726	SDLRMVA	24049	TCTGATCTTCGTATGGTTGCT	38372	AGCGACCTCAGAATGGTCGCA
9727	SDLSRPL	24050	AGTGATCTTTCGCGGCCTCTT	38373	AGCGACCTCAGCAGACCACTC
9728	SDMATKL	24051	AGTGATATGGCTACTAAGTTG	38374	AGCGACATGGCAACAAAACTC
9729	SDMPVPR	24052	AGTGATATGCCTGTTCCTCGT	38375	AGCGACATGCCAGTCCCAAGA
9730	SDMTARG	24053	TCGGATATGACGGCTCGGGGG	38376	AGCGACATGACAGCAAGAGGA
9731	SDNYERT	24054	AGTGATAATTATGAGCGTACG	38377	AGCGACAACTACGAAAGAACA
9732	SDPGRGA	24055	TCTGATCCTGGGCGTGGTGCG	38378	AGCGACCCAGGAAGAGGAGCA
9733	SDPKYSV	24056	AGTGATCCTAAGTATTCGGTG	38379	AGCGACCCAAAATACAGCGTC
9734	SDPNTYI	24057	TCTGATCCGAATACGTATATT	38380	AGCGACCCAAACACATACATC
9735	SDPRRTS	24058	TCTGATCCTAGGAGGACTAGT	38381	AGCGACCCAAGAAGAACAAGC
9736	SDPSLPV	24059	AGTGATCCGTCGTTGCCGGTT	38382	AGCGACCCAAGCCTCCCAGTC
9737	SDPVLGA	24060	TCTGATCCGGTGTTGGGGGCG	38383	AGCGACCCAGTCCTCGGAGCA
9738	SDQPTKA	24061	TCTGATCAGCCTACTAAGGCT	38384	AGCGACCAACCAACAAAAGCA
9739	SDQRILP	24062	AGTGATCAGCGGATTTTGCCT	38385	AGCGACCAAAGAATCCTCCCA
9740	SDQSLTY	24063	TCTGATCAGTCTCTGACGTAT	38386	AGCGACCAAAGCCTCACATAC
9741	SDQVKSS	24064	AGTGATCAGGTTAAGAGTTCT	38387	AGCGACCAAGTCAAAAGCAGC
9742	SDRESRI	24065	TCGGATCGGGAGTCTCGTATT	38388	AGCGACAGAGAAAGCAGAATC
9743	SDREVDP	24066	TCGGATAGGGAGGTTGATCCG	38389	AGCGACAGAGAAGTCGACCCA
9744	SDRGIRD	24067	AGTGATCGTGGGATTCGTGAT	38390	AGCGACAGAGGAATCAGAGAC
9745	SDRGYPK	24068	TCTGATAGGGGGTATCCTAAG	38391	AGCGACAGAGGATACCCAAAA
9746	SDRLCDE	24069	TCGGATCGGCTTTGTGATGAG	38392	AGCGACAGACTCTGCGACGAA
9747	SDRLQTV	24070	AGTGATCGGCTTCAGACGGTT	38393	AGCGACAGACTCCAAACAGTC
9748	SDRMMTF	24071	TCTGATAGGATGATGACTTTT	38394	AGCGACAGAATGATGACATTC
9749	SDRMSSP	24072	AGTGATCGTATGTCTAGTCCT	38395	AGCGACAGAATGAGCAGCCCA
9750	SDRPALL	24073	TCGGATAGGCCGGCGTTGTTG	38396	AGCGACAGACCAGCACTCCTC
9751	SDRPGLY	24074	TCTGATCGGCCTGGTCTGTAT	38397	AGCGACAGACCAGGACTCTAC
9752	SDRQPFT	24075	TCGGATCGTCAGCCTTTTACT	38398	AGCGACAGACAACCATTCACA
9753	SDRRAMS	24076	AGTGATCGTCGTGCTATGAGT	38399	AGCGACAGAAGAGCAATGAGC
9754	SDRRNMA	24077	TCTGATCGTCGTAATATGGCG	38400	AGCGACAGAAGAAACATGGCA

9755	SDRSATS	24078	AGTGATCGGAGTGCTACGTCT	38401	AGCGACAGAAGCGCAACAAGC
9756	SDRSDKP	24079	TCTGATCGTTCGGATAAGCCG	38402	AGCGACAGAAGCGACAAACCA
9757	SDSAHAP	24080	TCTGATTCGGCTCATGCTCCT	38403	AGCGACAGCGCACACGCACCA
9758	SDSGQSA	24081	TCGGATTCTGGGCAGTCTGCG	38404	AGCGACAGCGGACAAAGCGCA
9759	SDSKVGP	24082	TCTGATTCGAAGGTGGGTCCG	38405	AGCGACAGCAAAGTCGGACCA
9760	SDSRLGA	24083	TCGGATTCTCGTCTGGGGGCG	38406	AGCGACAGCAGACTCGGAGCA
9761	SDSRREY	24084	AGTGATTCTCGGAGGGAGTAT	38407	AGCGACAGCAGAAGAGAATAC
9762	SDSYGSR	24085	TCTGATTCGTATGGTTCTCGT	38408	AGCGACAGCTACGGAAGCAGA
9763	SDSYPRI	24086	TCGGATAGTTATCCGCGTATT	38409	AGCGACAGCTACCCAAGAATC
9764	SDTKLYP	24087	TCGGATACGAAGCTGTATCCG	38410	AGCGACACAAAACTCTACCCA
9765	SDTMRAE	24088	TCTGATACGATGAGGGCGGAG	38411	AGCGACACAATGAGAGCAGAA
9766	SDTRLTR	24089	TCGGATACGAGGCTGACGCGT	38412	AGCGACACAAGACTCACAAGA
9767	SDTRNGA	24090	TCGGATACTAGGAATGGGGCG	38413	AGCGACACAAGAAACGGAGCA
9768	SDTTLLD	24091	AGTGATACTACGCTGCTGGAT	38414	AGCGACACAACACTCCTCGAC
9769	SDTYMRL	24092	TCTGATACGTATATGCGGTTG	38415	AGCGACACATACATGAGACTC
9770	SDVAARS	24093	TCGGATGTTGCTGCTAGGAGT	38416	AGCGACGTCGCAGCAAGAAGC
9771	SDVAMRA	24094	TCTGATGTTGCTATGCGGGCG	38417	AGCGACGTCGCAATGAGAGCA
9772	SDVNQGL	24095	AGTGATGTTAATCAGGGGTTG	38418	AGCGACGTCAACCAAGGACTC
9773	SEAFRPA	24096	AGTGAGGCGTTTCGGCCGGCG	38419	AGCGAAGCATTCAGACCAGCA
9774	SEAPNDR	24097	TCTGAGGCTCCGAATGATCGG	38420	AGCGAAGCACCAAACGACAGA
9775	SEASASR	24098	AGTGAGGCGTCTGCGTCTAGG	38421	AGCGAAGCAAGCGCAAGCAGA
9776	SEAWLAS	24099	AGTGAGGCTTGGCTGGCGAGT	38422	AGCGAAGCATGGCTCGCAAGC
9777	SEDGDIK	24100	AGTGAGGATGGTGATATTAAG	38423	AGCGAAGACGGAGACATCAAA
9778	SEDRSRT	24101	TCGGAGGATCGTAGTCGGACG	38424	AGCGAAGACAGAAGCAGAACA
9779	SEESWGY	24102	AGTGAGGAGTCGTGGGGTTAT	38425	AGCGAAGAAAGCTGGGGATAC
9780	SEFVRMP	24103	TCTGAGTTTGTTCGGATGCCT	38426	AGCGAATTCGTCAGAATGCCA
9781	SEGDHAL	24104	TCTGAGGGGGATCATGCGCTT	38427	AGCGAAGGAGACCACGCACTC
9782	SEGFNAM	24105	TCGGAGGGTTTTAATGCGATG	38428	AGCGAAGGATTCAACGCAATG
9783	SEGHRGP	24106	AGTGAGGGGCATCGGGGTCCT	38429	AGCGAAGGACACAGAGGACCA
9784	SEGTVRE	24107	AGTGAGGGTACTGTTCGGGAG	38430	AGCGAAGGAACAGTCAGAGAA
9785	SEIHRLP	24108	TCTGAGATTCATAGGCTTCCG	38431	AGCGAAATCCACAGACTCCCA
9786	SEINRPE	24109	TCGGAGATTAATCGTCCTGAG	38432	AGCGAAATCAACAGACCAGAA
9787	SEITLPL	24110	TCGGAGATTACTCTTCCGCTT	38433	AGCGAAATCACACTCCCACTC
9788	SEKSNES	24111	TCTGAGAAGTCGAATGAGAGT	38434	AGCGAAAAAAGCAACGAAAGC
9789	SEKYAAM	24112	TCGGAGAAGTATGCTGCTATG	38435	AGCGAAAAATACGCAGCAATG
9790	SELEART	24113	AGTGAGCTGGAGGCTCGGACG	38436	AGCGAACTCGAAGCAAGAACA
9791	SELHGLL	24114	TCTGAGCTTCATGGGCTTCTG	38437	AGCGAACTCCACGGACTCCTC
9792	SELKTRP	24115	TCTGAGTTGAAGACGAGGCCT	38438	AGCGAACTCAAAACAAGACCA
9793	SELRSVG	24116	AGTGAGCTTAGGTCGGTGGGT	38439	AGCGAACTCAGAAGCGTCGGA
9794	SEMDLRS	24117	AGTGAGATGGATTTGCGGTCT	38440	AGCGAAATGGACCTCAGAAGC
9795	SENQMRS	24118	TCGGAGAATCAGATGAGGTCT	38441	AGCGAAAACCAAATGAGAAGC
9796	SENTSDH	24119	AGTGAGAATACGTCTGATCAT	38442	AGCGAAAACACAAGCGACCAC
9797	SEPIRTV	24120	TCTGAGCCTATTCGTACTGTT	38443	AGCGAACCAATCAGAACAGTC
9798	SEPRRTP	24121	AGTGAGCCTAGGCGGACTCCG	38444	AGCGAACCAAGAAGAACACCA
9799	SEPRSHP	24122	TCGGAGCCTCGGTCGCATCCG	38445	AGCGAACCAAGAAGCCACCCA

9800	SEPSDYV	24123	AGTGAGCCTTCTGATTATGTG	38446	AGCGAACCAAGCGACTACGTC
9801	SEPSLSS	24124	TCGGAGCCTTCTCTGTCGTCT	38447	AGCGAACCAAGCCTCAGCAGC
9802	SEPTARN	24125	TCTGAGCCGACGGCGAGGAAT	38448	AGCGAACCAACAGCAAGAAAC
9803	SEPTMIV	24126	TCGGAGCCGACTATGATTGTG	38449	AGCGAACCAACAATGATCGTC
9804	SEPYGRL	24127	TCGGAGCCGTATGGTCGTCTT	38450	AGCGAACCATACGGAAGACTC
9805	SEPYHAA	24128	TCTGAGCCTTATCATGCTGCG	38451	AGCGAACCATACCACGCAGCA
9806	SEQSRLL	24129	AGTGAGCAGTCGCGGTTGTTG	38452	AGCGAACAAAGCAGACTCCTC
9807	SERFFNG	24130	TCGGAGCGTTTTTTTAATGGT	38453	AGCGAAAGATTCTTCAACGGA
9808	SERHACS	24131	TCTGAGCGTCATGCTTGTTCT	38454	AGCGAAAGACACGCATGCAGC
9809	SERPAAA	24132	TCTGAGCGTCCGGCGGCGGCT	38455	AGCGAAAGACCAGCAGCAGCA
9810	SERPMPK	24133	TCGGAGAGGCCTATGCCTAAG	38456	AGCGAAAGACCAATGCCAAAA
9811	SERTLIM	24134	TCTGAGAGGACGCTGATTATG	38457	AGCGAAAGAACACTCATCATG
9812	SERVAAH	24135	TCTGAGCGGGTTGCTGCGCAT	38458	AGCGAAAGAGTCGCAGCACAC
9813	SERVEKH	24136	TCTGAGAGGGTTGAGAAGCAT	38459	AGCGAAAGAGTCGAAAAACAC
9814	SESSSQN	24137	TCTGAGAGTAGTTCGCAGAAT	38460	AGCGAAAGCAGCAGCCAAAAC
9815	SETTSRH	24138	TCGGAGACGACGTCTCGTCAT	38461	AGCGAAACAACAAGCAGACAC
9816	SEVGSAT	24139	AGTGAGGTGGGTTCTGCGACG	38462	AGCGAAGTCGGAAGCGCAACA
9817	SEVNLPS	24140	TCTGAGGTTAATCTTCCGTCG	38463	AGCGAAGTCAACCTCCCAAGC
9818	SEVRATA	24141	AGTGAGGTTCGGGCTACGGCG	38464	AGCGAAGTCAGAGCAACAGCA
9819	SEVSPRG	24142	TCGGAGGTTTCTCCGCGGGGG	38465	AGCGAAGTCAGCCCAAGAGGA
9820	SEWKVEH	24143	TCTGAGTGGAAGGTTGAGCAT	38466	AGCGAATGGAAAGTCGAACAC
9821	SEYYHSA	24144	TCGGAGTATTATCATAGTGCG	38467	AGCGAATACTACCACAGCGCA
9822	SFAPAHD	24145	AGTTTTGCGCCGGCGCATGAT	38468	AGCTTCGCACCAGCACACGAC
9823	SFASFPG	24146	TCGTTTGCGAGTTTTCCGGGT	38469	AGCTTCGCAAGCTTCCCAGGA
9824	SFDDGGP	24147	AGTTTTGATGATGGTGGTCCG	38470	AGCTTCGACGACGGAGGACCA
9825	SFDGVPF	24148	AGTTTTGATGGTGTGCCTTTT	38471	AGCTTCGACGGAGTCCCATTC
9826	SFDHTLG	24149	TCGTTTGATCATACTCTGGGG	38472	AGCTTCGACCACACACTCGGA
9827	SFDKFAE	24150	TCGTTTGATAAGTTTGCGGAG	38473	AGCTTCGACAAATTCGCAGAA
9828	SFDMALK	24151	AGTTTTGATATGGCTCTTAAG	38474	AGCTTCGACATGGCACTCAAA
9829	SFDSNRT	24152	TCTTTTGATTCTAATCGGACG	38475	AGCTTCGACAGCAACAGAACA
9830	SFESKMH	24153	TCGTTTGAGTCTAAGATGCAT	38476	AGCTTCGAAAGCAAAATGCAC
9831	SFETIGR	24154	AGTTTTGAGACGATTGGGCGT	38477	AGCTTCGAAACAATCGGAAGA
9832	SFETWAP	24155	AGTTTTGAGACGTGGGCGCCG	38478	AGCTTCGAAACATGGGCACCA
9833	SFGMKPS	24156	TCTTTTGGGATGAAGCCGTCG	38479	AGCTTCGGAATGAAACCAAGC
9834	SFGNGTV	24157	TCTTTTGGTAATGGGACTGTT	38480	AGCTTCGGAAACGGAACAGTC
9835	SFGSGPS	24158	TCTTTTGGTTCTGGTCCTTCG	38481	AGCTTCGGAAGCGGACCAAGC
9836	SFHEATN	24159	TCGTTTCATGAGGCGACTAAT	38482	AGCTTCCACGAAGCAACAAAC
9837	SFITDAP	24160	TCTTTTATTACGGATGCTCCT	38483	AGCTTCATCACAGACGCACCA
9838	SFKDHYA	24161	TCTTTTAAGGATCATTATGCT	38484	AGCTTCAAAGACCACTACGCA
9839	SFKSTNL	24162	TCTTTTAAGTCGACTAATCTG	38485	AGCTTCAAAAGCACAAACCTC
9840	SFKTGSA	24163	AGTTTTAAGACTGGTTCTGCG	38486	AGCTTCAAAACAGGAAGCGCA
9841	SFMPQLE	24164	TCGTTTATGCCGCAGTTGGAG	38487	AGCTTCATGCCACAACTCGAA
9842	SFNAGAS	24165	TCGTTTAATGCGGGGGCTTCT	38488	AGCTTCAACGCAGGAGCAAGC
9843	SFPDRPL	24166	AGTTTTCCTGATAGGCCTCTG	38489	AGCTTCCCAGACAGACCACTC
9844	SFPGERV	24167	TCTTTTCCGGGTGAGCGTGTT	38490	AGCTTCCCAGGAGAAAGAGTC

9845	SFQGART	24168	TCTTTTCAGGGGGCTCGTACT	38491	AGCTTCCAAGGAGCAAGAACA
9846	SFQSHGD	24169	AGTTTTCAGAGTCATGGTGAT	38492	AGCTTCCAAAGCCACGGAGAC
9847	SFRGGIS	24170	AGTTTTCGGGGTGGGATTAGT	38493	AGCTTCAGAGGAGGAATCAGC
9848	SFRQASC	24171	TCTTTTCGTCAGGCTAGTTGT	38494	AGCTTCAGACAAGCAAGCTGC
9849	SFRQPQS	24172	AGTTTTCGGCAGCCGCAGAGT	38495	AGCTTCAGACAACCACAAAGC
9850	SFSDPQN	24173	TCGTTTTCTGATCCTCAGAAT	38496	AGCTTCAGCGACCCACAAAAC
9851	SFSGPKS	24174	AGTTTTAGTGGTCCTAAGTCG	38497	AGCTTCAGCGGACCAAAAAGC
9852	SFSNPSQ	24175	TCTTTTTCGAATCCTTCGCAG	38498	AGCTTCAGCAACCCAAGCCAA
9853	SFSRATS	24176	TCGTTTTCGCGTGCGACTTCT	38499	AGCTTCAGCAGAGCAACAAGC
9854	SFSSTAS	24177	TCTTTTTCGTCTACTGCTTCT	38500	AGCTTCAGCAGCACAGCAAGC
9855	SFTGSVA	24178	AGTTTTACTGGTTCTGTTGCG	38501	AGCTTCACAGGAAGCGTCGCA
9856	SFTGSVP	24179	TCGTTTACTGGGTCTGTTCCT	38502	AGCTTCACAGGAAGCGTCCCA
9857	SFTQALE	24180	TCTTTTACTCAGGCGTTGGAG	38503	AGCTTCACACAAGCACTCGAA
9858	SFTRQEA	24181	AGTTTTACTCGTCAGGAGGCT	38504	AGCTTCACAAGACAAGAAGCA
9859	SFTTGGV	24182	TCTTTTACGACGGGTGGTGTG	38505	AGCTTCACAACAGGAGGAGTC
9860	SFTTQAT	24183	AGTTTTACGACGCAGGCGACT	38506	AGCTTCACAACACAAGCAACA
9861	SFVDRAG	24184	TCGTTTGTGGATCGTGCTGGT	38507	AGCTTCGTCGACAGAGCAGGA
9862	SFVQTTP	24185	TCGTTTGTTCAGACTACGCCT	38508	AGCTTCGTCCAAACAACACCA
9863	SFVRTST	24186	TCGTTTGTTAGGACGAGTACT	38509	AGCTTCGTCAGAACAAGCACA
9864	SGAAPTY	24187	AGTGGTGCTGCTCCTACGTAT	38510	AGCGGAGCAGCACCAACATAC
9865	SGAFHLS	24188	TCTGGGGCGTTTCATTTGAGT	38511	AGCGGAGCATTCCACCTCAGC
9866	SGAQPMF	24189	TCTGGGGCTCAGCCGATGTTT	38512	AGCGGAGCACAACCAATGTTC
9867	SGAQVPS	24190	AGTGGGGCGCAGGTTCCGTCT	38513	AGCGGAGCACAAGTCCCAAGC
9868	SGASVIA	24191	TCGGGTGCGAGTGTTATTGCT	38514	AGCGGAGCAAGCGTCATCGCA
9869	SGATHPY	24192	TCGGGGGCTACGCATCCTTAT	38515	AGCGGAGCAACACACCCATAC
9870	SGAVSGL	24193	TCGGGTGCTGTTAGTGGGCTT	38516	AGCGGAGCAGTCAGCGGACTC
9871	SGAYSSS	24194	TCTGGTGCGTATTCTTCGTCT	38517	AGCGGAGCATACAGCAGCAGC
9872	SGCSELP	24195	TCGGGGTGTTCTGAGCTGCCT	38518	AGCGGATGCAGCGAACTCCCA
9873	SGDPKDI	24196	TCTGGTGATCCTAAGGATATT	38519	AGCGGAGACCCAAAAGACATC
9874	SGDQGSR	24197	AGTGGGGATCAGGGTTCGAGG	38520	AGCGGAGACCAAGGAAGCAGA
9875	SGEAKSG	24198	TCTGGGGAGGCTAAGTCGGGG	38521	AGCGGAGAAGCAAAAAGCGGA
9876	SGELGGL	24199	AGTGGTGAGTTGGGTGGTTTG	38522	AGCGGAGAACTCGGAGGACTC
9877	SGELNPP	24200	TCGGGTGAGTTGAATCCTCCG	38523	AGCGGAGAACTCAACCCACCA
9878	SGELRYI	24201	TCTGGGGAGCTTCGTTATATT	38524	AGCGGAGAACTCAGATACATC
9879	SGERTSG	24202	TCTGGGGAGAGGACGTCGGGT	38525	AGCGGAGAAAGAACAAGCGGA
9880	SGFGAKQ	24203	AGTGGTTTTGGGGCGAAGCAG	38526	AGCGGATTCGGAGCAAAACAA
9881	SGFGPLT	24204	TCTGGGTTTGGTCCTCTTACT	38527	AGCGGATTCGGACCACTCACA
9882	SGGALGY	24205	TCTGGGGGTGCGCTTGGTTAT	38528	AGCGGAGGAGCACTCGGATAC
9883	SGGASTT	24206	TCGGGGGGTGCTTCGACTACT	38529	AGCGGAGGAGCAAGCACAACA
9884	SGGGTSL	24207	TCTGGTGGGGGGACGTCGTTG	38530	AGCGGAGGAGGAACAAGCCTC
9885	SGGHLTI	24208	AGTGGGGGTCATTTGACGATT	38531	AGCGGAGGACACCTCACAATC
9886	SGGLRAA	24209	TCGGGGGGGCTTCGGGCGGCG	38532	AGCGGAGGACTCAGAGCAGCA
9887	SGGQEWT	24210	TCTGGTGGGCAGGAGTGGACT	38533	AGCGGAGGACAAGAATGGACA
9888	SGGSFTT	24211	TCTGGGGGTTCGTTTACTACT	38534	AGCGGAGGAAGCTTCACAACA
9889	SGIGSRQ	24212	AGTGGGATTGGGTCTCGGCAG	38535	AGCGGAATCGGAAGCAGACAA

9890	SGILQSS	24213	TCGGGGATTCTGCAGTCGAGT	38536	AGCGGAATCCTCCAAAGCAGC
9891	SGISLRP	24214	TCGGGGATTAGTCTGCGGCCG	38537	AGCGGAATCAGCCTCAGACCA
9892	SGISRID	24215	AGTGGTATTAGTCGTATTGAT	38538	AGCGGAATCAGCAGAATCGAC
9893	SGKASPG	24216	TCGGGTAAGGCTTCTCCTGGG	38539	AGCGGAAAAGCAAGCCCAGGA
9894	SGKHTMN	24217	AGTGGGAAGCATACTATGAAT	38540	AGCGGAAAACACACAATGAAC
9895	SGKLVVS	24218	TCTGGTAAGTTGGTTGTTTCT	38541	AGCGGAAAACTCGTCGTCAGC
9896	SGKMGVY	24219	TCTGGTAAGATGGGTGTTTAT	38542	AGCGGAAAAATGGGAGTCTAC
9897	SGKNPGY	24220	TCGGGTAAGAATCCGGGTTAT	38543	AGCGGAAAAAACCCAGGATAC
9898	SGKPMGT	24221	AGTGGTAAGCCGATGGGGACG	38544	AGCGGAAAACCAATGGGAACA
9899	SGKSGFE	24222	TCTGGGAAGTCGGGTTTTGAG	38545	AGCGGAAAAAGCGGATTCGAA
9900	SGLAVHP	24223	AGTGGGTTGGCTGTTCATCCT	38546	AGCGGACTCGCAGTCCACCCA
9901	SGLEDVV	24224	TCGGGGCTGGAGGATGTTGTT	38547	AGCGGACTCGAAGACGTCGTC
9902	SGLGIST	24225	TCTGGTTTGGGGATTTCGACT	38548	AGCGGACTCGGAATCAGCACA
9903	SGLHALT	24226	AGTGGGCTGCATGCTCTGACT	38549	AGCGGACTCCACGCACTCACA
9904	SGLIATG	24227	AGTGGTCTGATTGCTACGGGG	38550	AGCGGACTCATCGCAACAGGA
9905	SGLNPKS	24228	TCGGGGCTTAATCCGAAGTCT	38551	AGCGGACTCAACCCAAAAAGC
9906	SGLNRTV	24229	AGTGGTCTGAATCGGACTGTT	38552	AGCGGACTCAACAGAACAGTC
9907	SGLSAYL	24230	AGTGGTCTGTCTGCTTATTTG	38553	AGCGGACTCAGCGCATACCTC
9908	SGMGHVA	24231	TCGGGGATGGGTCATGTGGCT	38554	AGCGGAATGGGACACGTCGCA
9909	SGMLMRG	24232	TCGGGTATGCTGATGCGGGGG	38555	AGCGGAATGCTCATGAGAGGA
9910	SGMTDSP	24233	TCGGGTATGACTGATTCGCCG	38556	AGCGGAATGACAGACAGCCCA
9911	SGNGVLL	24234	AGTGGTAATGGGGTTCTGTTG	38557	AGCGGAAACGGAGTCCTCCTC
9912	SGNLGYA	24235	AGTGGTAATCTGGGTTATGCT	38558	AGCGGAAACCTCGGATACGCA
9913	SGNMSAG	24236	AGTGGGAATATGAGTGCTGGG	38559	AGCGGAAACATGAGCGCAGGA
9914	SGNPSQA	24237	TCGGGTAATCCGTCTCAGGCT	38560	AGCGGAAACCCAAGCCAAGCA
9915	SGNTYSR	24238	AGTGGGAATACTTATTCTAGG	38561	AGCGGAAACACATACAGCAGA
9916	SGPDIFL	24239	TCTGGTCCTGATATTTTTCTT	38562	AGCGGACCAGACATCTTCCTC
9917	SGPHGGQ	24240	AGTGGGCCGCATGGGGGGCAG	38563	AGCGGACCACACGGAGGACAA
9918	SGPLNSP	24241	TCGGGTCCTCTTAATTCTCCT	38564	AGCGGACCACTCAACAGCCCA
9919	SGPRLGP	24242	AGTGGTCCTAGGCTTGGTCCG	38565	AGCGGACCAAGACTCGGACCA
9920	SGPSVLR	24243	AGTGGGCCGAGTGTGCTGCGG	38566	AGCGGACCAAGCGTCCTCAGA
9921	SGPTHAM	24244	TCTGGGCCGACGCATGCGATG	38567	AGCGGACCAACACACGCAATG
9922	SGPVGRT	24245	TCGGGTCCTGTGGGTCGGACT	38568	AGCGGACCAGTCGGAAGAACA
9923	SGPYKLE	24246	TCTGGTCCGTATAAGCTGGAG	38569	AGCGGACCATACAAACTCGAA
9924	SGPYPIK	24247	AGTGGTCCGTATCCTATTAAG	38570	AGCGGACCATACCCAATCAAA
9925	SGQASLT	24248	TCGGGGCAGGCTAGTTTGACT	38571	AGCGGACAAGCAAGCCTCACA
9926	SGQSISP	24249	AGTGGTCAGTCTATTTCGCCT	38572	AGCGGACAAAGCATCAGCCCA
9927	SGQVPSA	24250	TCGGGGCAGGTGCCGTCGGCG	38573	AGCGGACAAGTCCCAAGCGCA
9928	SGQYPSI	24251	TCTGGGCAGTATCCTTCTATT	38574	AGCGGACAATACCCAAGCATC
9929	SGRGPPP	24252	TCTGGTCGTGGTCCGCCGCCG	38575	AGCGGAAGAGGACCACCACCA
9930	SGRHSDD	24253	AGTGGGCGTCATTCTGATGAT	38576	AGCGGAAGACACAGCGACGAC
9931	SGRPSPA	24254	TCGGGTCGTCCTTCGCCGGCG	38577	AGCGGAAGACCAAGCCCAGCA
9932	SGRQPTV	24255	TCGGGGCGGCAGCCTACGGTT	38578	AGCGGAAGACAACCAACAGTC
9933	SGRTIIT	24256	TCGGGGAGGACGATTATTACG	38579	AGCGGAAGAACAATCATCACA
9934	SGRVTNS	24257	TCTGGTAGGGTGACGAATAGT	38580	AGCGGAAGAGTCACAAACAGC

9935	SGSDPRT	24258	TCTGGGAGTGATCCGAGGACT	38581	AGCGGAAGCGACCCAAGAACA
9936	SGSGVPQ	24259	TCGGGTAGTGGTGTGCCGCAG	38582	AGCGGAAGCGGAGTCCCACAA
9937	SGSKDSH	24260	TCTGGTTCTAAGGATTCTCAT	38583	AGCGGAAGCAAAGACAGCCAC
9938	SGSKGAF	24261	AGTGGGTCGAAGGGGGCGTTT	38584	AGCGGAAGCAAAGGAGCATTC
9939	SGSMSQV	24262	TCTGGTTCGATGTCTCAGGTG	38585	AGCGGAAGCATGAGCCAAGTC
9940	SGSNMLK	24263	TCTGGGTCGAATATGCTTAAG	38586	AGCGGAAGCAACATGCTCAAA
9941	SGSPRIS	24264	AGTGGGTCTCCTCGTATTTCG	38587	AGCGGAAGCCCAAGAATCAGC
9942	SGSQGTR	24265	AGTGGTAGTCAGGGTACGAGG	38588	AGCGGAAGCCAAGGAACAAGA
9943	SGSRIME	24266	TCTGGGTCGAGGATTATGGAG	38589	AGCGGAAGCAGAATCATGGAA
9944	SGSRNLG	24267	TCGGGGTCTCGGAATCTTGGG	38590	AGCGGAAGCAGAAACCTCGGA
9945	SGSRNMV	24268	TCGGGTTCGCGGAATATGGTG	38591	AGCGGAAGCAGAAACATGGTC
9946	SGSRSML	24269	TCTGGGTCGCGGTCGATGCTT	38592	AGCGGAAGCAGAAGCATGCTC
9947	SGSRVAP	24270	TCTGGTAGTCGTGTTGCTCCT	38593	AGCGGAAGCAGAGTCGCACCA
9948	SGSSASR	24271	AGTGGTTCGTCTGCGTCTCGG	38594	AGCGGAAGCAGCGCAAGCAGA
9949	SGSSGSA	24272	TCGGGTAGTTCTGGTAGTGCT	38595	AGCGGAAGCAGCGGAAGCGCA
9950	SGSSKSM	24273	TCTGGGAGTAGTAAGTCGATG	38596	AGCGGAAGCAGCAAAAGCATG
9951	SGSSTCI	24274	AGTGGGAGTTCTACGTGTATT	38597	AGCGGAAGCAGCACATGCATC
9952	SGSSTIN	24275	TCGGGGTCTAGTACGATTAAT	38598	AGCGGAAGCAGCACAATCAAC
9953	SGSSTPQ	24276	TCGGGTAGTTCTACGCCGCAG	38599	AGCGGAAGCAGCACACCACAA
9954	SGSVWPD	24277	TCTGGTAGTGTGTGGCCGGAT	38600	AGCGGAAGCGTCTGGCCAGAC
9955	SGSYPRD	24278	TCGGGTTCGTATCCTCGGGAT	38601	AGCGGAAGCTACCCAAGAGAC
9956	SGTALTL	24279	TCTGGGACGGCTCTTACTTTG	38602	AGCGGAACAGCACTCACACTC
9957	SGTDHLL	24280	TCGGGTACTGATCATCTGCTT	38603	AGCGGAACAGACCACCTCCTC
9958	SGTGQDG	24281	TCGGGGACGGGTCAGGATGGT	38604	AGCGGAACAGGACAAGACGGA
9959	SGTGRGT	24282	AGTGGGACTGGTAGGGGGACT	38605	AGCGGAACAGGAAGAGGAACA
9960	SGTLTQK	24283	AGTGGTACGCTGACGCAGAAG	38606	AGCGGAACACTCACACAAAAA
9961	SGTPMSR	24284	TCGGGGACGCCGATGTCTCGT	38607	AGCGGAACACCAATGAGCAGA
9962	SGTSVFA	24285	AGTGGGACTAGTGTGTTTGCT	38608	AGCGGAACAAGCGTCTTCGCA
9963	SGTTAWA	24286	TCGGGGACTACTGCGTGGGCG	38609	AGCGGAACAACAGCATGGGCA
9964	SGTTGYR	24287	TCGGGGACTACTGGTTATAGG	38610	AGCGGAACAACAGGATACAGA
9965	SGTVYRV	24288	TCGGGTACGGTGTATCGGGTT	38611	AGCGGAACAGTCTACAGAGTC
9966	SGVGMIS	24289	TCTGGGGTGGGGATGATTTCT	38612	AGCGGAGTCGGAATGATCAGC
9967	SGVHPFP	24290	AGTGGGGTTCATCCTTTCCG	38613	AGCGGAGTCCACCCATTCCCA
9968	SGVIKTS	24291	AGTGGGGTGATTAAGACGTCT	38614	AGCGGAGTCATCAAAACAAGC
9969	SGVNLSS	24292	TCTGGTGTGAATCTTTCTAGT	38615	AGCGGAGTCAACCTCAGCAGC
9970	SGVQSGP	24293	AGTGGGGTGCAGTCTGGTCCG	38616	AGCGGAGTCCAAAGCGGACCA
9971	SGVRQVA	24294	TCGGGTGTGCGGCAGGTGGCT	38617	AGCGGAGTCAGACAAGTCGCA
9972	SGVSMLP	24295	TCGGGTGTGTCGATGCTGCCT	38618	AGCGGAGTCAGCATGCTCCCA
9973	SGVSRYA	24296	TCTGGGGTTTCGAGGTATGCT	38619	AGCGGAGTCAGCAGATACGCA
9974	SGVSYVE	24297	AGTGGTGTGAGTTATGTTGAG	38620	AGCGGAGTCAGCTACGTCGAA
9975	SGYPNLD	24298	AGTGGTTATCCGAATTTGGAT	38621	AGCGGATACCCAAACCTCGAC
9976	SHAAQLP	24299	AGTCATGCTGCGCAGTTGCCT	38622	AGCCACGCAGCACAACTCCCA
9977	SHANLHA	24300	AGTCATGCGAATCTTCATGCG	38623	AGCCACGCAAACCTCCACGCA
9978	SHANTSS	24301	TCGCATGCGAATACGTCTAGT	38624	AGCCACGCAAACACAAGCAGC
9979	SHASNYP	24302	TCTCATGCGTCTAATTATCCG	38625	AGCCACGCAAGCAACTACCCA

9980	SHASVRS	24303	AGTCATGCGAGTGTGCGTTCG	38626	AGCCACGCAAGCGTCAGAAGC
9981	SHATTPS	24304	AGTCATGCTACGACGCCGTCT	38627	AGCCACGCAACAACACCAAGC
9982	SHAVRMG	24305	TCGCATGCGGTTCGGATGGGG	38628	AGCCACGCAGTCAGAATGGGA
9983	SHDNRGV	24306	TCGCATGATAATCGTGGGGTG	38629	AGCCACGACAACAGAGGAGTC
9984	SHENGST	24307	TCTCATGAGAATGGTTCTACT	38630	AGCCACGAAAACGGAAGCACA
9985	SHEPHTR	24308	TCTCATGAGCCGCATACTCGT	38631	AGCCACGAACCACACACAAGA
9986	SHESLGM	24309	TCGCATGAGTCTTTGGGGATG	38632	AGCCACGAAAGCCTCGGAATG
9987	SHFPMAP	24310	TCTCATTTTCCTATGGCGCCT	38633	AGCCACTTCCCAATGGCACCA
9988	SHFSAAE	24311	TCTCATTTTAGTGCGGCGGAG	38634	AGCCACTTCAGCGCAGCAGAA
9989	SHGPPRS	24312	AGTCATGGTCCGCCTCGTTCT	38635	AGCCACGGACCACCAAGAAGC
9990	SHGPYPY	24313	TCGCATGGTCCGTATCCGTAT	38636	AGCCACGGACCATACCCATAC
9991	SHGSAVN	24314	TCGCATGGGTCGGCGGTGAAT	38637	AGCCACGGAAGCGCAGTCAAC
9992	SHGSFPS	24315	TCTCATGGTTCGTTTCCGTCT	38638	AGCCACGGAAGCTTCCCAAGC
9993	SHGTKST	24316	TCTCATGGGACGAAGTCGACG	38639	AGCCACGGAACAAAAAGCACA
9994	SHHGSII	24317	TCGCATCATGGGTCTATTATT	38640	AGCCACCACGGAAGCATCATC
9995	SHIQLAP	24318	TCTCATATTCAGCTTGCTCCG	38641	AGCCACATCCAACTCGCACCA
9996	SHKRMVD	24319	AGTCATAAGCGTATGGTGGAT	38642	AGCCACAAAAGAATGGTCGAC
9997	SHKSPTP	24320	TCTCATAAGTCGCCTACTCCT	38643	AGCCACAAAAGCCCAACACCA
9998	SHLEIDM	24321	TCTCATCTTGAGATTGATATG	38644	AGCCACCTCGAAATCGACATG
9999	SHLNLRP	24322	TCGCATTTGAATCTTCGTCCT	38645	AGCCACCTCAACCTCAGACCA
10000	SHLPVSM	24323	AGTCATCTGCCGGTGTCGATG	38646	AGCCACCTCCCAGTCAGCATG
10001	SHLQNRI	24324	AGTCATTTGCAGAATCGGATT	38647	AGCCACCTCCAAAACAGAATC
10002	SHMTGST	24325	TCTCATATGACGGGTTCGACG	38648	AGCCACATGACAGGAAGCACA
10003	SHNAFPT	24326	AGTCATAATGCGTTTCCGACT	38649	AGCCACAACGCATTCCCAACA
10004	SHNALMD	24327	TCTCATAATGCGCTTATGGAT	38650	AGCCACAACGCACTCATGGAC
10005	SHNIPAG	24328	AGTCATAATATTCCTGCTGGT	38651	AGCCACAACATCCCAGCAGGA
10006	SHNKLSS	24329	TCGCATAATAAGCTGTCGAGT	38652	AGCCACAACAAACTCAGCAGC
10007	SHPAISA	24330	TCTCATCCTGCGATTTCTGCT	38653	AGCCACCCAGCAATCAGCGCA
10008	SHPALPP	24331	TCGCATCCTGCGCTGCCTCCG	38654	AGCCACCCAGCACTCCCACCA
10009	SHPDLSP	24332	TCTCATCCGGATCTTAGTCCT	38655	AGCCACCCAGACCTCAGCCCA
10010	SHPMLPT	24333	TCTCATCCTATGCTGCCTACT	38656	AGCCACCCAATGCTCCCAACA
10011	SHPMMPA	24334	TCGCATCCGATGATGCCTGCG	38657	AGCCACCCAATGATGCCAGCA
10012	SHPPLRL	24335	AGTCATCCTCCGCTTCGTCTG	38658	AGCCACCCACCACTCAGACTC
10013	SHPSSEP	24336	AGTCATCCTTCGAGTGAGCCT	38659	AGCCACCCAAGCAGCGAACCA
10014	SHQARAP	24337	AGTCATCAGGCGCGTGCTCCT	38660	AGCCACCAAGCAAGAGCACCA
10015	SHRGDEH	24338	TCTCATAGGGGGGATGAGCAT	38661	AGCCACAGAGGAGACGAACAC
10016	SHRPSTL	24339	TCTCATCGGCCTAGTACGCTG	38662	AGCCACAGACCAAGCACACTC
10017	SHRPTSS	24340	AGTCATAGGCCTACTTCTTCT	38663	AGCCACAGACCAACAAGCAGC
10018	SHSALMG	24341	TCTCATAGTGCGCTGATGGGG	38664	AGCCACAGCGCACTCATGGGA
10019	SHSAMQH	24342	TCTCATAGTGCGATGCAGCAT	38665	AGCCACAGCGCAATGCAACAC
10020	SHSHSDA	24343	TCTCATTCTCATTCTGATGCT	38666	AGCCACAGCCACAGCGACGCA
10021	SHSLGGN	24344	AGTCATTCGTTGGGTGGTAAT	38667	AGCCACAGCCTCGGAGGAAAC
10022	SHSPDIK	24345	AGTCATTCGCCTGATATTAAG	38668	AGCCACAGCCCAGACATCAAA
10023	SHSPLLP	24346	TCTCATTCGCCTTTGTTGCCG	38669	AGCCACAGCCCACTCCTCCCA
10024	SHSSIMV	24347	TCGCATAGTTCGATTATGGTG	38670	AGCCACAGCAGCATCATGGTC

10025	SHSSRLM	24348	AGTCATTCGTCTCGGCTGATG	38671	AGCCACAGCAGCAGACTCATG
10026	SHTHGNP	24349	AGTCATACTCATGGTAATCCG	38672	AGCCACACACACGGAAACCCA
10027	SHTKVSH	24350	TCTCATACTAAGGTGTCGCAT	38673	AGCCACACAAAAGTCAGCCAC
10028	SHTPRAS	24351	TCGCATACGCCGCGGGCTTCG	38674	AGCCACACACCAAGAGCAAGC
10029	SHTRPDA	24352	AGTCATACGCGTCCTGATGCT	38675	AGCCACACAAGACCAGACGCA
10030	SHTSLPR	24353	AGTCATACTAGTCTGCCGCGG	38676	AGCCACACAAGCCTCCCAAGA
10031	SHTSLVI	24354	AGTCATACTTCTCTTGTTATT	38677	AGCCACACAAGCCTCGTCATC
10032	SHVAGHA	24355	TCTCATGTGGCGGGTCATGCT	38678	AGCCACGTCGCAGGACACGCA
10033	SHVASKG	24356	TCTCATGTTGCTTCGAAGGGG	38679	AGCCACGTCGCAAGCAAAGGA
10034	SHVVNSL	24357	AGTCATGTTGTGAATAGTCTG	38680	AGCCACGTCGTCAACAGCCTC
10035	SHVYPGP	24358	TCTCATGTTTATCCGGGTCCG	38681	AGCCACGTCTACCCAGGACCA
10036	SIAAHQG	24359	AGTATTGCTGCGCATCAGGGG	38682	AGCATCGCAGCACACCAAGGA
10037	SIAQVGA	24360	AGTATTGCTCAGGTTGGTGCT	38683	AGCATCGCACAAGTCGGAGCA
10038	SIARAVT	24361	AGTATTGCTCGTGCTGTGACG	38684	AGCATCGCAAGAGCAGTCACA
10039	SIDSIAV	24362	TCTATTGATTCGATTGCGGTG	38685	AGCATCGACAGCATCGCAGTC
10040	SIDSSSL	24363	TCTATTGATTCGTCGTCTCTG	38686	AGCATCGACAGCAGCAGCCTC
10041	SIDSTYM	24364	TCTATTGATTCTACTTATATG	38687	AGCATCGACAGCACATACATG
10042	SIERELR	24365	TCGATTGAGCGTGAGCTTCGT	38688	AGCATCGAAAGAGAACTCAGA
10043	SIGGVLY	24366	AGTATTGGGGGTGTTCTTTAT	38689	AGCATCGGAGGAGTCCTCTAC
10044	SIGNFPD	24367	TCGATTGGGAATTTTCCGGAT	38690	AGCATCGGAAACTTCCCAGAC
10045	SIGSAPA	24368	TCTATTGGGTCTGCGCCGGCT	38691	AGCATCGGAAGCGCACCAGCA
10046	SIGTVVG	24369	AGTATTGGGACTGTTGTGGGG	38692	AGCATCGGAACAGTCGTCGGA
10047	SIGVHPG	24370	TCTATTGGGGTGCATCCGGGT	38693	AGCATCGGAGTCCACCCAGGA
10048	SIHLVTS	24371	AGTATTCATTTGGTTACTTCT	38694	AGCATCCACCTCGTCACAAGC
10049	SIHNGPQ	24372	TCTATTCATAATGGTCCGCAG	38695	AGCATCCACAACGGACCACAA
10050	SIIESVA	24373	TCTATTATTGAGTCGGTTGCG	38696	AGCATCATCGAAAGCGTCGCA
10051	SIIQAKP	24374	TCTATTATTCAGGCTAAGCCT	38697	AGCATCATCCAAGCAAAACCA
10052	SIISERR	24375	TCGATTATTAGTGAGAGGAGG	38698	AGCATCATCAGCGAAAGAAGA
10053	SIKVNPP	24376	AGTATTAAGGTTAATCCGCCT	38699	AGCATCAAAGTCAACCCACCA
10054	SILGAIP	24377	TCTATTCTTGGGGCGATTCCT	38700	AGCATCCTCGGAGCAATCCCA
10055	SILYGMP	24378	TCGATTCTTTATGGTATGCCG	38701	AGCATCCTCTACGGAATGCCA
10056	SIMNTGP	24379	TCTATTATGAATACGGGGCCT	38702	AGCATCATGAACACAGGACCA
10057	SIMRTDC	24380	TCTATTATGCGTACGGATTGT	38703	AGCATCATGAGAACAGACTGC
10058	SINEEPP	24381	TCTATTAATGAGGAGCCTCCT	38704	AGCATCAACGAAGAACCACCA
10059	SINVTHG	24382	TCGATTAATGTGACGCATGGT	38705	AGCATCAACGTCACACACGGA
10060	SIPMSGR	24383	AGTATTCCTATGTCTGGGCGT	38706	AGCATCCCAATGAGCGGAAGA
10061	SIPNLQA	24384	AGTATTCCGAATTTGCAGGCG	38707	AGCATCCCAAACCTCCAAGCA
10062	SIPNLYD	24385	TCTATTCCTAATTTGTATGAT	38708	AGCATCCCAAACCTCTACGAC
10063	SIPNSRQ	24386	AGTATTCCGAATTCGCGTCAG	38709	AGCATCCCAAACAGCAGACAA
10064	SIQKHLP	24387	TCGATTCAGAAGCATTTGCCT	38710	AGCATCCAAAAACACCTCCCA
10065	SIQWKDS	24388	TCTATTCAGTGGAAGGATAGT	38711	AGCATCCAATGGAAAGACAGC
10066	SISLPYP	24389	TCGATTAGTTTGCCTTATCCT	38712	AGCATCAGCCTCCCATACCCA
10067	SISPSPG	24390	TCTATTTCTCCTTCGCCGGGT	38713	AGCATCAGCCCAAGCCCAGGA
10068	SISSQDL	24391	TCTATTTCTAGTCAGGATCTT	38714	AGCATCAGCAGCCAAGACCTC
10069	SISSSSG	24392	TCGATTAGTTCGAGTTCTGGT	38715	AGCATCAGCAGCAGCAGCGGA

10070	SISVMKQ	24393	TCGATTTCTGTTATGAAGCAG	38716	AGCATCAGCGTCATGAAACAA
10071	SITPFNE	24394	TCTATTACTCCGTTTAATGAG	38717	AGCATCACACCATTCAACGAA
10072	SITSEKI	24395	AGTATTACGAGTGAGAAGATT	38718	AGCATCACAAGCGAAAAAATC
10073	SITTGRG	24396	TCGATTACGACGGGTCGGGGG	38719	AGCATCACAACAGGAAGAGGA
10074	SITTRTD	24397	TCTATTACGACTCGTACTGAT	38720	AGCATCACAACAAGAACAGAC
10075	SIVHPDS	24398	TCGATTGTTCATCCGGATTCT	38721	AGCATCGTCCACCCAGACAGC
10076	SIVLKGS	24399	TCGATTGTTCTGAAGGGGTCT	38722	AGCATCGTCCTCAAAGGAAGC
10077	SIVSRVE	24400	TCGATTGTTTCTCGGGTGGAG	38723	AGCATCGTCAGCAGAGTCGAA
10078	SIVTVSG	24401	TCGATTGTTACTGTTAGTGGT	38724	AGCATCGTCACAGTCAGCGGA
10079	SKAHENP	24402	TCGAAGGCTCATGAGAATCCT	38725	AGCAAAGCACACGAAAACCCA
10080	SKAPYSA	24403	TCTAAGGCGCCGTATTCTGCG	38726	AGCAAAGCACCATACAGCGCA
10081	SKASLNP	24404	TCGAAGGCGTCTTTGAATCCT	38727	AGCAAAGCAAGCCTCAACCCA
10082	SKAYTPL	24405	AGTAAGGCTTATACTCCGTTG	38728	AGCAAAGCATACACACCACTC
10083	SKDGSLN	24406	AGTAAGGATGGTTCGCTTAAT	38729	AGCAAAGACGGAAGCCTCAAC
10084	SKDHFPA	24407	TCTAAGGATCATTTTCCGGCT	38730	AGCAAAGACCACTTCCCAGCA
10085	SKDILRS	24408	AGTAAGGATATTCTGCGGTCT	38731	AGCAAAGACATCCTCAGAAGC
10086	SKDMLET	24409	TCGAAGGATATGTTGGAGACT	38732	AGCAAAGACATGCTCGAAACA
10087	SKDTLRN	24410	TCTAAGGATACGTTGCGTAAT	38733	AGCAAAGACACACTCAGAAAC
10088	SKDTPLA	24411	TCTAAGGATACTCCGCTGGCT	38734	AGCAAAGACACACCACTCGCA
10089	SKEIYTQ	24412	TCGAAGGAGATTTATACGCAG	38735	AGCAAAGAAATCTACACACAA
10090	SKENYPH	24413	AGTAAGGAGAATTATCCTCAT	38736	AGCAAAGAAAACTACCCACAC
10091	SKERFPY	24414	TCGAAGGAGAGGTTTCCGTAT	38737	AGCAAAGAAAGATTCCCATAC
10092	SKEYPEY	24415	TCGAAGGAGTATCCTGAGTAT	38738	AGCAAAGAATACCCAGAATAC
10093	SKFNGHL	24416	TCGAAGTTTAATGGGCATCTT	38739	AGCAAATTCAACGGACACCTC
10094	SKHEVYL	24417	TCGAAGCATGAGGTGTATCTT	38740	AGCAAACACGAAGTCTACCTC
10095	SKHTAFV	24418	TCTAAGCATACGGCGTTTGTT	38741	AGCAAACACACAGCATTCGTC
10096	SKIDLYT	24419	TCTAAGATTGATCTTTATACG	38742	AGCAAAATCGACCTCTACACA
10097	SKIDRDD	24420	AGTAAGATTGATCGGGATGAT	38743	AGCAAAATCGACAGAGACGAC
10098	SKIPHEV	24421	AGTAAGATTCCTCATGAGGTG	38744	AGCAAAATCCCACACGAAGTC
10099	SKLDDGR	24422	TCGAAGCTGGATGATGGGCGG	38745	AGCAAACTCGACGACGGAAGA
10100	SKLGSHL	24423	AGTAAGTTGGGTTCGCATCTG	38746	AGCAAACTCGGAAGCCACCTC
10101	SKLPPLH	24424	AGTAAGCTTCCTCCGCTTCAT	38747	AGCAAACTCCCACCACTCCAC
10102	SKLPVAL	24425	TCTAAGTTGCCGGTTGCGCTT	38748	AGCAAACTCCCAGTCGCACTC
10103	SKLTTEP	24426	TCTAAGCTTACTACTGAGCCT	38749	AGCAAACTCACAACAGAACCA
10104	SKMLEFV	24427	TCGAAGATGCTGGAGTTTGTG	38750	AGCAAAATGCTCGAATTCGTC
10105	SKMSRLE	24428	TCGAAGATGAGTAGGCTTGAG	38751	AGCAAAATGAGCAGACTCGAA
10106	SKNNPSL	24429	TCGAAGAATAATCCTAGTTTG	38752	AGCAAAAACAACCCAAGCCTC
10107	SKNSQDY	24430	TCGAAGAATTCTCAGGATTAT	38753	AGCAAAAACAGCCAAGACTAC
10108	SKNSVLN	24431	AGTAAGAATTCTGTGCTTAAT	38754	AGCAAAAACAGCGTCCTCAAC
10109	SKNVCEP	24432	TCGAAGAATGTTTGTGAGCCT	38755	AGCAAAAACGTCTGCGAACCA
10110	SKPHREV	24433	TCTAAGCCGCATCGGGAGGTT	38756	AGCAAACCACACAGAGAAGTC
10111	SKPLSGF	24434	AGTAAGCCTCTTTCTGGTTTT	38757	AGCAAACCACTCAGCGGATTC
10112	SKPSGPS	24435	TCGAAGCCTTCGGGTCCTTCT	38758	AGCAAACCAAGCGGACCAAGC
10113	SKPTPTH	24436	AGTAAGCCTACGCCTACTCAT	38759	AGCAAACCAACACCAACACAC
10114	SKQAASV	24437	TCTAAGCAGGCTGCGTCTGTG	38760	AGCAAACAAGCAGCAAGCGTC

10115	SKQMPMH	24438	AGTAAGCAGATGCCGATGCAT	38761	AGCAAACAAATGCCAATGCAC
10116	SKRTTWD	24439	TCGAAGCGGACGACTTGGGAT	38762	AGCAAAAGAACAACATGGGAC
10117	SKSGTSE	24440	TCTAAGTCGGGTACTTCGGAG	38763	AGCAAAAGCGGAACAAGCGAA
10118	SKSLKLS	24441	TCTAAGTCTCTTAAGCTGTCT	38764	AGCAAAAGCCTCAAACTCAGC
10119	SKSPNPY	24442	TCGAAGAGTCCTAATCCGTAT	38765	AGCAAAAGCCCAAACCCATAC
10120	SKSQFLA	24443	TCGAAGTCGCAGTTTCTTGCT	38766	AGCAAAAGCCAATTCCTCGCA
10121	SKSSMLI	24444	TCTAAGAGTTCGATGCTTATT	38767	AGCAAAAGCAGCATGCTCATC
10122	SKTDRMN	24445	TCTAAGACTGATCGTATGAAT	38768	AGCAAAACAGACAGAATGAAC
10123	SKTSDRT	24446	TCGAAGACTAGTGATAGGACG	38769	AGCAAAACAAGCGACAGAACA
10124	SKTVEQN	24447	TCTAAGACGGTGGAGCAGAAT	38770	AGCAAAACAGTCGAACAAAAC
10125	SKVPSLA	24448	AGTAAGGTGCCTAGTCTTGCT	38771	AGCAAAGTCCCAAGCCTCGCA
10126	SKVREPI	24449	TCTAAGGTGCGTGAGCCTATT	38772	AGCAAAGTCAGAGAACCAATC
10127	SKYATVV	24450	TCGAAGTATGCGACTGTTGTG	38773	AGCAAATACGCAACAGTCGTC
10128	SKYLRMD	24451	TCGAAGTATTTGCGTATGGAT	38774	AGCAAATACCTCAGAATGGAC
10129	SKYTLAY	24452	AGTAAGTATACTCTGGCTTAT	38775	AGCAAATACACACTCGCATAC
10130	SLADANA	24453	TCTCTTGCTGATGCTAATGCT	38776	AGCCTCGCAGACGCAAACGCA
10131	SLAGNSS	24454	AGTCTGGCTGGTAATAGTTCT	38777	AGCCTCGCAGGAAACAGCAGC
10132	SLAKMPG	24455	TCTTTGGCTAAGATGCCGGGT	38778	AGCCTCGCAAAAATGCCAGGA
10133	SLALVGR	24456	AGTTTGGCTCTTGTTGGGCGG	38779	AGCCTCGCACTCGTCGGAAGA
10134	SLAPTVM	24457	TCTTTGGCGCCGACTGTTATG	38780	AGCCTCGCACCAACAGTCATG
10135	SLAQKQP	24458	TCTCTTGCTCAGAAGCAGCCT	38781	AGCCTCGCACAAAAACAACCA
10136	SLAQLHS	24459	TCGCTGGCGCAGCTTCATTCT	38782	AGCCTCGCACAACTCCACAGC
10137	SLASSAM	24460	TCTCTGGCTTCTTCTGCGATG	38783	AGCCTCGCAAGCAGCGCAATG
10138	SLASTGF	24461	TCGTTGGCGTCGACTGGGTTT	38784	AGCCTCGCAAGCACAGGATTC
10139	SLATRIS	24462	AGTCTTGCGACTCGGATTTCT	38785	AGCCTCGCAACAAGAATCAGC
10140	SLATSPY	24463	AGTCTTGCTACTAGTCCGTAT	38786	AGCCTCGCAACAAGCCCATAC
10141	SLDATKD	24464	AGTTTGGATGCGACGAAGGAT	38787	AGCCTCGACGCAACAAAAGAC
10142	SLDFPRP	24465	TCGCTTGATTTTCCGCGGCCT	38788	AGCCTCGACTTCCCAAGACCA
10143	SLDHHNR	24466	TCGCTTGATCATCATAATCGT	38789	AGCCTCGACCACCACAACAGA
10144	SLDKALR	24467	TCGCTTGATAAGGCGCTGCGT	38790	AGCCTCGACAAAGCACTCAGA
10145	SLDMQKQ	24468	TCTCTGGATATGCAGAAGCAG	38791	AGCCTCGACATGCAAAAACAA
10146	SLDPKNS	24469	TCGCTGGATCCTAAGAATAGT	38792	AGCCTCGACCCAAAAAACAGC
10147	SLEIPKI	24470	TCTTTGGAGATTCCGAAGATT	38793	AGCCTCGAAATCCCAAAAATC
10148	SLEKRGE	24471	AGTCTGGAGAAGCGTGGTGAG	38794	AGCCTCGAAAAAAGAGGAGAA
10149	SLERHVY	24472	TCTTTGGAGCGTCATGTTTAT	38795	AGCCTCGAAAGACACGTCTAC
10150	SLESEHR	24473	TCGCTTGAGTCTGAGCATCGT	38796	AGCCTCGAAAGCGAACACAGA
10151	SLESMIH	24474	TCTCTGGAGAGTATGATTCAT	38797	AGCCTCGAAAGCATGATCCAC
10152	SLESRHY	24475	TCGCTTGAGAGTCGTCATTAT	38798	AGCCTCGAAAGCAGACACTAC
10153	SLEVVRK	24476	AGTCTGGAGGTGGTTCGTAAG	38799	AGCCTCGAAGTCGTCAGAAAA
10154	SLFKDVS	24477	TCGCTTTTTAAGGATGTGTCT	38800	AGCCTCTTCAAAGACGTCAGC
10155	SLFPAGG	24478	TCGTTGTTTCCTGCGGGGGGT	38801	AGCCTCTTCCCAGCAGGAGGA
10156	SLFSARP	24479	AGTCTGTTTAGTGCGCGTCCG	38802	AGCCTCTTCAGCGCAAGACCA
10157	SLGFRAG	24480	AGTTTGGGGTTTCGGGCGGGG	38803	AGCCTCGGATTCAGAGCAGGA
10158	SLGISNF	24481	TCGCTGGGGATTTCGAATTTT	38804	AGCCTCGGAATCAGCAACTTC
10159	SLGKTSP	24482	TCGCTTGGTAAGACTTCGCCT	38805	AGCCTCGGAAAAACAAGCCCA

10160	SLGMKSA	24483	AGTCTGGGGATGAAGTCTGCT	38806	AGCCTCGGAATGAAAAGCGCA
10161	SLGQSQY	24484	TCTCTTGGTCAGAGTCAGTAT	38807	AGCCTCGGACAAAGCCAATAC
10162	SLGRGSI	24485	TCGCTTGGGCGGGGTTCGATT	38808	AGCCTCGGAAGAGGAAGCATC
10163	SLGTGVG	24486	TCGTTGGGTACTGGTGTTGGG	38809	AGCCTCGGAACAGGAGTCGGA
10164	SLHAIKN	24487	TCGCTGCATGCGATTAAGAAT	38810	AGCCTCCACGCAATCAAAAAC
10165	SLHAVVS	24488	TCTCTTCATGCGGTTGTGTCG	38811	AGCCTCCACGCAGTCGTCAGC
10166	SLHDMSG	24489	AGTCTTCATGATATGTCTGGG	38812	AGCCTCCACGACATGAGCGGA
10167	SLHSSDS	24490	TCGCTGCATTCGAGTGATAGT	38813	AGCCTCCACAGCAGCGACAGC
10168	SLIDPYE	24491	TCTCTGATTGATCCGTATGAG	38814	AGCCTCATCGACCCATACGAA
10169	SLIDRHP	24492	TCGCTTATTGATCGTCATCCT	38815	AGCCTCATCGACAGACACCCA
10170	SLIGGQQ	24493	TCGCTGATTGGGGGTCAGCAG	38816	AGCCTCATCGGAGGACAACAA
10171	SLIRSST	24494	TCGTTGATTCGGTCGAGTACG	38817	AGCCTCATCAGAAGCAGCACA
10172	SLISEKG	24495	TCTCTGATTAGTGAGAAGGGT	38818	AGCCTCATCAGCGAAAAAGGA
10173	SLKASPP	24496	AGTTTGAAGGCGTCTCCTCCG	38819	AGCCTCAAAGCAAGCCCACCA
10174	SLKEAWL	24497	TCGCTTAAGGAGGCGTGGTTG	38820	AGCCTCAAAGAAGCATGGCTC
10175	SLKIPTA	24498	TCGCTGAAGATTCCTACGGCG	38821	AGCCTCAAAATCCCAACAGCA
10176	SLKNELA	24499	TCGCTTAAGAATGAGCTGGCT	38822	AGCCTCAAAAACGAACTCGCA
10177	SLKPGGG	24500	TCTCTTAAGCCTGGTGGTGGG	38823	AGCCTCAAACCAGGAGGAGGA
10178	SLKPYQS	24501	AGTCTGAAGCCTTATCAGAGT	38824	AGCCTCAAACCATACCAAAGC
10179	SLKQSHP	24502	TCTTTGAAGCAGTCGCATCCT	38825	AGCCTCAAACAAAGCCACCCA
10180	SLKSPQL	24503	TCTTTGAAGTCTCCGCAGCTT	38826	AGCCTCAAAAGCCCACAACTC
10181	SLKTYPE	24504	TCGCTGAAGACTTATCCTGAG	38827	AGCCTCAAAACATACCCAGAA
10182	SLLAKVP	24505	AGTCTTTTGGCGAAGGTTCCG	38828	AGCCTCCTCGCAAAAGTCCCA
10183	SLLDRPI	24506	TCGTTGTTGGATAGGCCTATT	38829	AGCCTCCTCGACAGACCAATC
10184	SLLGPTQ	24507	TCGCTGTTGGGGCCGACTCAG	38830	AGCCTCCTCGGACCAACACAA
10185	SLLKPVQ	24508	TCTCTTTTGAAGCCTGTTCAG	38831	AGCCTCCTCAAACCAGTCCAA
10186	SLLLLCA	24509	TCTCTGCTTCTTCTTTGTGCT	38832	AGCCTCCTCCTCCTCTGCGCA
10187	SLLLNRG	24510	AGTCTGCTTTTGAATCGGGGT	38833	AGCCTCCTCCTCAACAGAGGA
10188	SLLLQNP	24511	AGTTTGCTTCTGCAGAATCCT	38834	AGCCTCCTCCTCCAAAACCCA
10189	SLLNSDT	24512	AGTCTGCTGAATTCTGATACT	38835	AGCCTCCTCAACAGCGACACA
10190	SLLRQVP	24513	AGTCTTTTGAGGCAGGTGCCT	38836	AGCCTCCTCAGACAAGTCCCA
10191	SLLSVSH	24514	AGTCTTCTTTCGGTGTCGCAT	38837	AGCCTCCTCAGCGTCAGCCAC
10192	SLLTASV	24515	AGTTTGCTTACTGCTAGTGTT	38838	AGCCTCCTCACAGCAAGCGTC
10193	SLLTSAP	24516	TCGCTTCTGACTAGTGCTCCG	38839	AGCCTCCTCACAAGCGCACCA
10194	SLLVNLS	24517	AGTCTGCTTGTGAATCTTTCT	38840	AGCCTCCTCGTCAACCTCAGC
10195	SLLYPTP	24518	TCTTTGCTGTATCCGACTCCT	38841	AGCCTCCTCTACCCAACACCA
10196	SLMAAGL	24519	TCGTTGATGGCGGCGGGGCTT	38842	AGCCTCATGGCAGCAGGACTC
10197	SLMASIG	24520	TCTCTGATGGCGAGTATTGGT	38843	AGCCTCATGGCAAGCATCGGA
10198	SLMHDVS	24521	TCTCTTATGCATGATGTGTCT	38844	AGCCTCATGCACGACGTCAGC
10199	SLMSLDT	24522	AGTCTGATGAGTCTTGATACT	38845	AGCCTCATGAGCCTCGACACA
10200	SLMSPSM	24523	TCGTTGATGTCGCCGTCTATG	38846	AGCCTCATGAGCCCAAGCATG
10201	SLNLRGN	24524	AGTCTTAATCTGAGGGGTAAT	38847	AGCCTCAACCTCAGAGGAAAC
10202	SLNNARN	24525	TCGTTGAATAATGCGCGGAAT	38848	AGCCTCAACAACGCAAGAAAC
10203	SLNNGLT	24526	AGTCTGAATAATGGGTTGACT	38849	AGCCTCAACAACGGACTCACA
10204	SLNNRPS	24527	AGTCTGAATAATCGGCCGAGT	38850	AGCCTCAACAACAGACCAAGC

10205	SLNPKSP	24528	AGTTTGAATCCTAAGTCTCCT	38851	AGCCTCAACCCAAAAAGCCCA
10206	SLNPSGM	24529	TCTTTGAATCCTTCTGGGATG	38852	AGCCTCAACCCAAGCGGAATG
10207	SLNRQGN	24530	TCGCTGAATAGGCAGGGTAAT	38853	AGCCTCAACAGACAAGGAAAC
10208	SLNSYSP	24531	TCTCTGAATTCTTATTCGCCG	38854	AGCCTCAACAGCTACAGCCCA
10209	SLNTGTI	24532	TCTCTGAATACTGGTACTATT	38855	AGCCTCAACACAGGAACAATC
10210	SLNTLGT	24533	AGTCTGAATACTTTGGGTACG	38856	AGCCTCAACACACTCGGAACA
10211	SLNTMNA	24534	TCGTTGAATACGATGAATGCT	38857	AGCCTCAACACAATGAACGCA
10212	SLNTTPE	24535	TCGCTTAATACGACGCCTGAG	38858	AGCCTCAACACAACACCAGAA
10213	SLNVADA	24536	AGTCTTAATGTTGCTGATGCT	38859	AGCCTCAACGTCGCAGACGCA
10214	SLPAQQV	24537	TCTCTTCCGGCGCAGCAGGTT	38860	AGCCTCCCAGCACAACAAGTC
10215	SLPASTL	24538	TCTTTGCCTGCGTCGACTCTG	38861	AGCCTCCCAGCAAGCACACTC
10216	SLPESNS	24539	AGTTTGCCTGAGTCTAATAGT	38862	AGCCTCCCAGAAAGCAACAGC
10217	SLPGSVM	24540	AGTCTGCCGGGGTCTGTTATG	38863	AGCCTCCCAGGAAGCGTCATG
10218	SLPGTVR	24541	TCGTTGCCGGGTACGGTGAGG	38864	AGCCTCCCAGGAACAGTCAGA
10219	SLPHIRH	24542	TCGCTTCCTCATATTCGTCAT	38865	AGCCTCCCACACATCAGACAC
10220	SLPHSCG	24543	AGTTTGCCGCATTCGTGTGGT	38866	AGCCTCCCACACAGCTGCGGA
10221	SLPIGGS	24544	TCTCTGCCTATTGGGGGTTCT	38867	AGCCTCCCAATCGGAGGAAGC
10222	SLPKPSH	24545	TCGCTGCCGAAGCCGTCTCAT	38868	AGCCTCCCAAAACCAAGCCAC
10223	SLPLKVN	24546	TCTTTGCCGCTTAAGGTTAAT	38869	AGCCTCCCACTCAAAGTCAAC
10224	SLPLRDL	24547	TCTCTTCCTTTGCGTGATTTG	38870	AGCCTCCCACTCAGAGACCTC
10225	SLPNIGT	24548	TCGCTGCCGAATATTGGTACT	38871	AGCCTCCCAAACATCGGAACA
10226	SLPQPPL	24549	AGTCTGCCGCAGCCTCCTTTG	38872	AGCCTCCCACAACCACCACTC
10227	SLPQTLR	24550	AGTTTGCCTCAGACTTTGAGG	38873	AGCCTCCCACAAACACTCAGA
10228	SLPRGSN	24551	TCGCTGCCTCGTGGTTCTAAT	38874	AGCCTCCCAAGAGGAAGCAAC
10229	SLPSLLG	24552	TCTCTTCCGTCTCTGCTGGGT	38875	AGCCTCCCAAGCCTCCTCGGA
10230	SLPSSPS	24553	TCTTTGCCTTCGTCTCCGTCT	38876	AGCCTCCCAAGCAGCCCAAGC
10231	SLPSTHV	24554	TCTTTGCCGTCTACGCATGTG	38877	AGCCTCCCAAGCACACACGTC
10232	SLPTGPI	24555	TCTTTGCCGACTGGGCCTATT	38878	AGCCTCCCAACAGGACCAATC
10233	SLPTSTM	24556	AGTCTGCCGACGTCTACTATG	38879	AGCCTCCCAACAAGCACAATG
10234	SLPVPSR	24557	AGTCTGCCTGTTCCGAGTAGG	38880	AGCCTCCCAGTCCCAAGCAGA
10235	SLPVRGV	24558	TCGCTTCCTGTGCGGGGGGTG	38881	AGCCTCCCAGTCAGAGGAGTC
10236	SLPVSPS	24559	TCTCTTCCTGTGTCTCCGTCT	38882	AGCCTCCCAGTCAGCCCAAGC
10237	SLPVTGR	24560	TCTCTGCCTGTTACTGGTCGT	38883	AGCCTCCCAGTCACAGGAAGA
10238	SLQFTSS	24561	TCGTTGCAGTTTACGTCGTCG	38884	AGCCTCCAATTCACAAGCAGC
10239	SLQRDLV	24562	TCTCTTCAGAGGGATCTGGTT	38885	AGCCTCCAAAGAGACCTCGTC
10240	SLQRPTI	24563	TCTCTGCAGCGGCCGACTATT	38886	AGCCTCCAAAGACCAACAATC
10241	SLQSSRG	24564	TCTTTGCAGTCGTCTCGGGGT	38887	AGCCTCCAAAGCAGCAGAGGA
10242	SLQTDNE	24565	TCGCTTCAGACTGATAATGAG	38888	AGCCTCCAAACAGACAACGAA
10243	SLQTSRV	24566	TCTCTTCAGACGAGTCGTGTG	38889	AGCCTCCAAACAAGCAGAGTC
10244	SLQWTSA	24567	TCTCTTCAGTGGACTAGTGCG	38890	AGCCTCCAATGGACAAGCGCA
10245	SLRANTY	24568	TCTCTGCGTGCGAATACTTAT	38891	AGCCTCAGAGCAAACACATAC
10246	SLRAVVP	24569	TCGCTGCGGGCTGTTGTGCCT	38892	AGCCTCAGAGCAGTCGTCCCA
10247	SLRDSYH	24570	AGTCTGCGGGATTCTTATCAT	38893	AGCCTCAGAGACAGCTACCAC
10248	SLREDAQ	24571	TCTCTTCGGGAGGATGCTCAG	38894	AGCCTCAGAGAAGACGCACAA
10249	SLRGSSS	24572	TCTTTGCGGGGTTCTAGTAGT	38895	AGCCTCAGAGGAAGCAGCAGC

10250	SLRHSET	24573	TCTTTGCGTCATAGTGAGACG	38896	AGCCTCAGACACAGCGAAACA
10251	SLRISAT	24574	AGTTTGCGTATTTCTGCTACG	38897	AGCCTCAGAATCAGCGCAACA
10252	SLRPDQH	24575	TCGCTTCGTCCTGATCAGCAT	38898	AGCCTCAGACCAGACCAACAC
10253	SLRPNSS	24576	TCGTTGAGGCCGAATTCTTCT	38899	AGCCTCAGACCAAACAGCAGC
10254	SLRSLNS	24577	TCGCTTAGGTCGCTGAATTCG	38900	AGCCTCAGAAGCCTCAACAGC
10255	SLRTGDY	24578	TCTTTGCGTACTGGTGATTAT	38901	AGCCTCAGAACAGGAGACTAC
10256	SLRTIAA	24579	TCTCTTCGGACGATTGCTGCG	38902	AGCCTCAGAACAATCGCAGCA
10257	SLRTNVV	24580	TCTTTGAGGACTAATGTGGTG	38903	AGCCTCAGAACAAACGTCGTC
10258	SLRTSMV	24581	TCTCTGCGTACGTCGATGGTG	38904	AGCCTCAGAACAAGCATGGTC
10259	SLRVAEL	24582	TCGCTTCGTGTGGCGGAGCTG	38905	AGCCTCAGAGTCGCAGAACTC
10260	SLRVPVA	24583	TCGCTGCGGGTTCCGGTTGCT	38906	AGCCTCAGAGTCCCAGTCGCA
10261	SLSAHDR	24584	TCGTTGTCGGCTCATGATAGG	38907	AGCCTCAGCGCACACGACAGA
10262	SLSETFR	24585	AGTCTTTCTGAGACGTTTAGG	38908	AGCCTCAGCGAAACATTCAGA
10263	SLSGARA	24586	AGTCTGAGTGGTGCTCGGGCT	38909	AGCCTCAGCGGAGCAAGAGCA
10264	SLSGNTD	24587	AGTCTTTCTGGTAATACTGAT	38910	AGCCTCAGCGGAAACACAGAC
10265	SLSGRPS	24588	TCGTTGTCGGGTCGGCCGAGT	38911	AGCCTCAGCGGAAGACCAAGC
10266	SLSHFPA	24589	TCGTTGTCGCATTTTCCGGCT	38912	AGCCTCAGCCACTTCCCAGCA
10267	SLSHSDG	24590	TCTTTGTCTCATTCGGATGGG	38913	AGCCTCAGCCACAGCGACGGA
10268	SLSIDKA	24591	TCTCTTTCTATTGATAAGGCT	38914	AGCCTCAGCATCGACAAAGCA
10269	SLSKMPS	24592	TCTCTTTCGAAGATGCCTAGT	38915	AGCCTCAGCAAAATGCCAAGC
10270	SLSKPVG	24593	AGTCTGTCTAAGCCGGTTGGT	38916	AGCCTCAGCAAACCAGTCGGA
10271	SLSPRTF	24594	TCTTTGTCGCCGCGTACTTTT	38917	AGCCTCAGCCCAAGAACATTC
10272	SLSQGSN	24595	TCTCTTTCGCAGGGTTCTAAT	38918	AGCCTCAGCCAAGGAAGCAAC
10273	SLSRAGP	24596	TCTCTTTCTCGGGCTGGGCCT	38919	AGCCTCAGCAGAGCAGGACCA
10274	SLSSAIG	24597	TCGCTTTCGAGTGCTATTGGG	38920	AGCCTCAGCAGCGCAATCGGA
10275	SLSSRNI	24598	TCGCTTTCGTCTCGGAATATT	38921	AGCCTCAGCAGCAGAAACATC
10276	SLSTTSK	24599	AGTTTGTCGACGACGTCTAAG	38922	AGCCTCAGCACAACAAGCAAA
10277	SLSVEPT	24600	TCGTTGAGTGTTGAGCCTACT	38923	AGCCTCAGCGTCGAACCAACA
10278	SLSYANH	24601	TCGCTGTCTTATGCGAATCAT	38924	AGCCTCAGCTACGCAAACCAC
10279	SLSYAQE	24602	TCTTTGTCGTATGCGCAGGAG	38925	AGCCTCAGCTACGCACAAGAA
10280	SLTAGGH	24603	TCGCTTACGGCTGGGGGGCAT	38926	AGCCTCACAGCAGGAGGACAC
10281	SLTFSTG	24604	TCGTTGACGTTTAGTACTGGG	38927	AGCCTCACATTCAGCACAGGA
10282	SLTGDGV	24605	TCGCTTACGGGTGATGGTGTT	38928	AGCCTCACAGGAGACGGAGTC
10283	SLTHINH	24606	TCTCTTACTCATATTAATCAT	38929	AGCCTCACACACATCAACCAC
10284	SLTHIPM	24607	TCTTTGACGCATATTCCGATG	38930	AGCCTCACACACATCCCAATG
10285	SLTIAAV	24608	TCGCTTACGATTGCTGCGGTT	38931	AGCCTCACAATCGCAGCAGTC
10286	SLTNEAK	24609	TCTCTTACGAATGAGGCTAAG	38932	AGCCTCACAAACGAAGCAAAA
10287	SLTNIAQ	24610	AGTCTTACGAATATTGCTCAG	38933	AGCCTCACAAACATCGCACAA
10288	SLTPIMR	24611	TCGCTGACTCCTATTATGCGG	38934	AGCCTCACACCAATCATGAGA
10289	SLTPRST	24612	AGTCTGACGCCTCGTTCTACT	38935	AGCCTCACACCAAGAAGCACA
10290	SLTPSFA	24613	TCTTTGACTCCGTCGTTTGCT	38936	AGCCTCACACCAAGCTTCGCA
10291	SLTSATT	24614	AGTTTGACTAGTGCTACTACT	38937	AGCCTCACAAGCGCAACAACA
10292	SLTSRPM	24615	AGTCTTACTTCTCGGCCGATG	38938	AGCCTCACAAGCAGACCAATG
10293	SLTSTMS	24616	TCTTTGACTTCTACGATGAGT	38939	AGCCTCACAAGCACAATGAGC
10294	SLTVLRN	24617	TCGCTTACTGTTTTGCGTAAT	38940	AGCCTCACAGTCCTCAGAAAC

10295	SLTYDNS	24618	TCTCTTACTTATGATAATTCT	38941	AGCCTCACATACGACAACAGC
10296	SLTYERD	24619	TCTTTGACTTATGAGCGTGAT	38942	AGCCTCACATACGAAAGAGAC
10297	SLTYGAL	24620	AGTCTGACGTATGGGGCTTTG	38943	AGCCTCACATACGGAGCACTC
10298	SLVERTS	24621	TCGCTTGTTGAGCGTACGTCT	38944	AGCCTCGTCGAAAGAACAAGC
10299	SLVGTVD	24622	TCGTTGGTTGGGACTGTTGAT	38945	AGCCTCGTCGGAACAGTCGAC
10300	SLVHRST	24623	TCGCTTGTGCATCGTTCTACT	38946	AGCCTCGTCCACAGAAGCACA
10301	SLVNETS	24624	AGTTTGGTGAATGAGACGAGT	38947	AGCCTCGTCAACGAAACAAGC
10302	SLVQKLS	24625	TCTCTTGTGCAGAAGCTGTCT	38948	AGCCTCGTCCAAAAACTCAGC
10303	SLVRSGD	24626	AGTCTTGTTCGGAGTGGTGAT	38949	AGCCTCGTCAGAAGCGGAGAC
10304	SLVRSQN	24627	TCGCTGGTGCGTTCTCAGAAT	38950	AGCCTCGTCAGAAGCCAAAAC
10305	SLVSRIS	24628	AGTCTGGTGTCTCGGATTTCT	38951	AGCCTCGTCAGCAGAATCAGC
10306	SLVTAGS	24629	TCTCTGGTTACGGCGGGGAGT	38952	AGCCTCGTCACAGCAGGAAGC
10307	SLVVQSA	24630	TCTCTTGTGGTTCAGTCGGCT	38953	AGCCTCGTCGTCCAAAGCGCA
10308	SLVYDPL	24631	TCGCTTGTTTATGATCCTCTG	38954	AGCCTCGTCTACGACCCACTC
10309	SLYSGNV	24632	TCGTTGTATAGTGGTAATGTT	38955	AGCCTCTACAGCGGAAACGTC
10310	SLYVPKH	24633	TCTCTGTATGTGCCTAAGCAT	38956	AGCCTCTACGTCCCAAAACAC
10311	SLYYKEE	24634	TCGCTTTATTATAAGGAGGAG	38957	AGCCTCTACTACAAAGAAGAA
10312	SMAATPA	24635	AGTATGGCTGCGACGCCTGCG	38958	AGCATGGCAGCAACACCAGCA
10313	SMALSGI	24636	TCGATGGCTTTGAGTGGGATT	38959	AGCATGGCACTCAGCGGAATC
10314	SMAVSVP	24637	TCTATGGCTGTGTCTGTGCCG	38960	AGCATGGCAGTCAGCGTCCCA
10315	SMDCLSP	24638	TCTATGGATTGTCTTTCGCCT	38961	AGCATGGACTGCCTCAGCCCA
10316	SMDPGAR	24639	TCGATGGATCCGGGTGCTCGG	38962	AGCATGGACCCAGGAGCAAGA
10317	SMDRKTG	24640	TCGATGGATAGGAAGACTGGT	38963	AGCATGGACAGAAAAACAGGA
10318	SMDVSDT	24641	TCGATGGATGTTAGTGATACG	38964	AGCATGGACGTCAGCGACACA
10319	SMESRLL	24642	AGTATGGAGTCTAGGCTTCTG	38965	AGCATGGAAAGCAGACTCCTC
10320	SMGAGPT	24643	AGTATGGGTGCGGGGCCGACG	38966	AGCATGGGAGCAGGACCAACA
10321	SMGDNRR	24644	AGTATGGGTGATAATCGGAGG	38967	AGCATGGGAGACAACAGAAGA
10322	SMGSSAL	24645	TCGATGGGGAGTAGTGCTTTG	38968	AGCATGGGAAGCAGCGCACTC
10323	SMHALSV	24646	TCGATGCATGCGCTTAGTGTT	38969	AGCATGCACGCACTCAGCGTC
10324	SMHQTVH	24647	TCTATGCATCAGACTGTTCAT	38970	AGCATGCACCAAACAGTCCAC
10325	SMHRTSP	24648	AGTATGCATCGGACTAGTCCT	38971	AGCATGCACAGAACAAGCCCA
10326	SMHTTTT	24649	AGTATGCATACGACTACGACT	38972	AGCATGCACACAACAACAACA
10327	SMHVPGV	24650	TCTATGCATGTGCCTGGTGTT	38973	AGCATGCACGTCCCAGGAGTC
10328	SMKAVLN	24651	TCGATGAAGGCTGTTTTGAAT	38974	AGCATGAAAGCAGTCCTCAAC
10329	SMLDSLL	24652	TCGATGCTTGATTCTCTTCTG	38975	AGCATGCTCGACAGCCTCCTC
10330	SMLNVTV	24653	TCTATGCTGAATGTTACGGTT	38976	AGCATGCTCAACGTCACAGTC
10331	SMLSASL	24654	TCTATGCTTAGTGCTAGTCTG	38977	AGCATGCTCAGCGCAAGCCTC
10332	SMMAVKP	24655	TCTATGATGGCTGTGAAGCCT	38978	AGCATGATGGCAGTCAAACCA
10333	SMMEPFK	24656	TCTATGATGGAGCCGTTTAAG	38979	AGCATGATGGAACCATTCAAA
10334	SMMNTVG	24657	AGTATGATGAATACTGTTGGT	38980	AGCATGATGAACACAGTCGGA
10335	SMMQKVP	24658	TCGATGATGCAGAAGGTTCCG	38981	AGCATGATGCAAAAAGTCCCA
10336	SMMTGLA	24659	TCTATGATGACGGGTTTGGCG	38982	AGCATGATGACAGGACTCGCA
10337	SMMYIEP	24660	TCGATGATGTATATTGAGCCT	38983	AGCATGATGTACATCGAACCA
10338	SMNLGST	24661	TCTATGAATCTTGGGTCGACT	38984	AGCATGAACCTCGGAAGCACA
10339	SMNPGSA	24662	TCTATGAATCCGGGTTCGGCT	38985	AGCATGAACCCAGGAAGCGCA

10340	SMNPMTV	24663	TCGATGAATCCGATGACTGTG	38986	AGCATGAACCCAATGACAGTC
10341	SMNVYDT	24664	TCGATGAATGTGTATGATACT	38987	AGCATGAACGTCTACGACACA
10342	SMPFSVA	24665	AGTATGCCTTTTTCTGTTGCT	38988	AGCATGCCATTCAGCGTCGCA
10343	SMPGVAN	24666	TCGATGCCTGGGGTGGCTAAT	38989	AGCATGCCAGGAGTCGCAAAC
10344	SMPHTLS	24667	TCTATGCCTCATACGCTGTCT	38990	AGCATGCCACACACACTCAGC
10345	SMPMPSP	24668	AGTATGCCGATGCCGAGTCCG	38991	AGCATGCCAATGCCAAGCCCA
10346	SMPNAPS	24669	TCTATGCCGAATGCGCCTAGT	38992	AGCATGCCAAACGCACCAAGC
10347	SMPNPYQ	24670	TCGATGCCTAATCCTTATCAG	38993	AGCATGCCAAACCCATACCAA
10348	SMPRDLI	24671	TCTATGCCTCGGGATTTGATT	38994	AGCATGCCAAGAGACCTCATC
10349	SMPREPG	24672	TCGATGCCGCGGGAGCCGGGG	38995	AGCATGCCAAGAGAACCAGGA
10350	SMPSPRV	24673	TCTATGCCGTCTCCGCGGGTT	38996	AGCATGCCAAGCCCAAGAGTC
10351	SMRAAAF	24674	TCGATGCGGGCTGCGGCTTTT	38997	AGCATGAGAGCAGCAGCATTC
10352	SMRDTDR	24675	TCTATGAGGGATACGGATCGG	38998	AGCATGAGAGACACAGACAGA
10353	SMRPSDN	24676	TCTATGAGGCCGTCTGATAAT	38999	AGCATGAGACCAAGCGACAAC
10354	SMRSGEP	24677	TCTATGAGGTCTGGTGAGCCT	39000	AGCATGAGAAGCGGAGAACCA
10355	SMRSRDT	24678	TCTATGCGGAGTCGTGATACG	39001	AGCATGAGAAGCAGAGACACA
10356	SMRSSPL	24679	AGTATGCGTAGTTCTCCGTTG	39002	AGCATGAGAAGCAGCCCACTC
10357	SMSGFDV	24680	TCGATGTCTGGTTTTGATGTT	39003	AGCATGAGCGGATTCGACGTC
10358	SMSGRIT	24681	TCGATGTCGGGGAGGATTACG	39004	AGCATGAGCGGAAGAATCACA
10359	SMSLSGL	24682	TCGATGTCTCTGTCTGGGCTT	39005	AGCATGAGCCTCAGCGGACTC
10360	SMSPSHP	24683	TCTATGTCGCCTTCTCATCCG	39006	AGCATGAGCCCAAGCCACCCA
10361	SMSQPTY	24684	TCTATGAGTCAGCCGACGTAT	39007	AGCATGAGCCAACCAACATAC
10362	SMSRPQP	24685	TCGATGTCTAGGCCGCAGCCT	39008	AGCATGAGCAGACCACAACCA
10363	SMSSFPP	24686	AGTATGTCGAGTTTTCCGCCG	39009	AGCATGAGCAGCTTCCCACCA
10364	SMSVEPY	24687	AGTATGAGTGTGGAGCCTTAT	39010	AGCATGAGCGTCGAACCATAC
10365	SMTADLI	24688	TCGATGACTGCGGATCTGATT	39011	AGCATGACAGCAGACCTCATC
10366	SMTALTA	24689	TCTATGACGGCGCTGACGGCG	39012	AGCATGACAGCACTCACAGCA
10367	SMTGPEL	24690	TCGATGACTGGGCCTGAGCTT	39013	AGCATGACAGGACCAGAACTC
10368	SMTLGTA	24691	TCTATGACTTTGGGGACTGCG	39014	AGCATGACACTCGGAACAGCA
10369	SMTPSVT	24692	TCGATGACGCCTAGTGTGACT	39015	AGCATGACACCAAGCGTCACA
10370	SMTTIGP	24693	AGTATGACGACGATTGGTCCG	39016	AGCATGACAACAATCGGACCA
10371	SMVQGRV	24694	TCGATGGTGCAGGGTCGGGTG	39017	AGCATGGTCCAAGGAAGAGTC
10372	SMYAAGS	24695	TCGATGTATGCTGCTGGTAGT	39018	AGCATGTACGCAGCAGGAAGC
10373	SMYDPRA	24696	TCTATGTATGATCCGCGTGCT	39019	AGCATGTACGACCCAAGAGCA
10374	SNAAIPL	24697	AGTAATGCGGCGATTCCGTTG	39020	AGCAACGCAGCAATCCCACTC
10375	SNALNIG	24698	TCTAATGCTCTTAATATTGGT	39021	AGCAACGCACTCAACATCGGA
10376	SNARAPV	24699	TCTAATGCGAGGGCGCCTGTT	39022	AGCAACGCAAGAGCACCAGTC
10377	SNARPPS	24700	TCGAATGCTAGGCCGCCGTCG	39023	AGCAACGCAAGACCACCAAGC
10378	SNASHSV	24701	TCTAATGCGTCTCATAGTGTG	39024	AGCAACGCAAGCCACAGCGTC
10379	SNASMMH	24702	TCTAATGCGAGTATGATGCAT	39025	AGCAACGCAAGCATGATGCAC
10380	SNATTPT	24703	TCGAATGCTACGACGCCTACG	39026	AGCAACGCAACAACACCAACA
10381	SNCPKDC	24704	TCTAATTGTCCTAAGGATTGT	39027	AGCAACTGCCCAAAAGACTGC
10382	SNCSSLK	24705	AGTAATTGTTCTTCGCTTAAG	39028	AGCAACTGCAGCAGCCTCAAA
10383	SNENRSS	24706	TCTAATGAGAATCGGAGTTCG	39029	AGCAACGAAAACAGAAGCAGC
10384	SNERTTN	24707	TCGAATGAGAGGACGACTAAT	39030	AGCAACGAAAGAACAACAAAC

10385	SNFTEAM	24708	AGTAATTTTACTGAGGCGATG	39031	AGCAACTTCACAGAAGCAATG
10386	SNGHDAS	24709	TCTAATGGTCATGATGCTTCT	39032	AGCAACGGACACGACGCAAGC
10387	SNGHPPW	24710	TCTAATGGTCATCCTCCTTGG	39033	AGCAACGGACACCCACCATGG
10388	SNGIDSG	24711	TCTAATGGGATTGATTCTGGG	39034	AGCAACGGAATCGACAGCGGA
10389	SNGLNRL	24712	TCGAATGGTCTGAATCGTCTT	39035	AGCAACGGACTCAACAGACTC
10390	SNGNRDS	24713	TCTAATGGTAATCGTGATTCG	39036	AGCAACGGAAACAGAGACAGC
10391	SNGQTSP	24714	TCGAATGGTCAGACTTCGCCT	39037	AGCAACGGACAAACAAGCCCA
10392	SNGSKVV	24715	AGTAATGGTTCGAAGGTTGTG	39038	AGCAACGGAAGCAAAGTCGTC
10393	SNGSPKA	24716	AGTAATGGTTCTCCGAAGGCG	39039	AGCAACGGAAGCCCAAAAGCA
10394	SNGSTYK	24717	AGTAATGGTAGTACGTATAAG	39040	AGCAACGGAAGCACATACAAA
10395	SNGTRSY	24718	TCTAATGGTACGAGGTCGTAT	39041	AGCAACGGAACAAGAAGCTAC
10396	SNHAHSL	24719	TCTAATCATGCGCATAGTCTT	39042	AGCAACCACGCACACAGCCTC
10397	SNHEIDY	24720	TCGAATCATGAGATTGATTAT	39043	AGCAACCACGAAATCGACTAC
10398	SNHGGVS	24721	TCTAATCATGGTGGGGTTTCG	39044	AGCAACCACGGAGGAGTCAGC
10399	SNIGGGY	24722	AGTAATATTGGGGGTGGGTAT	39045	AGCAACATCGGAGGAGGATAC
10400	SNILQAT	24723	TCGAATATTCTGCAGGCGACT	39046	AGCAACATCCTCCAAGCAACA
10401	SNKAAYA	24724	AGTAATAAGGCTGCTTATGCG	39047	AGCAACAAAGCAGCATACGCA
10402	SNKFVTA	24725	TCTAATAAGTTTGTTACTGCG	39048	AGCAACAAATTCGTCACAGCA
10403	SNKGLTG	24726	AGTAATAAGGGTTTGACTGGG	39049	AGCAACAAAGGACTCACAGGA
10404	SNKGPVT	24727	TCGAATAAGGGTCCTGTGACG	39050	AGCAACAAAGGACCAGTCACA
10405	SNKYNEV	24728	AGTAATAAGTATAATGAGGTT	39051	AGCAACAAATACAACGAAGTC
10406	SNLETSR	24729	TCGAATCTGGAGACGTCGCGT	39052	AGCAACCTCGAAACAAGCAGA
10407	SNLGFPA	24730	TCGAATCTGGGGTTTCCTGCG	39053	AGCAACCTCGGATTCCCAGCA
10408	SNLGISA	24731	AGTAATCTGGGTATTTCGGCT	39054	AGCAACCTCGGAATCAGCGCA
10409	SNLLHAS	24732	TCGAATCTTTTGCATGCTTCT	39055	AGCAACCTCCTCCACGCAAGC
10410	SNLSPEQ	24733	AGTAATTTGTCTCCTGAGCAG	39056	AGCAACCTCAGCCCAGAACAA
10411	SNLTMSN	24734	TCTAATCTGACGATGAGTAAT	39057	AGCAACCTCACAATGAGCAAC
10412	SNMDTSK	24735	AGTAATATGGATACGTCTAAG	39058	AGCAACATGGACACAAGCAAA
10413	SNMMLSE	24736	TCGAATATGATGCTTTCTGAG	39059	AGCAACATGATGCTCAGCGAA
10414	SNMSVSG	24737	AGTAATATGTCGGTGTCGGGT	39060	AGCAACATGAGCGTCAGCGGA
10415	SNMVPMS	24738	AGTAATATGGTTCCTATGTCT	39061	AGCAACATGGTCCCAATGAGC
10416	SNNGEHV	24739	AGTAATAATGGGGAGCATGTG	39062	AGCAACAACGGAGAACACGTC
10417	SNNQRVV	24740	AGTAATAATCAGCGTGTTGTG	39063	AGCAACAACCAAAGAGTCGTC
10418	SNPALSR	24741	TCTAATCCTGCGCTGAGTCGT	39064	AGCAACCCAGCACTCAGCAGA
10419	SNPASYV	24742	TCGAATCCTGCTTCTTATGTG	39065	AGCAACCCAGCAAGCTACGTC
10420	SNPLRTL	24743	AGTAATCCGCTTAGGACGTTG	39066	AGCAACCCACTCAGAACACTC
10421	SNPMTLT	24744	TCTAATCCGATGACGCTTACT	39067	AGCAACCCAATGACACTCACA
10422	SNPPPLS	24745	TCGAATCCGCCTCCTTTGTCG	39068	AGCAACCCACCACCACTCAGC
10423	SNPPVQK	24746	AGTAATCCTCCTGTGCAGAAG	39069	AGCAACCCACCAGTCCAAAAA
10424	SNPSAAP	24747	TCGAATCCGAGTGCGGCGCCT	39070	AGCAACCCAAGCGCAGCACCA
10425	SNQQGMA	24748	TCGAATCAGCAGGGTATGGCG	39071	AGCAACCAACAAGGAATGGCA
10426	SNQSPPP	24749	TCGAATCAGAGTCCTCCGCCG	39072	AGCAACCAAAGCCCACCACCA
10427	SNSGRAP	24750	TCGAATAGTGGGCGGGCTCCG	39073	AGCAACAGCGGAAGAGCACCA
10428	SNSHSPE	24751	TCTAATTCGCATTCTCCGGAG	39074	AGCAACAGCCACAGCCCAGAA
10429	SNSISAA	24752	TCGAATTCGATTTCTGCTGCG	39075	AGCAACAGCATCAGCGCAGCA

10430	SNSLPVM	24753	TCTAATTCGCTTCCTGTGATG	39076	AGCAACAGCCTCCCAGTCATG
10431	SNSPRGY	24754	TCTAATAGTCCTCGTGGGTAT	39077	AGCAACAGCCCAAGAGGATAC
10432	SNSQPNV	24755	TCGAATTCGCAGCCTAATGTG	39078	AGCAACAGCCAACCAAACGTC
10433	SNSRVAG	24756	TCGAATTCGAGGGTGGCGGGG	39079	AGCAACAGCAGAGTCGCAGGA
10434	SNSSAVH	24757	AGTAATAGTTCTGCTGTGCAT	39080	AGCAACAGCAGCGCAGTCCAC
10435	SNSTIIY	24758	TCGAATTCGACGATTATTTAT	39081	AGCAACAGCACAATCATCTAC
10436	SNSYMML	24759	TCTAATTCTTATATGATGCTG	39082	AGCAACAGCTACATGATGCTC
10437	SNTLSQL	24760	AGTAATACTCTGAGTCAGTTG	39083	AGCAACACACTCAGCCAACTC
10438	SNTNLSE	24761	AGTAATACTAATCTTTCTGAG	39084	AGCAACACAAACCTCAGCGAA
10439	SNTTAAV	24762	TCGAATACTACTGCTGCTGTG	39085	AGCAACACAACAGCAGCAGTC
10440	SNVAIVQ	24763	TCGAATGTTGCGATTGTTCAG	39086	AGCAACGTCGCAATCGTCCAA
10441	SNVEIME	24764	AGTAATGTTGAGATTATGGAG	39087	AGCAACGTCGAAATCATGGAA
10442	SNVGTHF	24765	TCGAATGTGGGTACTCATTTT	39088	AGCAACGTCGGAACACACTTC
10443	SNVHSLH	24766	TCGAATGTGCATTCTCTGCAT	39089	AGCAACGTCCACAGCCTCCAC
10444	SNVNGAD	24767	AGTAATGTTAATGGTGCTGAT	39090	AGCAACGTCAACGGAGCAGAC
10445	SNVREVA	24768	TCTAATGTTAGGGAGGTTGCG	39091	AGCAACGTCAGAGAAGTCGCA
10446	SNVSPRP	24769	TCGAATGTTAGTCCGCGGCCT	39092	AGCAACGTCAGCCCAAGACCA
10447	SNVVVLH	24770	TCGAATGTGGTGGTGCTGCAT	39093	AGCAACGTCGTCGTCCTCCAC
10448	SNYSLNH	24771	TCGAATTATTCGCTGAATCAT	39094	AGCAACTACAGCCTCAACCAC
10449	SPAAEIK	24772	TCTCCGGCGGCTGAGATTAAG	39095	AGCCCAGCAGCAGAAATCAAA
10450	SPALNRS	24773	AGTCCTGCTCTGAATCGGAGT	39096	AGCCCAGCACTCAACAGAAGC
10451	SPANQYD	24774	TCTCCGGCGAATCAGTATGAT	39097	AGCCCAGCAAACCAATACGAC
10452	SPAPYAL	24775	AGTCCGGCGCCGTATGCTCTT	39098	AGCCCAGCACCATACGCACTC
10453	SPAQSDD	24776	TCTCCTGCTCAGTCTGATGAT	39099	AGCCCAGCACAAAGCGACGAC
10454	SPARAGY	24777	TCGCCTGCGCGGGCTGGGTAT	39100	AGCCCAGCAAGAGCAGGATAC
10455	SPARNLI	24778	AGTCCGGCGCGGAATTTGATT	39101	AGCCCAGCAAGAAACCTCATC
10456	SPASHHR	24779	TCTCCTGCGTCTCATCATCGT	39102	AGCCCAGCAAGCCACCACAGA
10457	SPAVGCH	24780	TCTCCGGCTGTGGGGTGTCAT	39103	AGCCCAGCAGTCGGATGCCAC
10458	SPCPGDA	24781	TCTCCGTGTCCTGGTGATGCG	39104	AGCCCATGCCCAGGAGACGCA
10459	SPDLPGL	24782	AGTCCGGATTTGCCTGGTTTG	39105	AGCCCAGACCTCCCAGGACTC
10460	SPDLRTP	24783	TCTCCTGATCTTAGGACGCCT	39106	AGCCCAGACCTCAGAACACCA
10461	SPDRAQL	24784	TCTCCTGATCGTGCGCAGCTG	39107	AGCCCAGACAGAGCACAACTC
10462	SPDSNGP	24785	TCGCCTGATTCGAATGGGCCG	39108	AGCCCAGACAGCAACGGACCA
10463	SPDVVVS	24786	AGTCCGGATGTTGTTGTGAGT	39109	AGCCCAGACGTCGTCGTCAGC
10464	SPEFGTG	24787	TCGCCTGAGTTTGGTACGGGT	39110	AGCCCAGAATTCGGAACAGGA
10465	SPELPKA	24788	AGTCCTGAGCTTCCTAAGGCG	39111	AGCCCAGAACTCCCAAAAGCA
10466	SPESRMP	24789	TCTCCTGAGTCTCGTATGCCG	39112	AGCCCAGAAAGCAGAATGCCA
10467	SPFDANV	24790	AGTCCTTTTGATGCGAATGTG	39113	AGCCCATTCGACGCAAACGTC
10468	SPFPPQL	24791	TCTCCTTTTCCGCCGCAGCTG	39114	AGCCCATTCCCACCACAACTC
10469	SPFRDQE	24792	TCTCCTTTTAGGGATCAGGAG	39115	AGCCCATTCAGAGACCAAGAA
10470	SPFTMRP	24793	TCGCCTTTTACGATGCGTCCT	39116	AGCCCATTCACAATGAGACCA
10471	SPGDPAE	24794	TCGCCTGGGGATCCGGCGGAG	39117	AGCCCAGGAGACCCAGCAGAA
10472	SPGGHVS	24795	TCGCCGGGGGGTCATGTTAGT	39118	AGCCCAGGAGGACACGTCAGC
10473	SPGHPPS	24796	AGTCCGGGTCATCCTCCGAGT	39119	AGCCCAGGACACCCACCAAGC
10474	SPGIRDF	24797	AGTCCTGGTATTCGTGATTTT	39120	AGCCCAGGAATCAGAGACTTC

10475	SPGISRL	24798	TCTCCGGGTATTTCTAGGCTG	39121	AGCCCAGGAATCAGCAGACTC
10476	SPGPHKS	24799	TCGCCGGGTCCGCATAAGTCG	39122	AGCCCAGGACCACACAAAAGC
10477	SPGSGKS	24800	TCTCCTGGGTCTGGTAAGTCT	39123	AGCCCAGGAAGCGGAAAAAGC
10478	SPGSPMS	24801	TCGCCTGGTTCGCCGATGTCT	39124	AGCCCAGGAAGCCCAATGAGC
10479	SPGTLPT	24802	TCGCCGGGGACTTTGCCGACT	39125	AGCCCAGGAACACTCCCAACA
10480	SPGVMPG	24803	AGTCCTGGTGTTATGCCGGGG	39126	AGCCCAGGAGTCATGCCAGGA
10481	SPHDETS	24804	AGTCCTCATGATGAGACTTCG	39127	AGCCCACACGACGAAACAAGC
10482	SPHDSPL	24805	AGTCCTCATGATAGTCCGCTG	39128	AGCCCACACGACAGCCCACTC
10483	SPHITHM	24806	TCGCCGCATATTACTCATATG	39129	AGCCCACACATCACACACATG
10484	SPHKNAH	24807	AGTCCGCATAAGAATGCGCAT	39130	AGCCCACACAAAAACGCACAC
10485	SPHLRGA	24808	TCGCCTCATTTGCGGGGTGCG	39131	AGCCCACACCTCAGAGGAGCA
10486	SPHPENH	24809	TCTCCGCATCCTGAGAATCAT	39132	AGCCCACACCCAGAAAACCAC
10487	SPIERRT	24810	TCTCCGATTGAGCGGCGGACG	39133	AGCCCAATCGAAAGAAGAACA
10488	SPIQTNS	24811	TCGCCGATTCAGACGAATTCT	39134	AGCCCAATCCAAACAAACAGC
10489	SPIQTQG	24812	TCTCCGATTCAGACTCAGGGT	39135	AGCCCAATCCAAACACAAGGA
10490	SPISIKN	24813	TCGCCGATTTCTATTAAGAAT	39136	AGCCCAATCAGCATCAAAAAC
10491	SPITPGR	24814	TCTCCTATTACGCCTGGTCGG	39137	AGCCCAATCACACCAGGAAGA
10492	SPITYNT	24815	TCGCCGATTACGTATAATACG	39138	AGCCCAATCACATACAACACA
10493	SPKIPTH	24816	AGTCCGAAGATTCCGACGCAT	39139	AGCCCAAAAATCCCAACACAC
10494	SPKIPWT	24817	TCGCCTAAGATTCCTTGGACT	39140	AGCCCAAAAATCCCATGGACA
10495	SPKMLRS	24818	TCTCCTAAGATGCTGAGGTCG	39141	AGCCCAAAAATGCTCAGAAGC
10496	SPKVAGV	24819	TCGCCGAAGGTTGCGGGTGTG	39142	AGCCCAAAAGTCGCAGGAGTC
10497	SPLAEAR	24820	TCGCCGCTGGCGGAGGCTCGT	39143	AGCCCACTCGCAGAAGCAAGA
10498	SPLATRV	24821	AGTCCGCTGGCTACTCGGGTT	39144	AGCCCACTCGCAACAAGAGTC
10499	SPLIVNT	24822	AGTCCTCTTATTGTGAATACT	39145	AGCCCACTCATCGTCAACACA
10500	SPLLLAS	24823	TCTCCGTTGCTTTTGGCGAGT	39146	AGCCCACTCCTCCTCGCAAGC
10501	SPLPPSN	24824	AGTCCTCTTCCGCCTTCTAAT	39147	AGCCCACTCCCACCAAGCAAC
10502	SPLRERV	24825	TCGCCTCTTCGTGAGCGTGTT	39148	AGCCCACTCAGAGAAAGAGTC
10503	SPLRSDV	24826	TCGCCGTTGCGTTCTGATGTG	39149	AGCCCACTCAGAAGCGACGTC
10504	SPLTDLS	24827	AGTCCGCTGACGGATCTTTCT	39150	AGCCCACTCACAGACCTCAGC
10505	SPLTDSY	24828	AGTCCTCTTACTGATTCGTAT	39151	AGCCCACTCACAGACAGCTAC
10506	SPLTTVP	24829	TCGCCTCTGACGACGGTGCCT	39152	AGCCCACTCACAACAGTCCCA
10507	SPLVSTA	24830	TCTCCGTTGGTTTCGACTGCT	39153	AGCCCACTCGTCAGCACAGCA
10508	SPMKAGT	24831	AGTCCGATGAAGGCGGGTACG	39154	AGCCCAATGAAAGCAGGAACA
10509	SPMRIEP	24832	TCGCCTATGCGGATTGAGCCT	39155	AGCCCAATGAGAATCGAACCA
10510	SPMRPQE	24833	TCGCCTATGCGTCCGCAGGAG	39156	AGCCCAATGAGACCACAAGAA
10511	SPNALLD	24834	TCTCCGAATGCTCTTCTGGAT	39157	AGCCCAAACGCACTCCTCGAC
10512	SPNATTD	24835	AGTCCGAATGCTACTACTGAT	39158	AGCCCAAACGCAACAACAGAC
10513	SPNMDRL	24836	AGTCCGAATATGGATCGGCTT	39159	AGCCCAAACATGGACAGACTC
10514	SPNMGQF	24837	TCGCCTAATATGGGTCAGTTT	39160	AGCCCAAACATGGGACAATTC
10515	SPNRESM	24838	AGTCCGAATCGGGAGTCTATG	39161	AGCCCAAACAGAGAAAGCATG
10516	SPNTPTF	24839	TCTCCGAATACGCCGACGTTT	39162	AGCCCAAACACACCAACATTC
10517	SPNTRTA	24840	AGTCCTAATACTAGGACTGCT	39163	AGCCCAAACACAAGAACAGCA
10518	SPPNFPE	24841	TCTCCTCCGAATTTTCCTGAG	39164	AGCCCACCAAACTTCCCAGAA
10519	SPPQANA	24842	TCGCCTCCTCAGGCTAATGCT	39165	AGCCCACCACAAGCAAACGCA

10520	SPPQVTK	24843	AGTCCGCCTCAGGTGACTAAG	39166	AGCCCACCACAAGTCACAAAA
10521	SPPRNME	24844	TCTCCTCCGAGGAATATGGAG	39167	AGCCCACCAAGAAACATGGAA
10522	SPPRVGL	24845	AGTCCGCCGCGTGTGGGGTTG	39168	AGCCCACCAAGAGTCGGACTC
10523	SPPTARD	24846	AGTCCGCCTACTGCTCGTGAT	39169	AGCCCACCAACAGCAAGAGAC
10524	SPPVSFE	24847	AGTCCGCCGGTGTCGTTTGAG	39170	AGCCCACCAGTCAGCTTCGAA
10525	SPQGNGA	24848	AGTCCGCAGGGTAATGGTGCG	39171	AGCCCACAAGGAAACGGAGCA
10526	SPQGTYV	24849	TCTCCTCAGGGTACTTATGTG	39172	AGCCCACAAGGAACATACGTC
10527	SPQITRP	24850	AGTCCGCAGATTACGCGTCCG	39173	AGCCCACAAATCACAAGACCA
10528	SPQRIED	24851	TCGCCTCAGAGGATTGAGGAT	39174	AGCCCACAAAGAATCGAAGAC
10529	SPQRPMN	24852	TCTCCGCAGCGTCCGATGAAT	39175	AGCCCACAAAGACCAATGAAC
10530	SPRARID	24853	TCTCCGAGGGCTCGTATTGAT	39176	AGCCCAAGAGCAAGAATCGAC
10531	SPRDPEI	24854	AGTCCTCGGGATCCTGAGATT	39177	AGCCCAAGAGACCCAGAAATC
10532	SPRECGL	24855	TCGCCTCGTGAGTGTGGTCTG	39178	AGCCCAAGAGAATGCGGACTC
10533	SPRGMGL	24856	TCGCCGAGGGGTATGGGGTTG	39179	AGCCCAAGAGGAATGGGACTC
10534	SPRGMPL	24857	TCGCCGCGTGGTATGCCGCTT	39180	AGCCCAAGAGGAATGCCACTC
10535	SPRHNLG	24858	TCGCCGAGGCATAATCTTGGT	39181	AGCCCAAGACACAACCTCGGA
10536	SPRIRDD	24859	TCTCCTCGTATTAGGGATGAT	39182	AGCCCAAGAATCAGAGACGAC
10537	SPRPSYA	24860	AGTCCGCGTCCGTCGTATGCT	39183	AGCCCAAGACCAAGCTACGCA
10538	SPRQLSV	24861	TCTCCGCGGCAGTTGTCTGTT	39184	AGCCCAAGACAACTCAGCGTC
10539	SPRQNIP	24862	TCTCCGCGGCAGAATATTCCG	39185	AGCCCAAGACAAAACATCCCA
10540	SPRQSIS	24863	TCTCCTCGGCAGAGTATTTCG	39186	AGCCCAAGACAAAGCATCAGC
10541	SPRTALP	24864	TCGCCTCGGACTGCGCTTCCT	39187	AGCCCAAGAACAGCACTCCCA
10542	SPRTGLG	24865	TCTCCTAGGACGGGTTTGGGT	39188	AGCCCAAGAACAGGACTCGGA
10543	SPRWHED	24866	TCTCCTCGTTGGCATGAGGAT	39189	AGCCCAAGATGGCACGAAGAC
10544	SPSALLH	24867	AGTCCGTCTGCTCTTTTGCAT	39190	AGCCCAAGCGCACTCCTCCAC
10545	SPSAMGI	24868	TCTCCGTCGGCGATGGGGATT	39191	AGCCCAAGCGCAATGGGAATC
10546	SPSGNNG	24869	AGTCCTTCGGGGAATAATGGG	39192	AGCCCAAGCGGAAACAACGGA
10547	SPSGPVR	24870	AGTCCTTCGGGTCCGGTGAGG	39193	AGCCCAAGCGGACCAGTCAGA
10548	SPSGSLA	24871	TCGCCTTCGGGTTCGTTGGCG	39194	AGCCCAAGCGGAAGCCTCGCA
10549	SPSGVAG	24872	TCGCCTAGTGGGGTGGCGGGG	39195	AGCCCAAGCGGAGTCGCAGGA
10550	SPSLSRS	24873	TCTCCTTCTCTGTCGCGGTCG	39196	AGCCCAAGCCTCAGCAGAAGC
10551	SPSLTAG	24874	TCGCCTTCGCTGACGGCTGGG	39197	AGCCCAAGCCTCACAGCAGGA
10552	SPSLTSD	24875	AGTCCGTCGCTTACGAGTGAT	39198	AGCCCAAGCCTCACAAGCGAC
10553	SPSMPAR	24876	TCTCCTAGTATGCCTGCTCGT	39199	AGCCCAAGCATGCCAGCAAGA
10554	SPSRHEI	24877	TCTCCGAGTAGGCATGAGATT	39200	AGCCCAAGCAGACACGAAATC
10555	SPSRMNS	24878	TCGCCGAGTCGGATGAATAGT	39201	AGCCCAAGCAGAATGAACAGC
10556	SPSRPST	24879	TCTCCTTCTAGGCCTAGTACG	39202	AGCCCAAGCAGACCAAGCACA
10557	SPSRTSL	24880	AGTCCGTCTAGGACGTCTTTG	39203	AGCCCAAGCAGAACAAGCCTC
10558	SPSSLKE	24881	AGTCCGAGTAGTCTTAAGGAG	39204	AGCCCAAGCAGCCTCAAAGAA
10559	SPSTGKL	24882	TCTCCGTCTACGGGTAAGTTG	39205	AGCCCAAGCACAGGAAAACTC
10560	SPSTLPP	24883	TCTCCGTCTACTCTTCCGCCT	39206	AGCCCAAGCACACTCCCACCA
10561	SPSTNNT	24884	AGTCCGAGTACTAATAATACG	39207	AGCCCAAGCACAAACAACACA
10562	SPSTRMG	24885	AGTCCGTCGACTCGGATGGGG	39208	AGCCCAAGCACAAGAATGGGA
10563	SPSVAYH	24886	TCTCCGAGTGTTGCGTATCAT	39209	AGCCCAAGCGTCGCATACCAC
10564	SPSVELF	24887	TCGCCGAGTGTTGAGTTGTTT	39210	AGCCCAAGCGTCGAACTCTTC

10565	SPTAKMW	24888	TCGCCGACGGCTAAGATGTGG	39211	AGCCCAACAGCAAAAATGTGG
10566	SPTCVAC	24889	AGTCCTACTTGTGTGGCGTGT	39212	AGCCCAACATGCGTCGCATGC
10567	SPTDFMN	24890	TCTCCTACGGATTTTATGAAT	39213	AGCCCAACAGACTTCATGAAC
10568	SPTFVGT	24891	AGTCCGACGTTTGTTGGGACT	39214	AGCCCAACATTCGTCGGAACA
10569	SPTGVQP	24892	TCTCCTACTGGTGTGCAGCCG	39215	AGCCCAACAGGAGTCCAACCA
10570	SPTITAR	24893	TCGCCTACGATTACTGCTCGG	39216	AGCCCAACAATCACAGCAAGA
10571	SPTLSPG	24894	TCTCCGACGCTTTCGCCGGGG	39217	AGCCCAACACTCAGCCCAGGA
10572	SPTRNIV	24895	TCGCCTACTCGGAATATTGTT	39218	AGCCCAACAAGAAACATCGTC
10573	SPTSSVT	24896	TCGCCTACTTCTTCTGTGACT	39219	AGCCCAACAAGCAGCGTCACA
10574	SPTTQRT	24897	AGTCCTACTACGCAGAGGACT	39220	AGCCCAACAACACAAAGAACA
10575	SPTVNPI	24898	TCTCCGACTGTTAATCCTATT	39221	AGCCCAACAGTCAACCCAATC
10576	SPTVVLA	24899	TCGCCGACGGTTGTTCTGGCG	39222	AGCCCAACAGTCGTCCTCGCA
10577	SPTYTID	24900	TCGCCGACTTATACTATTGAT	39223	AGCCCAACATACACAATCGAC
10578	SPVARNN	24901	AGTCCTGTTGCTAGGAATAAT	39224	AGCCCAGTCGCAAGAAACAAC
10579	SPVGGKD	24902	TCGCCTGTTGGTGGGAAGGAT	39225	AGCCCAGTCGGAGGAAAAGAC
10580	SPVGSSG	24903	TCGCCGGTTGGTTCGTCTGGT	39226	AGCCCAGTCGGAAGCAGCGGA
10581	SPVMLQS	24904	TCTCCTGTGATGCTTCAGTCT	39227	AGCCCAGTCATGCTCCAAAGC
10582	SPVRHPS	24905	AGTCCTGTTCGTCATCCGTCT	39228	AGCCCAGTCAGACACCCAAGC
10583	SPVSDNP	24906	TCTCCTGTTAGTGATAATCCT	39229	AGCCCAGTCAGCGACAACCCA
10584	SPVVAQP	24907	TCGCCTGTGGTGGCGCAGCCG	39230	AGCCCAGTCGTCGCACAACCA
10585	SPVVPRA	24908	TCGCCTGTGGTTCCGCGTGCT	39231	AGCCCAGTCGTCCCAAGAGCA
10586	SPYGHQN	24909	AGTCCGTATGGTCATCAGAAT	39232	AGCCCATACGGACACCAAAAC
10587	SPYKQNS	24910	TCTCCTTATAAGCAGAATTCT	39233	AGCCCATACAAACAAAACAGC
10588	SPYNITS	24911	TCGCCGTATAATATTACTTCG	39234	AGCCCATACAACATCACAAGC
10589	SPYPALL	24912	TCGCCTTATCCTGCGCTTCTT	39235	AGCCCATACCCAGCACTCCTC
10590	SQAGAIP	24913	TCTCAGGCTGGTGCGATTCCT	39236	AGCCAAGCAGGAGCAATCCCA
10591	SQAMQTL	24914	TCTCAGGCGATGCAGACGTTG	39237	AGCCAAGCAATGCAAACACTC
10592	SQAPRDP	24915	AGTCAGGCTCCTAGGGATCCT	39238	AGCCAAGCACCAAGAGACCCA
10593	SQATGRS	24916	AGTCAGGCGACTGGTCGTTCG	39239	AGCCAAGCAACAGGAAGAAGC
10594	SQATQHN	24917	TCTCAGGCTACGCAGCATAAT	39240	AGCCAAGCAACACAACACAAC
10595	SQAVPPS	24918	AGTCAGGCTGTTCCTCCGAGT	39241	AGCCAAGCAGTCCCACCAAGC
10596	SQDMYRG	24919	TCGCAGGATATGTATCGGGGT	39242	AGCCAAGACATGTACAGAGGA
10597	SQDNVQE	24920	TCGCAGGATAATGTTCAGGAG	39243	AGCCAAGACAACGTCCAAGAA
10598	SQDWNLT	24921	TCGCAGGATTGGAATCTTACT	39244	AGCCAAGACTGGAACCTCACA
10599	SQELPGS	24922	TCGCAGGAGCTGCCTGGGTCG	39245	AGCCAAGAACTCCCAGGAAGC
10600	SQESYMD	24923	TCTCAGGAGTCGTATATGGAT	39246	AGCCAAGAAAGCTACATGGAC
10601	SQFEARP	24924	AGTCAGTTTGAGGCTCGGCCG	39247	AGCCAATTCGAAGCAAGACCA
10602	SQFKPTF	24925	AGTCAGTTTAAGCCGACGTTT	39248	AGCCAATTCAAACCAACATTC
10603	SQFLADI	24926	TCTCAGTTTCTTGCGGATATT	39249	AGCCAATTCCTCGCAGACATC
10604	SQGARND	24927	AGTCAGGGTGCGCGTAATGAT	39250	AGCCAAGGAGCAAGAAACGAC
10605	SQGFNSS	24928	TCGCAGGGTTTTAATTCGAGT	39251	AGCCAAGGATTCAACAGCAGC
10606	SQGHALP	24929	AGTCAGGGGCATGCTCTTCCT	39252	AGCCAAGGACACGCACTCCCA
10607	SQGSVQG	24930	TCGCAGGGTAGTGTTCAGGGT	39253	AGCCAAGGAAGCGTCCAAGGA
10608	SQGVRVG	24931	TCTCAGGGTGTGAGGGTTGGG	39254	AGCCAAGGAGTCAGAGTCGGA
10609	SQHLSVN	24932	TCGCAGCATCTTTCTGTTAAT	39255	AGCCAACACCTCAGCGTCAAC

10610	SQHPIRE	24933	TCTCAGCATCCGATTAGGGAG	39256	AGCCAACACCCAATCAGAGAA
10611	SQHPPGD	24934	AGTCAGCATCCGCCGGGTGAT	39257	AGCCAACACCCACCAGGAGAC
10612	SQHRDHP	24935	TCTCAGCATCGTGATCATCCG	39258	AGCCAACACAGAGACCACCCA
10613	SQHVASP	24936	TCGCAGCATGTTGCGTCTCCT	39259	AGCCAACACGTCGCAAGCCCA
10614	SQISCGL	24937	TCTCAGATTAGTTGTGGGCTT	39260	AGCCAAATCAGCTGCGGACTC
10615	SQKPMVA	24938	AGTCAGAAGCCGATGGTTGCG	39261	AGCCAAAAACCAATGGTCGCA
10616	SQKSHGN	24939	TCTCAGAAGTCTCATGGGAAT	39262	AGCCAAAAAAGCCACGGAAAC
10617	SQLDING	24940	TCTCAGCTTGATATTAATGGG	39263	AGCCAACTCGACATCAACGGA
10618	SQMDDTL	24941	TCTCAGATGGATGATACTTTG	39264	AGCCAAATGGACGACACACTC
10619	SQMLPAP	24942	AGTCAGATGCTTCCGGCTCCG	39265	AGCCAAATGCTCCCAGCACCA
10620	SQMLTGP	24943	TCTCAGATGCTTACTGGGCCG	39266	AGCCAAATGCTCACAGGACCA
10621	SQMREPV	24944	TCGCAGATGCGTGAGCCGGTG	39267	AGCCAAATGAGAGAACCAGTC
10622	SQNLVIS	24945	TCTCAGAATTTGGTGATTAGT	39268	AGCCAAAACCTCGTCATCAGC
10623	SQNSLSE	24946	TCGCAGAATTCTTTGTCGGAG	39269	AGCCAAAACAGCCTCAGCGAA
10624	SQNTGQN	24947	TCTCAGAATACTGGGCAGAAT	39270	AGCCAAAACACAGGACAAAAC
10625	SQPHFAS	24948	AGTCAGCCTCATTTTGCGTCT	39271	AGCCAACCACACTTCGCAAGC
10626	SQPMARM	24949	TCTCAGCCGATGGCTAGGATG	39272	AGCCAACCAATGGCAAGAATG
10627	SQPMPPA	24950	AGTCAGCCTATGCCTCCTGCG	39273	AGCCAACCAATGCCACCAGCA
10628	SQPNPAV	24951	TCGCAGCCTAATCCTGCTGTG	39274	AGCCAACCAAACCCAGCAGTC
10629	SQPTTAR	24952	AGTCAGCCGACTACTGCTAGG	39275	AGCCAACCAACAACAGCAAGA
10630	SQPVTAG	24953	TCTCAGCCGGTTACTGCGGGT	39276	AGCCAACCAGTCACAGCAGGA
10631	SQQDPIL	24954	TCTCAGCAGGATCCTATTTTG	39277	AGCCAACAAGACCCAATCCTC
10632	SQRAPIP	24955	TCGCAGCGGGCGCCGATTCCT	39278	AGCCAAAGAGCACCAATCCCA
10633	SQRATAL	24956	AGTCAGCGTGCTACTGCGCTT	39279	AGCCAAAGAGCAACAGCACTC
10634	SQRILDT	24957	AGTCAGCGGATTCTTGATACT	39280	AGCCAAAGAATCCTCGACACA
10635	SQRSGRE	24958	AGTCAGCGTAGTGGTCGGGAG	39281	AGCCAAAGAAGCGGAAGAGAA
10636	SQRSTLT	24959	TCGCAGCGTAGTACGCTTACG	39282	AGCCAAAGAAGCACACTCACA
10637	SQRVASE	24960	TCTCAGCGGGTGGCTTCGGAG	39283	AGCCAAAGAGTCGCAAGCGAA
10638	SQRVSQS	24961	TCGCAGAGGGTTTCTCAGTCG	39284	AGCCAAAGAGTCAGCCAAAGC
10639	SQSFSVD	24962	TCTCAGTCGTTTTCTGTTGAT	39285	AGCCAAAGCTTCAGCGTCGAC
10640	SQSGSSN	24963	TCTCAGAGTGGTTCTTCGAAT	39286	AGCCAAAGCGGAAGCAGCAAC
10641	SQSMRSS	24964	TCGCAGAGTATGAGGTCTTCG	39287	AGCCAAAGCATGAGAAGCAGC
10642	SQSPVLK	24965	TCTCAGTCTCCTGTGCTGAAG	39288	AGCCAAAGCCCAGTCCTCAAA
10643	SQSQMLP	24966	TCTCAGTCTCAGATGCTTCCG	39289	AGCCAAAGCCAAATGCTCCCA
10644	SQSRFSA	24967	TCGCAGTCGCGGTTTTCGGCG	39290	AGCCAAAGCAGATTCAGCGCA
10645	SQSRMQP	24968	TCTCAGTCGCGGATGCAGCCT	39291	AGCCAAAGCAGAATGCAACCA
10646	SQSSIRL	24969	TCTCAGAGTTCTATTAGGCTT	39292	AGCCAAAGCAGCATCAGACTC
10647	SQSSNYP	24970	TCTCAGAGTAGTAATTATCCG	39293	AGCCAAAGCAGCAACTACCCA
10648	SQSTYNI	24971	AGTCAGTCGACGTATAATATT	39294	AGCCAAAGCACATACAACATC
10649	SQTGLLT	24972	TCTCAGACGGGTCTGCTTACT	39295	AGCCAAACAGGACTCCTCACA
10650	SQTIPDS	24973	AGTCAGACTATTCCGGATTCG	39296	AGCCAAACAATCCCAGACAGC
10651	SQTKSQH	24974	AGTCAGACGAAGTCGCAGCAT	39297	AGCCAAACAAAAAGCCAACAC
10652	SQTPRST	24975	AGTCAGACGCCTCGTTCTACG	39298	AGCCAAACACCAAGAAGCACA
10653	SQTQHRI	24976	TCGCAGACTCAGCATAGGATT	39299	AGCCAAACACAACACAGAATC
10654	SQTVGVS	24977	TCTCAGACTGTTGGGGTGTCT	39300	AGCCAAACAGTCGGAGTCAGC

10655	SQVGAPT	24978	TCTCAGGTGGGTGCTCCGACT	39301	AGCCAAGTCGGAGCACCAACA
10656	SQVGMYR	24979	TCGCAGGTTGGTATGTATAGG	39302	AGCCAAGTCGGAATGTACAGA
10657	SQWVPTN	24980	TCTCAGTGGGTGCCTACGAAT	39303	AGCCAATGGGTCCCAACAAAC
10658	SQYASLD	24981	AGTCAGTATGCGTCTTTGGAT	39304	AGCCAATACGCAAGCCTCGAC
10659	SQYTKFQ	24982	TCGCAGTATACTAAGTTTCAG	39305	AGCCAATACACAAAATTCCAA
10660	SQYVPSS	24983	AGTCAGTATGTGCCTTCTTCG	39306	AGCCAATACGTCCCAAGCAGC
10661	SRAAMDG	24984	TCTCGGGCGGCGATGGATGGT	39307	AGCAGAGCAGCAATGGACGGA
10662	SRADIFL	24985	AGTCGTGCTGATATTTTTCTT	39308	AGCAGAGCAGACATCTTCCTC
10663	SRAGRSE	24986	TCGCGGGCGGGTCGTTCGGAG	39309	AGCAGAGCAGGAAGAAGCGAA
10664	SRAGTTT	24987	TCGCGGGCGGGGACTACGACG	39310	AGCAGAGCAGGAACAACAACA
10665	SRAILAD	24988	TCGCGGGCTATTCTTGCGGAT	39311	AGCAGAGCAATCCTCGCAGAC
10666	SRALTGP	24989	TCTCGGGCGCTTACTGGTCCG	39312	AGCAGAGCACTCACAGGACCA
10667	SRALVSA	24990	TCTCGGGCGCTGGTTTCTGCG	39313	AGCAGAGCACTCGTCAGCGCA
10668	SRANLHS	24991	TCTCGGGCGAATCTTCATTCT	39314	AGCAGAGCAAACCTCCACAGC
10669	SRAPSLP	24992	TCGCGTGCGCCGTCTCTTCCT	39315	AGCAGAGCACCAAGCCTCCCA
10670	SRASMAV	24993	TCTCGTGCTAGTATGGCGGTT	39316	AGCAGAGCAAGCATGGCAGTC
10671	SRAVSDA	24994	AGTCGGGCGGTTTCGGATGCT	39317	AGCAGAGCAGTCAGCGACGCA
10672	SRDAIHD	24995	TCTCGGGATGCGATTCATGAT	39318	AGCAGAGACGCAATCCACGAC
10673	SRDAKQS	24996	TCTCGTGATGCTAAGCAGTCG	39319	AGCAGAGACGCAAAACAAAGC
10674	SRDLLSP	24997	AGTCGTGATCTGTTGTCGCCG	39320	AGCAGAGACCTCCTCAGCCCA
10675	SRDMTNF	24998	TCGCGGGATATGACGAATTTT	39321	AGCAGAGACATGACAAACTTC
10676	SRDNQTV	24999	AGTCGTGATAATCAGACTGTT	39322	AGCAGAGACAACCAAACAGTC
10677	SRDRTLN	25000	AGTCGGGATAGGACTTTGAAT	39323	AGCAGAGACAGAACACTCAAC
10678	SRDSGTS	25001	TCTCGTGATTCGGGTACTAGT	39324	AGCAGAGACAGCGGAACAAGC
10679	SRDSQRE	25002	AGTCGTGATAGTCAGCGTGAG	39325	AGCAGAGACAGCCAAAGAGAA
10680	SRDTGHT	25003	TCTCGTGATACTGGGCATACG	39326	AGCAGAGACACAGGACACACA
10681	SRDTSHH	25004	TCGCGGGATACGTCGCATCAT	39327	AGCAGAGACACAAGCCACCAC
10682	SRDVPQN	25005	TCGCGTGATGTTCCTCAGAAT	39328	AGCAGAGACGTCCCACAAAAC
10683	SRDYQLN	25006	TCGAGGGATTATCAGTTGAAT	39329	AGCAGAGACTACCAACTCAAC
10684	SREKVSA	25007	TCGAGGGAGAAGGTGTCGGCG	39330	AGCAGAGAAAAAGTCAGCGCA
10685	SRELSRL	25008	TCGAGGGAGCTGTCGCGTCTG	39331	AGCAGAGAACTCAGCAGACTC
10686	SREMAPS	25009	AGTCGGGAGATGGCTCCTAGT	39332	AGCAGAGAAATGGCACCAAGC
10687	SREPANI	25010	TCTCGTGAGCCTGCTAATATT	39333	AGCAGAGAACCAGCAAACATC
10688	SREQLSG	25011	TCGAGGGAGCAGCTGAGTGGG	39334	AGCAGAGAACAACTCAGCGGA
10689	SRESRFD	25012	AGTAGGGAGTCTCGGTTTGAT	39335	AGCAGAGAAAGCAGATTCGAC
10690	SRESYQQ	25013	TCTCGTGAGTCTTATCAGCAG	39336	AGCAGAGAAAGCTACCAACAA
10691	SRETRAV	25014	TCGCGTGAGACTCGTGCGGTT	39337	AGCAGAGAAACAAGAGCAGTC
10692	SREVDKT	25015	TCTCGGGAGGTGGATAAGACT	39338	AGCAGAGAAGTCGACAAAACA
10693	SREVVAS	25016	AGTCGTGAGGTTGTTGCGTCG	39339	AGCAGAGAAGTCGTCGCAAGC
10694	SRFEANT	25017	TCTCGGTTTGAGGCGAATACT	39340	AGCAGATTCGAAGCAAACACA
10695	SRFEQLG	25018	AGTCGGTTTGAGCAGCTGGGG	39341	AGCAGATTCGAACAACTCGGA
10696	SRFHPTE	25019	AGTCGGTTTCATCCTACGGAG	39342	AGCAGATTCCACCCAACAGAA
10697	SRFQGSG	25020	TCGCGTTTTCAGGGTTCGGGT	39343	AGCAGATTCCAAGGAAGCGGA
10698	SRFTTQV	25021	AGTCGGTTTACTACTCAGGTT	39344	AGCAGATTCACAACACAAGTC
10699	SRGDPLF	25022	TCGCGGGGTGATCCGCTGTTT	39345	AGCAGAGGAGACCCACTCTTC

10700	SRGDRPM	25023	TCTCGGGGGGATCGTCCGATG	39346	AGCAGAGGAGACAGACCAATG
10701	SRGDTMV	25024	TCTAGGGGTGATACTATGGTT	39347	AGCAGAGGAGACACAATGGTC
10702	SRGEHYV	25025	AGTCGTGGTGAGCATTATGTT	39348	AGCAGAGGAGAACACTACGTC
10703	SRGHETS	25026	TCGAGGGGTCATGAGACGTCT	39349	AGCAGAGGACACGAAACAAGC
10704	SRGKEVI	25027	TCGCGTGGGAAGGAGGTGATT	39350	AGCAGAGGAAAAGAAGTCATC
10705	SRGSESI	25028	TCGCGTGGTTCTGAGTCGATT	39351	AGCAGAGGAAGCGAAAGCATC
10706	SRGVDNL	25029	AGTCGTGGGGTGGATAATCTT	39352	AGCAGAGGAGTCGACAACCTC
10707	SRGVSSP	25030	TCGCGTGGTGTGTCTTCTCCT	39353	AGCAGAGGAGTCAGCAGCCCA
10708	SRHPVPH	25031	TCGCGGCATCCGGTGCCGCAT	39354	AGCAGACACCCAGTCCCACAC
10709	SRHQATS	25032	TCTAGGCATCAGGCTACTTCG	39355	AGCAGACACCAAGCAACAAGC
10710	SRHTSLS	25033	TCGAGGCATACGTCGCTTTCT	39356	AGCAGACACACAAGCCTCAGC
10711	SRHYTTE	25034	TCGAGGCATTATACTACTGAG	39357	AGCAGACACTACACAACAGAA
10712	SRIAEPK	25035	AGTAGGATTGCGGAGCCTAAG	39358	AGCAGAATCGCAGAACCAAAA
10713	SRIGISA	25036	TCTCGGATTGGTATTTCGGCT	39359	AGCAGAATCGGAATCAGCGCA
10714	SRILRLD	25037	TCGCGGATTTTGCGGCTGGAT	39360	AGCAGAATCCTCAGACTCGAC
10715	SRLGGHS	25038	TCGCGTCTTGGGGGGCATTCG	39361	AGCAGACTCGGAGGACACAGC
10716	SRLPTQD	25039	TCGAGGCTTCCGACTCAGGAT	39362	AGCAGACTCCCAACACAAGAC
10717	SRLPYPN	25040	TCGCGTCTGCCTTATCCTAAT	39363	AGCAGACTCCCATACCCAAAC
10718	SRLSGAE	25041	TCTCGTTTGTCGGGGGCGGAG	39364	AGCAGACTCAGCGGAGCAGAA
10719	SRLSHEL	25042	AGTAGGCTGTCGCATGAGTTG	39365	AGCAGACTCAGCCACGAACTC
10720	SRLTPPS	25043	TCTCGGCTGACTCCGCCGAGT	39366	AGCAGACTCACACCACCAAGC
10721	SRLTPYP	25044	TCTAGGCTTACGCCTTATCCT	39367	AGCAGACTCACACCATACCCA
10722	SRLVPVA	25045	TCTAGGTTGGTGCCGGTTGCG	39368	AGCAGACTCGTCCCAGTCGCA
10723	SRMAISD	25046	TCTCGTATGGCTATTAGTGAT	39369	AGCAGAATGGCAATCAGCGAC
10724	SRMGQTS	25047	TCTCGGATGGGGCAGACTTCG	39370	AGCAGAATGGGACAAACAAGC
10725	SRMSFAP	25048	TCGAGGATGAGTTTTGCGCCG	39371	AGCAGAATGAGCTTCGCACCA
10726	SRMSQGF	25049	AGTCGTATGAGTCAGGGTTTT	39372	AGCAGAATGAGCCAAGGATTC
10727	SRNSLAL	25050	TCTCGGAATTCGTTGGCGCTT	39373	AGCAGAAACAGCCTCGCACTC
10728	SRNSLLD	25051	TCTAGGAATAGTCTTTTGGAT	39374	AGCAGAAACAGCCTCCTCGAC
10729	SRNTNTD	25052	TCGAGGAATACTAATACGGAT	39375	AGCAGAAACACAAACACAGAC
10730	SRNTPVD	25053	TCGCGGAATACTCCTGTTGAT	39376	AGCAGAAACACACCAGTCGAC
10731	SRPAIGS	25054	TCGCGTCCGGCGATTGGTTCG	39377	AGCAGACCAGCAATCGGAAGC
10732	SRPAPVL	25055	TCGCGTCCTGCTCCTGTTCTT	39378	AGCAGACCAGCACCAGTCCTC
10733	SRPATNP	25056	TCTCGTCCTGCGACTAATCCG	39379	AGCAGACCAGCAACAAACCCA
10734	SRPEPPY	25057	AGTCGGCCGGAGCCTCCGTAT	39380	AGCAGACCAGAACCACCATAC
10735	SRPGFQN	25058	AGTAGGCCGGGTTTTCAGAAT	39381	AGCAGACCAGGATTCCAAAAC
10736	SRPGLTF	25059	TCTAGGCCGGGGCTTACGTTT	39382	AGCAGACCAGGACTCACATTC
10737	SRPITPL	25060	TCTCGTCCTATTACTCCTTTG	39383	AGCAGACCAATCACACCACTC
10738	SRPMSLE	25061	AGTCGGCCGATGTCGTTGGAG	39384	AGCAGACCAATGAGCCTCGAA
10739	SRPRDTD	25062	TCTCGTCCGCGTGATACTGAT	39385	AGCAGACCAAGAGACACAGAC
10740	SRPSAYQ	25063	TCTCGTCCTTCGGCTTATCAG	39386	AGCAGACCAAGCGCATACCAA
10741	SRPSDVW	25064	TCTAGGCCGTCTGATGTTTGG	39387	AGCAGACCAAGCGACGTCTGG
10742	SRPSNDA	25065	TCTAGGCCTTCTAATGATGCT	39388	AGCAGACCAAGCAACGACGCA
10743	SRPSSES	25066	TCGCGGCCTAGTTCTGAGTCT	39389	AGCAGACCAAGCAGCGAAAGC
10744	SRPTAQE	25067	AGTCGTCCGACGGCGCAGGAG	39390	AGCAGACCAACAGCACAAGAA

10745	SRPTSAS	25068	TCGCGGCCTACGTCTGCTTCT	39391	AGCAGACCAACAAGCGCAAGC
10746	SRPVVSS	25069	TCGCGTCCTGTGGTGTCGAGT	39392	AGCAGACCAGTCGTCAGCAGC
10747	SRQALSD	25070	TCTAGGCAGGCTCTTAGTGAT	39393	AGCAGACAAGCACTCAGCGAC
10748	SRQDHWP	25071	AGTCGTCAGGATCATTGGCCT	39394	AGCAGACAAGACCACTGGCCA
10749	SRQDPVI	25072	TCGCGTCAGGATCCTGTTATT	39395	AGCAGACAAGACCCAGTCATC
10750	SRQLAPS	25073	AGTCGGCAGCTTGCTCCGAGT	39396	AGCAGACAACTCGCACCAAGC
10751	SRQMEHV	25074	AGTAGGCAGATGGAGCATGTG	39397	AGCAGACAAATGGAACACGTC
10752	SRQQERG	25075	TCTCGTCAGCAGGAGAGGGGG	39398	AGCAGACAACAAGAAAGAGGA
10753	SRQQTPD	25076	AGTCGGCAGCAGACGCCGGAT	39399	AGCAGACAACAAACACCAGAC
10754	SRQSPSL	25077	AGTAGGCAGTCGCCTTCGCTG	39400	AGCAGACAAAGCCCAAGCCTC
10755	SRQSVHG	25078	TCTCGTCAGTCTGTTCATGGT	39401	AGCAGACAAAGCGTCCACGGA
10756	SRRPSDI	25079	AGTCGTAGGCCTTCGGATATT	39402	AGCAGAAGACCAAGCGACATC
10757	SRSALTD	25080	AGTAGGTCGGCTCTTACTGAT	39403	AGCAGAAGCGCACTCACAGAC
10758	SRSERMP	25081	TCGCGTTCGGAGCGTATGCCT	39404	AGCAGAAGCGAAAGAATGCCA
10759	SRSGQGD	25082	TCGCGTTCGGGTCAGGGTGAT	39405	AGCAGAAGCGGACAAGGAGAC
10760	SRSGSLP	25083	AGTCGGAGTGGTAGTCTTCCG	39406	AGCAGAAGCGGAAGCCTCCCA
10761	SRSGTPF	25084	TCTCGGTCTGGTACTCCGTTT	39407	AGCAGAAGCGGAACACCATTC
10762	SRSHPSQ	25085	TCGCGTAGTCATCCGAGTCAG	39408	AGCAGAAGCCACCCAAGCCAA
10763	SRSIMQG	25086	TCTCGGTCGATTATGCAGGGG	39409	AGCAGAAGCATCATGCAAGGA
10764	SRSISTD	25087	TCGCGGTCTATTTCGACGGAT	39410	AGCAGAAGCATCAGCACAGAC
10765	SRSLEST	25088	AGTCGTTCTCTTGAGAGTACG	39411	AGCAGAAGCCTCGAAAGCACA
10766	SRSLGTN	25089	TCGAGGTCTTTGGGTACGAAT	39412	AGCAGAAGCCTCGGAACAAAC
10767	SRSLHLV	25090	TCGAGGAGTTTGCATCTTGTG	39413	AGCAGAAGCCTCCACCTCGTC
10768	SRSLRPD	25091	AGTCGTTCTTTGAGGCCTGAT	39414	AGCAGAAGCCTCAGACCAGAC
10769	SRSNANI	25092	TCGCGGTCGAATGCTAATATT	39415	AGCAGAAGCAACGCAAACATC
10770	SRSNGVI	25093	AGTAGGAGTAATGGTGTTATT	39416	AGCAGAAGCAACGGAGTCATC
10771	SRSPGVH	25094	TCTAGGTCTCCGGGTGTGCAT	39417	AGCAGAAGCCCAGGAGTCCAC
10772	SRSPMQP	25095	TCTCGTTCTCCTATGCAGCCT	39418	AGCAGAAGCCCAATGCAACCA
10773	SRSPPLP	25096	TCTCGTTCGCCGCCGCTGCCT	39419	AGCAGAAGCCCACCACTCCCA
10774	SRSPPMT	25097	TCGAGGAGTCCGCCGATGACG	39420	AGCAGAAGCCCACCAATGACA
10775	SRSRTET	25098	TCTCGTTCTCGTACGGAGACG	39421	AGCAGAAGCAGAACAGAAACA
10776	SRSSGGN	25099	TCTAGGTCGTCGGGTGGTAAT	39422	AGCAGAAGCAGCGGAGGAAAC
10777	SRSSGGS	25100	TCGCGGAGTTCGGGTGGTTCT	39423	AGCAGAAGCAGCGGAGGAAGC
10778	SRSVSGT	25101	AGTCGTAGTGTTTCGGGGACG	39424	AGCAGAAGCGTCAGCGGAACA
10779	SRSVSLS	25102	TCGCGGTCTGTTTCGTTGTCG	39425	AGCAGAAGCGTCAGCCTCAGC
10780	SRTANAA	25103	TCGCGTACTGCTAATGCTGCT	39426	AGCAGAACAGCAAACGCAGCA
10781	SRTASFP	25104	AGTAGGACTGCGTCGTTTCCG	39427	AGCAGAACAGCAAGCTTCCCA
10782	SRTASSG	25105	TCGCGTACGGCTTCGTCTGGT	39428	AGCAGAACAGCAAGCAGCGGA
10783	SRTDTIK	25106	AGTAGGACTGATACGATTAAG	39429	AGCAGAACAGACACAATCAAA
10784	SRTEALG	25107	TCTCGGACTGAGGCGCTTGGT	39430	AGCAGAACAGAAGCACTCGGA
10785	SRTERSA	25108	AGTCGTACGGAGCGTTCTGCG	39431	AGCAGAACAGAAAGAAGCGCA
10786	SRTGAYP	25109	TCTCGTACGGGGGCGTATCCT	39432	AGCAGAACAGGAGCATACCCA
10787	SRTGSTL	25110	TCGAGGACTGGTTCGACTTTG	39433	AGCAGAACAGGAAGCACACTC
10788	SRTHDQA	25111	AGTCGGACTCATGATCAGGCT	39434	AGCAGAACACACGACCAAGCA
10789	SRTLVGE	25112	TCGCGTACTCTGGTTGGTGAG	39435	AGCAGAACACTCGTCGGAGAA

10790	SRTPHID	25113	TCTAGGACGCCGCATATTGAT	39436	AGCAGAACACCACACATCGAC
10791	SRTPMSM	25114	AGTAGGACTCCGATGTCGATG	39437	AGCAGAACACCAATGAGCATG
10792	SRTSMPS	25115	TCTCGTACTAGTATGCCTTCT	39438	AGCAGAACAAGCATGCCAAGC
10793	SRTSRLD	25116	AGTCGTACTTCGCGGCTGGAT	39439	AGCAGAACAAGCAGACTCGAC
10794	SRTVASG	25117	AGTCGGACTGTGGCTTCGGGT	39440	AGCAGAACAGTCGCAAGCGGA
10795	SRTVQAM	25118	TCTCGGACTGTGCAGGCGATG	39441	AGCAGAACAGTCCAAGCAATG
10796	SRVATTL	25119	TCGCGTGTTGCTACGACGTTG	39442	AGCAGAGTCGCAACAACACTC
10797	SRVIHVS	25120	AGTAGGGTGATTCATGTTAGT	39443	AGCAGAGTCATCCACGTCAGC
10798	SRVNAPS	25121	AGTCGTGTTAATGCGCCGAGT	39444	AGCAGAGTCAACGCACCAAGC
10799	SRVNAQA	25122	TCTCGGGTTAATGCTCAGGCT	39445	AGCAGAGTCAACGCACAAGCA
10800	SRVPHSD	25123	AGTCGTGTGCCTCATAGTGAT	39446	AGCAGAGTCCCACACAGCGAC
10801	SRVPNLS	25124	TCGCGGGTTCCTAATCTTTCG	39447	AGCAGAGTCCCAAACCTCAGC
10802	SRVQNGV	25125	AGTCGTGTGCAGAATGGGGTG	39448	AGCAGAGTCCAAAACGGAGTC
10803	SRVSAVM	25126	AGTCGTGTTAGTGCTGTGATG	39449	AGCAGAGTCAGCGCAGTCATG
10804	SRVSGQS	25127	AGTCGGGTGTCTGGGCAGTCG	39450	AGCAGAGTCAGCGGACAAAGC
10805	SRVSQVM	25128	AGTAGGGTTTCTCAGGTGATG	39451	AGCAGAGTCAGCCAAGTCATG
10806	SRWVTIE	25129	TCTCGTTGGGTTACTATTGAG	39452	AGCAGATGGGTCACAATCGAA
10807	SRYATSG	25130	TCGAGGTATGCTACTTCTGGG	39453	AGCAGATACGCAACAAGCGGA
10808	SRYEDPE	25131	AGTCGTTATGAGGATCCGGAG	39454	AGCAGATACGAAGACCCAGAA
10809	SRYGSDS	25132	AGTCGTTATGGGTCGGATTCT	39455	AGCAGATACGGAAGCGACAGC
10810	SRYNGMG	25133	TCTCGGTATAATGGGATGGGT	39456	AGCAGATACAACGGAATGGGA
10811	SRYPEAT	25134	AGTCGGTATCCTGAGGCTACT	39457	AGCAGATACCCAGAAGCAACA
10812	SSACIKA	25135	TCTTCTGCTTGTATTAAGGCT	39458	AGCAGCGCATGCATCAAAGCA
10813	SSAEARL	25136	TCGAGTGCTGAGGCTCGTCTG	39459	AGCAGCGCAGAAGCAAGACTC
10814	SSAGAPL	25137	TCGTCGGCGGGTGCGCCTTTG	39460	AGCAGCGCAGGAGCACCACTC
10815	SSAGWVG	25138	AGTAGTGCGGGTTGGGTGGGT	39461	AGCAGCGCAGGATGGGTCGGA
10816	SSAIPMK	25139	AGTTCTGCTATTCCGATGAAG	39462	AGCAGCGCAATCCCAATGAAA
10817	SSANAPR	25140	TCTTCTGCTAATGCTCCGCGT	39463	AGCAGCGCAAACGCACCAAGA
10818	SSANAST	25141	AGTAGTGCTAATGCGAGTACT	39464	AGCAGCGCAAACGCAAGCACA
10819	SSAPVSP	25142	TCGTCGGCGCCGGTTTCTCCT	39465	AGCAGCGCACCAGTCAGCCCA
10820	SSAQVSV	25143	TCTTCGGCTCAGGTGTCTGTG	39466	AGCAGCGCACAAGTCAGCGTC
10821	SSATMTT	25144	TCGTCGGCGACTATGACTACG	39467	AGCAGCGCAACAATGACAACA
10822	SSDASRR	25145	TCTTCGGATGCTAGTCGTCGT	39468	AGCAGCGACGCAAGCAGAAGA
10823	SSDHGLK	25146	TCTAGTGATCATGGGCTTAAG	39469	AGCAGCGACCACGGACTCAAA
10824	SSDHIGC	25147	TCTTCGGATCATATTGGTTGT	39470	AGCAGCGACCACATCGGATGC
10825	SSDIRPS	25148	TCTAGTGATATTAGGCCGTCT	39471	AGCAGCGACATCAGACCAAGC
10826	SSDSVKH	25149	AGTAGTGATTCGGTGAAGCAT	39472	AGCAGCGACAGCGTCAAACAC
10827	SSDTSPG	25150	TCGTCTGATACGAGTCCTGGG	39473	AGCAGCGACACAAGCCCAGGA
10828	SSDTVTE	25151	AGTTCGGATACTGTGACTGAG	39474	AGCAGCGACACAGTCACAGAA
10829	SSEAARG	25152	TCTTCTGAGGCTGCTAGGGGG	39475	AGCAGCGAAGCAGCAAGAGGA
10830	SSEDVGF	25153	TCTAGTGAGGATGTTGGTTTT	39476	AGCAGCGAAGACGTCGGATTC
10831	SSEHGRN	25154	AGTAGTGAGCATGGGCGGAAT	39477	AGCAGCGAACACGGAAGAAAC
10832	SSEKHSP	25155	TCTTCGGAGAAGCATTCGCCT	39478	AGCAGCGAAAAACACAGCCCA
10833	SSEKRPG	25156	TCTTCGGAGAAGCGTCCTGGT	39479	AGCAGCGAAAAAAGACCAGGA
10834	SSEMSGN	25157	TCTAGTGAGATGTCGGGTAAT	39480	AGCAGCGAAATGAGCGGAAAC

10835	SSERAHG	25158	TCGTCTGAGAGGGCGCATGGT	39481	AGCAGCGAAAGAGCACACGGA
10836	SSERASS	25159	AGTAGTGAGCGGGCGTCTTCT	39482	AGCAGCGAAAGAGCAAGCAGC
10837	SSESLGR	25160	TCTTCTGAGTCGCTGGGGAGG	39483	AGCAGCGAAAGCCTCGGAAGA
10838	SSESRWI	25161	TCGTCGGAGTCTCGTTGGATT	39484	AGCAGCGAAAGCAGATGGATC
10839	SSFAVGG	25162	TCTAGTTTTGCGGTTGGGGGG	39485	AGCAGCTTCGCAGTCGGAGGA
10840	SSFDRGA	25163	TCGAGTTTTGATAGGGGGGCG	39486	AGCAGCTTCGACAGAGGAGCA
10841	SSFKGTF	25164	AGTTCGTTTAAGGGTACGTTT	39487	AGCAGCTTCAAAGGAACATTC
10842	SSFLTPS	25165	TCGTCTTTTTTGACTCCTTCT	39488	AGCAGCTTCCTCACACCAAGC
10843	SSFPSKA	25166	TCTAGTTTTCCTTCTAAGGCG	39489	AGCAGCTTCCCAAGCAAAGCA
10844	SSFRTPL	25167	TCGTCGTTTCGGACGCCTCTG	39490	AGCAGCTTCAGAACACCACTC
10845	SSGASSP	25168	TCTTCGGGTGCTTCGTCGCCT	39491	AGCAGCGGAGCAAGCAGCCCA
10846	SSGDRSH	25169	TCTAGTGGGGATCGGAGTCAT	39492	AGCAGCGGAGACAGAAGCCAC
10847	SSGEGYK	25170	TCGTCTGGTGAGGGGTATAAG	39493	AGCAGCGGAGAAGGATACAAA
10848	SSGFGKP	25171	TCTTCTGGGTTTGGTAAGCCT	39494	AGCAGCGGATTCGGAAAACCA
10849	SSGIGHF	25172	TCGTCGGGGATTGGGCATTTT	39495	AGCAGCGGAATCGGACACTTC
10850	SSGLARA	25173	TCTAGTGGGCTTGCTCGTGCT	39496	AGCAGCGGACTCGCAAGAGCA
10851	SSGLISV	25174	AGTTCGGGTCTGATTTCTGTT	39497	AGCAGCGGACTCATCAGCGTC
10852	SSGNNLH	25175	TCGAGTGGGAATAATCTTCAT	39498	AGCAGCGGAAACAACCTCCAC
10853	SSGPSLA	25176	AGTTCTGGGCCTTCTCTTGCT	39499	AGCAGCGGACCAAGCCTCGCA
10854	SSGQVRQ	25177	TCGTCGGGGCAGGTGCGTCAG	39500	AGCAGCGGACAAGTCAGACAA
10855	SSGRPVA	25178	TCGTCGGGTCGTCCTGTTGCT	39501	AGCAGCGGAAGACCAGTCGCA
10856	SSGTMSY	25179	AGTTCTGGTACTATGTCTTAT	39502	AGCAGCGGAACAATGAGCTAC
10857	SSHFRAD	25180	TCGTCGCATTTTAGGGCTGAT	39503	AGCAGCCACTTCAGAGCAGAC
10858	SSHFVVT	25181	TCGAGTCATTTTGTTGTGACT	39504	AGCAGCCACTTCGTCGTCACA
10859	SSHHQFP	25182	AGTTCGCATCATCAGTTTCCG	39505	AGCAGCCACCACCAATTCCCA
10860	SSHKVAW	25183	AGTTCGCATAAGGTGGCTTGG	39506	AGCAGCCACAAAGTCGCATGG
10861	SSHMSPW	25184	AGTAGTCATATGTCGCCGTGG	39507	AGCAGCCACATGAGCCCATGG
10862	SSHPSRI	25185	TCGTCTCATCCTTCGAGGATT	39508	AGCAGCCACCCAAGCAGAATC
10863	SSHQEKL	25186	AGTTCTCATCAGGAGAAGCTT	39509	AGCAGCCACCAAGAAAAACTC
10864	SSHRALV	25187	TCGTCTCATAGGGCTCTTGTT	39510	AGCAGCCACAGAGCACTCGTC
10865	SSHSLYT	25188	TCTTCTCATAGTCTTTATACT	39511	AGCAGCCACAGCCTCTACACA
10866	SSHSYVT	25189	TCTTCTCATTCGTATGTTACG	39512	AGCAGCCACAGCTACGTCACA
10867	SSHVTGY	25190	TCGTCTCATGTTACGGGTTAT	39513	AGCAGCCACGTCACAGGATAC
10868	SSIHNAV	25191	AGTAGTATTCATAATGCTGTT	39514	AGCAGCATCCACAACGCAGTC
10869	SSIILGD	25192	TCTAGTATTATTTTGGGTGAT	39515	AGCAGCATCATCCTCGGAGAC
10870	SSIPRHP	25193	TCGAGTATTCCTAGGCATCCG	39516	AGCAGCATCCCAAGACACCCA
10871	SSIPSNV	25194	TCTAGTATTCCTTCGAATGTT	39517	AGCAGCATCCCAAGCAACGTC
10872	SSIQTAQ	25195	TCGAGTATTCAGACGGCTCAG	39518	AGCAGCATCCAAACAGCACAA
10873	SSIRPSP	25196	TCTAGTATTAGGCCTAGTCCT	39519	AGCAGCATCAGACCAAGCCCA
10874	SSISGSS	25197	TCTTCTATTTCGGGTAGTTCG	39520	AGCAGCATCAGCGGAAGCAGC
10875	SSISPNG	25198	TCGTCGATTAGTCCTAATGGT	39521	AGCAGCATCAGCCCAAACGGA
10876	SSKESPL	25199	TCGAGTAAGGAGAGTCCGCTG	39522	AGCAGCAAAGAAAGCCCACTC
10877	SSKGYHL	25200	TCGTCTAAGGGGTATCATTTG	39523	AGCAGCAAAGGATACCACCTC
10878	SSKGYLV	25201	AGTTCGAAGGGGTATCTGGTT	39524	AGCAGCAAAGGATACCTCGTC
10879	SSKLETE	25202	TCGTCTAAGTTGGAGACTGAG	39525	AGCAGCAAACTCGAAACAGAA

10880	SSKMTGS	25203	TCGAGTAAGATGACGGGGAGT	39526	AGCAGCAAAATGACAGGAAGC
10881	SSKQVTN	25204	AGTAGTAAGCAGGTGACGAAT	39527	AGCAGCAAACAAGTCACAAAC
10882	SSKYAEN	25205	AGTTCTAAGTATGCTGAGAAT	39528	AGCAGCAAATACGCAGAAAAC
10883	SSLASGA	25206	TCTTCTCTTGCTTCTGGTGCT	39529	AGCAGCCTCGCAAGCGGAGCA
10884	SSLDREF	25207	TCGTCTCTTGATAGGGAGTTT	39530	AGCAGCCTCGACAGAGAATTC
10885	SSLGETL	25208	TCTTCGCTGGGTGAGACTCTG	39531	AGCAGCCTCGGAGAAACACTC
10886	SSLIELL	25209	TCGAGTTTGATTGAGCTGCTT	39532	AGCAGCCTCATCGAACTCCTC
10887	SSLKIET	25210	TCTAGTCTTAAGATTGAGACG	39533	AGCAGCCTCAAAATCGAAACA
10888	SSLKLNG	25211	TCTTCTCTTAAGTTGAATGGT	39534	AGCAGCCTCAAACTCAACGGA
10889	SSLNTGA	25212	AGTTCTCTGAATACTGGTGCG	39535	AGCAGCCTCAACACAGGAGCA
10890	SSLPAGR	25213	TCGTCTTTGCCTGCTGGTCGT	39536	AGCAGCCTCCCAGCAGGAAGA
10891	SSLRNNI	25214	TCTTCGCTGCGTAATAATATT	39537	AGCAGCCTCAGAAACAACATC
10892	SSLRPAT	25215	TCTTCGCTTAGGCCTGCTACG	39538	AGCAGCCTCAGACCAGCAACA
10893	SSLSDRD	25216	AGTAGTCTTTCGGATCGGGAT	39539	AGCAGCCTCAGCGACAGAGAC
10894	SSLSRTG	25217	TCTTCTTTGTCGCGTACTGGG	39540	AGCAGCCTCAGCAGAACAGGA
10895	SSMAKKE	25218	TCGAGTATGGCTAAGAAGGAG	39541	AGCAGCATGGCAAAAAAAGAA
10896	SSMALGT	25219	TCTAGTATGGCTTTGGGTACG	39542	AGCAGCATGGCACTCGGAACA
10897	SSMVDQV	25220	TCTAGTATGGTTGATCAGGTT	39543	AGCAGCATGGTCGACCAAGTC
10898	SSNAMLP	25221	AGTAGTAATGCTATGCTGCCT	39544	AGCAGCAACGCAATGCTCCCA
10899	SSNEHMR	25222	TCTTCGAATGAGCATATGCGT	39545	AGCAGCAACGAACACATGAGA
10900	SSNLKLS	25223	AGTTCTAATCTTAAGCTTAGT	39546	AGCAGCAACCTCAAACTCAGC
10901	SSNPMLR	25224	AGTTCTAATCCTATGTTGAGG	39547	AGCAGCAACCCAATGCTCAGA
10902	SSNPQRV	25225	TCGTCGAATCCGCAGAGGGTG	39548	AGCAGCAACCCACAAAGAGTC
10903	SSNRASV	25226	AGTTCTAATAGGGCGAGTGTT	39549	AGCAGCAACAGAGCAAGCGTC
10904	SSNRGEL	25227	TCGTCGAATAGGGGTGAGCTG	39550	AGCAGCAACAGAGGAGAACTC
10905	SSNSFPR	25228	TCTTCGAATAGTTTTCCTCGT	39551	AGCAGCAACAGCTTCCCAAGA
10906	SSNSGVP	25229	AGTTCTAATTCTGGTGTGCCG	39552	AGCAGCAACAGCGGAGTCCCA
10907	SSNSRAI	25230	TCGTCTAATAGTCGTGCTATT	39553	AGCAGCAACAGCAGAGCAATC
10908	SSNSSFA	25231	AGTAGTAATTCGAGTTTTGCG	39554	AGCAGCAACAGCAGCTTCGCA
10909	SSNSVIA	25232	TCGTCGAATAGTGTTATTGCG	39555	AGCAGCAACAGCGTCATCGCA
10910	SSPALNY	25233	TCTTCTCCTGCGCTGAATTAT	39556	AGCAGCCCAGCACTCAACTAC
10911	SSPEGLA	25234	TCTTCGCCTGAGGGGCTGGCT	39557	AGCAGCCCAGAAGGACTCGCA
10912	SSPMRSE	25235	AGTTCTCCGATGCGTTCTGAG	39558	AGCAGCCCAATGAGAAGCGAA
10913	SSPPGNG	25236	TCTTCTCCTCCGGGGAATGGG	39559	AGCAGCCCACCAGGAAACGGA
10914	SSPRGFG	25237	TCGTCTCCTCGGGGTTTTGGT	39560	AGCAGCCCAAGAGGATTCGGA
10915	SSPRHSE	25238	AGTAGTCCTCGTCATAGTGAG	39561	AGCAGCCCAAGACACAGCGAA
10916	SSPSLTL	25239	TCTAGTCCTAGTCTTACTCTT	39562	AGCAGCCCAAGCCTCACACTC
10917	SSPSSNG	25240	TCTAGTCCTAGTTCTAATGGG	39563	AGCAGCCCAAGCAGCAACGGA
10918	SSPTCCP	25241	AGTTCGCCTACGTGTTGTCCT	39564	AGCAGCCCAACATGCTGCCCA
10919	SSPTMFV	25242	AGTTCGCCTACTATGTTTGTT	39565	AGCAGCCCAACAATGTTCGTC
10920	SSPTPLK	25243	TCGAGTCCTACTCCTCTTAAG	39566	AGCAGCCCAACACCACTCAAA
10921	SSPVASS	25244	AGTTCGCCGGTTGCTTCGTCG	39567	AGCAGCCCAGTCGCAAGCAGC
10922	SSPVKTL	25245	AGTTCTCCTGTTAAGACTCTG	39568	AGCAGCCCAGTCAAAACACTC
10923	SSPYPMM	25246	AGTAGTCCGTATCCTATGATG	39569	AGCAGCCCATACCCAATGATG
10924	SSQERNV	25247	AGTTCTCAGGAGCGTAATGTT	39570	AGCAGCCAAGAAAGAAACGTC

10925	SSQGPIR	25248	TCTTCGCAGGGGCCTATTAGG	39571	AGCAGCCAAGGACCAATCAGA
10926	SSQKPVL	25249	AGTTCTCAGAAGCCGGTGCTT	39572	AGCAGCCAAAAACCAGTCCTC
10927	SSQLLLD	25250	TCTAGTCAGCTGCTGTTGGAT	39573	AGCAGCCAACTCCTCCTCGAC
10928	SSQMLYP	25251	TCTTCGCAGATGCTTTATCCG	39574	AGCAGCCAAATGCTCTACCCA
10929	SSQPLEL	25252	TCTAGTCAGCCTCTTGAGCTG	39575	AGCAGCCAACCACTCGAACTC
10930	SSQPMSY	25253	AGTTCGCAGCCGATGTCTTAT	39576	AGCAGCCAACCAATGAGCTAC
10931	SSQRVPS	25254	TCTTCGCAGCGTGTTCCGAGT	39577	AGCAGCCAAAGAGTCCCAAGC
10932	SSQSMTL	25255	AGTTCGCAGAGTATGACTCTT	39578	AGCAGCCAAAGCATGACACTC
10933	SSQVKTL	25256	TCGTCTCAGGTTAAGACGTTG	39579	AGCAGCCAAGTCAAAACACTC
10934	SSQWHAG	25257	TCGAGTCAGTGGCATGCGGGT	39580	AGCAGCCAATGGCACGCAGGA
10935	SSRAGTE	25258	AGTTCGCGGGCTGGTACGGAG	39581	AGCAGCAGAGCAGGAACAGAA
10936	SSRDMTS	25259	AGTTCTAGGGATATGACTTCT	39582	AGCAGCAGAGACATGACAAGC
10937	SSRDVGR	25260	TCGTCTAGGGATGTTGGGCGT	39583	AGCAGCAGAGACGTCGGAAGA
10938	SSRGPIA	25261	TCTTCTCGGGGGCCGATTGCT	39584	AGCAGCAGAGGACCAATCGCA
10939	SSRGSPS	25262	AGTTCTAGGGGGAGTCCGTCT	39585	AGCAGCAGAGGAAGCCCAAGC
10940	SSRGVPG	25263	TCGTCTCGTGGGGTGCCTGGG	39586	AGCAGCAGAGGAGTCCCAGGA
10941	SSRINPM	25264	AGTAGTCGTATTAATCCTATG	39587	AGCAGCAGAATCAACCCAATG
10942	SSRIPDT	25265	AGTTCGCGGATTCCGGATACG	39588	AGCAGCAGAATCCCAGACACA
10943	SSRLNEQ	25266	TCTTCTAGGCTGAATGAGCAG	39589	AGCAGCAGACTCAACGAACAA
10944	SSRLSAD	25267	AGTAGTCGTCTGTCTGCGGAT	39590	AGCAGCAGACTCAGCGCAGAC
10945	SSRLSES	25268	TCGTCGAGGTTGTCTGAGAGT	39591	AGCAGCAGACTCAGCGAAAGC
10946	SSRPGMS	25269	TCTTCGCGTCCGGGTATGAGT	39592	AGCAGCAGACCAGGAATGAGC
10947	SSRPGQH	25270	AGTTCTCGTCCGGGTCAGCAT	39593	AGCAGCAGACCAGGACAACAC
10948	SSRPNDD	25271	TCTTCGAGGCCGAATGATGAT	39594	AGCAGCAGACCAAACGACGAC
10949	SSRPSGS	25272	AGTTCTCGGCCGTCGGGTTCG	39595	AGCAGCAGACCAAGCGGAAGC
10950	SSRSAQS	25273	AGTAGTCGTAGTGCTCAGAGT	39596	AGCAGCAGAAGCGCACAAAGC
10951	SSRSPDL	25274	TCGTCGAGGTCGCCTGATCTG	39597	AGCAGCAGAAGCCCAGACCTC
10952	SSRTNSY	25275	TCTTCGCGGACTAATTCTTAT	39598	AGCAGCAGAACAAACAGCTAC
10953	SSRTVEA	25276	AGTAGTCGTACGGTTGAGGCG	39599	AGCAGCAGAACAGTCGAAGCA
10954	SSSALVL	25277	TCGTCGTCGGCGCTTGTGCTT	39600	AGCAGCAGCGCACTCGTCCTC
10955	SSSAVAS	25278	TCTAGTTCTGCGGTGGCTTCG	39601	AGCAGCAGCGCAGTCGCAAGC
10956	SSSESAW	25279	TCTTCTAGTGAGTCTGCGTGG	39602	AGCAGCAGCGAAAGCGCATGG
10957	SSSGTHP	25280	TCTAGTTCTGGGACTCATCCT	39603	AGCAGCAGCGGAACACACCCA
10958	SSSIIRT	25281	AGTTCGTCGATTATTCGGACT	39604	AGCAGCAGCATCATCAGAACA
10959	SSSIRAN	25282	TCGAGTTCGATTCGGGCTAAT	39605	AGCAGCAGCATCAGAGCAAAC
10960	SSSKPHL	25283	TCTTCTAGTAAGCCTCATTTG	39606	AGCAGCAGCAAACCACACCTC
10961	SSSLDSR	25284	TCGAGTTCGCTTGATAGTCGG	39607	AGCAGCAGCCTCGACAGCAGA
10962	SSSLQLG	25285	TCGAGTTCGCTTCAGCTGGGT	39608	AGCAGCAGCCTCCAACTCGGA
10963	SSSLSHS	25286	TCGAGTTCGTTGTCGCATTCG	39609	AGCAGCAGCCTCAGCCACAGC
10964	SSSMRER	25287	TCGTCTTCGATGAGGGAGAGG	39610	AGCAGCAGCATGAGAGAAAGA
10965	SSSNTLT	25288	TCGAGTAGTAATACGCTGACT	39611	AGCAGCAGCAACACACTCACA
10966	SSSRAVE	25289	TCGAGTAGTAGGGCGGTTGAG	39612	AGCAGCAGCAGAGCAGTCGAA
10967	SSSRPTQ	25290	TCGTCTTCGCGGCCTACTCAG	39613	AGCAGCAGCAGACCAACACAA
10968	SSSSKTP	25291	TCTTCTTCGTCTAAGACTCCT	39614	AGCAGCAGCAGCAAAACACCA
10969	SSSSLYT	25292	TCGTCTTCTAGTCTTTATACT	39615	AGCAGCAGCAGCCTCTACACA

10970	SSSSPRA	25293	AGTTCTAGTTCGCCGCGTGCT	39616	AGCAGCAGCAGCCCAAGAGCA
10971	SSSSSRP	25294	TCGTCTAGTTCGTCGCGGCCG	39617	AGCAGCAGCAGCAGCAGACCA
10972	SSSSVRA	25295	AGTTCTTCGTCTGTTCGGGCG	39618	AGCAGCAGCAGCGTCAGAGCA
10973	SSSTPPL	25296	AGTTCGTCTACTCCGCCGTTG	39619	AGCAGCAGCACACCACCACTC
10974	SSSTPPS	25297	TCGAGTTCGACTCCTCCTTCT	39620	AGCAGCAGCACACCACCAAGC
10975	SSSTPPT	25298	AGTTCTTCGACTCCGCCGACT	39621	AGCAGCAGCACACCACCAACA
10976	SSSTSTG	25299	TCGAGTTCTACGTCTACTGGT	39622	AGCAGCAGCACAAGCACAGGA
10977	SSSTVQF	25300	TCTTCGTCTACTGTTCAGTTT	39623	AGCAGCAGCACAGTCCAATTC
10978	SSSVSNN	25301	AGTTCGTCGGTTAGTAATAAT	39624	AGCAGCAGCGTCAGCAACAAC
10979	SSSYNGK	25302	TCTAGTTCGTATAATGGTAAG	39625	AGCAGCAGCTACAACGGAAAA
10980	SSTESIR	25303	TCGAGTACGGAGTCTATTAGG	39626	AGCAGCACAGAAAGCATCAGA
10981	SSTHEKP	25304	TCGAGTACGCATGAGAAGCCG	39627	AGCAGCACACACGAAAAACCA
10982	SSTKSLA	25305	TCGAGTACGAAGTCGCTTGCT	39628	AGCAGCACAAAAAGCCTCGCA
10983	SSTPPKY	25306	TCTTCTACGCCGCCGAAGTAT	39629	AGCAGCACACCACCAAAATAC
10984	SSTPTSH	25307	TCGTCTACTCCTACTTCGCAT	39630	AGCAGCACACCAACAAGCCAC
10985	SSTPTTA	25308	TCTTCTACGCCGACTACTGCG	39631	AGCAGCACACCAACAACAGCA
10986	SSTRDAH	25309	AGTTCGACGCGTGATGCTCAT	39632	AGCAGCACAAGAGACGCACAC
10987	SSTRTPP	25310	TCGAGTACGCGTACGCCTCCT	39633	AGCAGCACAAGAACACCACCA
10988	SSTSSRF	25311	TCTAGTACTTCTAGTCGGTTT	39634	AGCAGCACAAGCAGCAGATTC
10989	SSTSTLL	25312	AGTTCGACGTCGACGCTTTTG	39635	AGCAGCACAAGCACACTCCTC
10990	SSTTMIE	25313	TCGTCTACTACTATGATTGAG	39636	AGCAGCACAACAATGATCGAA
10991	SSVASTV	25314	AGTTCGGTTGCTTCGACTGTT	39637	AGCAGCGTCGCAAGCACAGTC
10992	SSVGSAG	25315	TCGTCTGTTGGGAGTGCTGGT	39638	AGCAGCGTCGGAAGCGCAGGA
10993	SSVHLYP	25316	TCGAGTGTGCATCTTTATCCT	39639	AGCAGCGTCCACCTCTACCCA
10994	SSVHSRM	25317	TCGTCTGTTCATTCGAGGATG	39640	AGCAGCGTCCACAGCAGAATG
10995	SSVNTSG	25318	TCTTCTGTTAATACGTCTGGT	39641	AGCAGCGTCAACACAAGCGGA
10996	SSVPRPS	25319	TCGAGTGTGCCTCGTCCGTCT	39642	AGCAGCGTCCCAAGACCAAGC
10997	SSVRLLS	25320	AGTTCGGTGCGTTTGTTGTCG	39643	AGCAGCGTCAGACTCCTCAGC
10998	SSVSGLS	25321	TCGAGTGTTTCGGGGTTGAGT	39644	AGCAGCGTCAGCGGACTCAGC
10999	SSVTRTG	25322	TCTTCTGTTACGCGGACGGGG	39645	AGCAGCGTCACAAGAACAGGA
11000	SSVTVSS	25323	TCTTCTGTGACGGTTTCTTCT	39646	AGCAGCGTCACAGTCAGCAGC
11001	SSVVHGV	25324	TCGAGTGTTGTTCATGGGGTG	39647	AGCAGCGTCGTCCACGGAGTC
11002	SSVVPSM	25325	TCGTCGGTGGTTCCGTCTATG	39648	AGCAGCGTCGTCCCAAGCATG
11003	SSWQPFE	25326	TCTAGTTGGCAGCCTTTTGAG	39649	AGCAGCTGGCAACCATTCGAA
11004	SSYAPLH	25327	AGTTCTTATGCTCCGTTGCAT	39650	AGCAGCTACGCACCACTCCAC
11005	SSYASGS	25328	AGTAGTTATGCGTCTGGGTCG	39651	AGCAGCTACGCAAGCGGAAGC
11006	SSYDSSK	25329	AGTTCGTATGATTCTAGTAAG	39652	AGCAGCTACGACAGCAGCAAA
11007	SSYEKGT	25330	TCGAGTTATGAGAAGGGGACT	39653	AGCAGCTACGAAAAAGGAACA
11008	SSYHGLT	25331	TCGTCTTATCATGGGCTTACG	39654	AGCAGCTACCACGGACTCACA
11009	SSYHPAE	25332	TCTAGTTATCATCCTGCGGAG	39655	AGCAGCTACCACCCAGCAGAA
11010	SSYPGHS	25333	TCTTCGTATCCTGGGCATTCG	39656	AGCAGCTACCCAGGACACAGC
11011	SSYSVPE	25334	TCGTCGTATAGTGTTCCGGAG	39657	AGCAGCTACAGCGTCCCAGAA
11012	STAITIH	25335	TCTACGGCTATTACTATTCAT	39658	AGCACAGCAATCACAATCCAC
11013	STALGIV	25336	TCGACTGCGCTTGGTATTGTT	39659	AGCACAGCACTCGGAATCGTC
11014	STANAQT	25337	AGTACTGCTAATGCTCAGACT	39660	AGCACAGCAAACGCACAAACA

11015	STAPGAA	25338	AGTACGGCTCCGGGTGCTGCG	39661	AGCACAGCACCAGGAGCAGCA
11016	STARAST	25339	TCTACGGCTCGGGCTAGTACT	39662	AGCACAGCAAGAGCAAGCACA
11017	STARLRD	25340	TCGACGGCGCGGCTGCGGGAT	39663	AGCACAGCAAGACTCAGAGAC
11018	STATQLM	25341	AGTACGGCGACGCAGTTGATG	39664	AGCACAGCAACACAACTCATG
11019	STCHPSG	25342	TCTACGTGTCATCCTTCGGGT	39665	AGCACATGCCACCCAAGCGGA
11020	STDEHVM	25343	TCTACGGATGAGCATGTGATG	39666	AGCACAGACGAACACGTCATG
11021	STDHTAY	25344	TCGACTGATCATACGGCTTAT	39667	AGCACAGACCACACAGCATAC
11022	STDLRQA	25345	AGTACTGATTTGAGGCAGGCT	39668	AGCACAGACCTCAGACAAGCA
11023	STDMRHI	25346	TCGACGGATATGCGGCATATT	39669	AGCACAGACATGAGACACATC
11024	STDNDLR	25347	TCGACTGATAATGATCTTCGG	39670	AGCACAGACAACGACCTCAGA
11025	STDTNHQ	25348	AGTACGGATACGAATCATCAG	39671	AGCACAGACACAAACCACCAA
11026	STDVKTQ	25349	TCTACGGATGTGAAGACGCAG	39672	AGCACAGACGTCAAAACACAA
11027	STEFKSA	25350	TCTACGGAGTTTAAGTCGGCT	39673	AGCACAGAATTCAAAAGCGCA
11028	STERPMP	25351	TCTACGGAGCGTCCTATGCCT	39674	AGCACAGAAAGACCAATGCCA
11029	STETAQS	25352	TCTACTGAGACTGCGCAGAGT	39675	AGCACAGAAACAGCACAAAGC
11030	STFKNVV	25353	TCGACGTTTAAGAATGTTGTT	39676	AGCACATTCAAAAACGTCGTC
11031	STFNSAG	25354	TCGACGTTTAATTCGGCTGGT	39677	AGCACATTCAACAGCGCAGGA
11032	STFSSSM	25355	AGTACTTTTAGTTCTTCGATG	39678	AGCACATTCAGCAGCAGCATG
11033	STFVTAG	25356	TCGACGTTTGTGACTGCGGGG	39679	AGCACATTCGTCACAGCAGGA
11034	STFVTRS	25357	TCGACTTTTGTGACTAGGAGT	39680	AGCACATTCGTCACAAGAAGC
11035	STGALPS	25358	AGTACGGGTGCTTTGCCTTCT	39681	AGCACAGGAGCACTCCCAAGC
11036	STGAMLH	25359	TCTACGGGTGCTATGCTGCAT	39682	AGCACAGGAGCAATGCTCCAC
11037	STGAPPD	25360	AGTACTGGGGCTCCTCCTGAT	39683	AGCACAGGAGCACCACCAGAC
11038	STGMGAF	25361	AGTACTGGTATGGGTGCTTTT	39684	AGCACAGGAATGGGAGCATTC
11039	STGPFLP	25362	TCGACTGGTCCGTTTCTTCCG	39685	AGCACAGGACCATTCCTCCCA
11040	STGSAQT	25363	TCGACGGGGTCGGCTCAGACT	39686	AGCACAGGAAGCGCACAAACA
11041	STGSTLQ	25364	TCGACGGGTTCGACGCTGCAG	39687	AGCACAGGAAGCACACTCCAA
11042	STGYGGL	25365	AGTACGGGGTATGGTGGTCTG	39688	AGCACAGGATACGGAGGACTC
11043	STHISPP	25366	AGTACGCATATTTCTCCTCCT	39689	AGCACACACATCAGCCCACCA
11044	STHMRLA	25367	AGTACGCATATGCGGCTTGCG	39690	AGCACACACATGAGACTCGCA
11045	STHNLTS	25368	TCTACTCATAATCTGACTTCG	39691	AGCACACACAACCTCACAAGC
11046	STHRDSS	25369	AGTACTCATCGGGATTCGAGT	39692	AGCACACACAGAGACAGCAGC
11047	STHRSLA	25370	TCTACGCATCGTAGTCTTGCT	39693	AGCACACACAGAAGCCTCGCA
11048	STHSYPV	25371	TCGACGCATTCGTATCCGGTG	39694	AGCACACACAGCTACCCAGTC
11049	STHVSST	25372	TCGACTCATGTGTCGAGTACG	39695	AGCACACACGTCAGCAGCACA
11050	STIAGTP	25373	AGTACTATTGCGGGTACGCCG	39696	AGCACAATCGCAGGAACACCA
11051	STISALA	25374	AGTACTATTAGTGCTCTTGCG	39697	AGCACAATCAGCGCACTCGCA
11052	STKESQL	25375	AGTACTAAGGAGTCGCAGCTT	39698	AGCACAAAAGAAAGCCAACTC
11053	STKSGTP	25376	AGTACTAAGTCTGGGACTCCT	39699	AGCACAAAAAGCGGAACACCA
11054	STKTPPA	25377	TCTACGAAGACTCCTCCTGCG	39700	AGCACAAAAACACCACCAGCA
11055	STKYSSV	25378	AGTACGAAGTATTCGTCTGTT	39701	AGCACAAAATACAGCAGCGTC
11056	STLARDN	25379	TCGACTCTTGCGCGGGATAAT	39702	AGCACACTCGCAAGAGACAAC
11057	STLARVP	25380	AGTACGTTGGCGCGGGTGCCT	39703	AGCACACTCGCAAGAGTCCCA
11058	STLCPVL	25381	AGTACTCTGTGTCCTGTTCTT	39704	AGCACACTCTGCCCAGTCCTC
11059	STLGGGY	25382	TCTACTCTGGGTGGGGGTTAT	39705	AGCACACTCGGAGGAGGATAC

11060	STLNNVP	25383	TCGACGTTGAATAATGTTCCG	39706	AGCACACTCAACAACGTCCCA
11061	STLPSPE	25384	TCGACTCTTCCTTCGCCTGAG	39707	AGCACACTCCCAAGCCCAGAA
11062	STLPSRP	25385	AGTACTCTGCCGTCTCGTCCT	39708	AGCACACTCCCAAGCAGACCA
11063	STLRCGE	25386	TCTACGCTGAGGTGTGGGGAG	39709	AGCACACTCAGATGCGGAGAA
11064	STLVKNA	25387	TCGACGTTGGTGAAGAATGCT	39710	AGCACACTCGTCAAAAACGCA
11065	STLVRAE	25388	TCTACTTTGGTTCGTGCTGAG	39711	AGCACACTCGTCAGAGCAGAA
11066	STMAGRH	25389	TCTACTATGGCGGGGAGGCAT	39712	AGCACAATGGCAGGAAGACAC
11067	STMIAHS	25390	TCGACTATGATTGCTCATTCT	39713	AGCACAATGATCGCACACAGC
11068	STMLLPS	25391	AGTACTATGCTGTTGCCGTCT	39714	AGCACAATGCTCCTCCCAAGC
11069	STMNRGL	25392	TCGACGATGAATCGTGGTCTG	39715	AGCACAATGAACAGAGGACTC
11070	STMRPQL	25393	AGTACGATGCGTCCGCAGTTG	39716	AGCACAATGAGACCACAACTC
11071	STMSVKE	25394	TCTACGATGTCTGTTAAGGAG	39717	AGCACAATGAGCGTCAAAGAA
11072	STNATSN	25395	TCGACTAATGCTACTTCTAAT	39718	AGCACAAACGCAACAAGCAAC
11073	STNIVEY	25396	TCTACTAATATTGTGGAGTAT	39719	AGCACAAACATCGTCGAATAC
11074	STNRSTV	25397	TCGACGAATCGGTCGACGGTG	39720	AGCACAAACAGAAGCACAGTC
11075	STNTALW	25398	TCGACTAATACTGCTCTGTGG	39721	AGCACAAACACAGCACTCTGG
11076	STNTPRG	25399	AGTACTAATACGCCGCGTGGT	39722	AGCACAAACACACCAAGAGGA
11077	STNTQAY	25400	TCGACTAATACGCAGGCTTAT	39723	AGCACAAACACACAAGCATAC
11078	STNTREE	25401	TCGACGAATACTAGGGAGGAG	39724	AGCACAAACACAAGAGAAGAA
11079	STNVGLA	25402	TCGACGAATGTGGGGCTTGCT	39725	AGCACAAACGTCGGACTCGCA
11080	STPAKYG	25403	AGTACTCCGGCGAAGTATGGT	39726	AGCACACCAGCAAAATACGGA
11081	STPASRA	25404	AGTACGCCTGCGTCTCGTGCG	39727	AGCACACCAGCAAGCAGAGCA
11082	STPDNHT	25405	AGTACTCCGGATAATCATACG	39728	AGCACACCAGACAACCACACA
11083	STPDRQT	25406	AGTACTCCGGATCGTCAGACG	39729	AGCACACCAGACAGACAAACA
11084	STPHTNA	25407	TCGACGCCGCATACGAATGCG	39730	AGCACACCACACACAAACGCA
11085	STPKPSP	25408	TCTACGCCGAAGCCTTCGCCT	39731	AGCACACCAAAACCAAGCCCA
11086	STPLIAK	25409	AGTACGCCGTTGATTGCTAAG	39732	AGCACACCACTCATCGCAAAA
11087	STPLPRT	25410	TCTACGCCGTTGCCTAGGACG	39733	AGCACACCACTCCCAAGAACA
11088	STPLQTP	25411	AGTACTCCGTTGCAGACTCCG	39734	AGCACACCACTCCAAACACCA
11089	STPLRTS	25412	AGTACTCCGCTGCGTACGAGT	39735	AGCACACCACTCAGAACAAGC
11090	STPNARI	25413	TCGACTCCTAATGCTCGGATT	39736	AGCACACCAAACGCAAGAATC
11091	STPNMNR	25414	TCGACTCCGAATATGAATAGG	39737	AGCACACCAAACATGAACAGA
11092	STPPARS	25415	AGTACTCCTCCGGCTCGTTCT	39738	AGCACACCACCAGCAAGAAGC
11093	STPPLYE	25416	TCTACGCCGCCGCTGTATGAG	39739	AGCACACCACCACTCTACGAA
11094	STPPTTL	25417	AGTACGCCTCCTACTACGCTG	39740	AGCACACCACCAACAACACTC
11095	STPRPHD	25418	TCTACTCCTCGTCCGCATGAT	39741	AGCACACCAAGACCACACGAC
11096	STPTGAL	25419	TCTACGCCTACTGGGGCTCTG	39742	AGCACACCAACAGGAGCACTC
11097	STQQRSG	25420	TCGACGCAGCAGCGTTCTGGT	39743	AGCACACAACAAAGAAGCGGA
11098	STQRAAA	25421	TCTACTCAGCGTGCTGCTGCG	39744	AGCACACAAAGAGCAGCAGCA
11099	STQVHLL	25422	TCGACGCAGGTTCATCTGTTG	39745	AGCACACAAGTCCACCTCCTC
11100	STQVHMM	25423	TCGACGCAGGTGCATATGATG	39746	AGCACACAAGTCCACATGATG
11101	STQVPNK	25424	AGTACTCAGGTGCCGAATAAG	39747	AGCACACAAGTCCCAAACAAA
11102	STQWRTE	25425	TCTACTCAGTGGCGGACTGAG	39748	AGCACACAATGGAGAACAGAA
11103	STQYSPV	25426	TCGACTCAGTATAGTCCGGTG	39749	AGCACACAATACAGCCCAGTC
11104	STRAPTA	25427	TCGACTCGGGCGCCTACGGCG	39750	AGCACAAGAGCACCAACAGCA

11105	STRDTSN	25428	TCTACGCGTGATACTTCGAAT	39751	AGCACAAGAGACACAAGCAAC
11106	STREAKP	25429	TCTACGCGTGAGGCGAAGCCG	39752	AGCACAAGAGAAGCAAAACCA
11107	STREDVL	25430	AGTACTCGGGAGGATGTGTTG	39753	AGCACAAGAGAAGACGTCCTC
11108	STRFNST	25431	AGTACTAGGTTTAATTCTACT	39754	AGCACAAGATTCAACAGCACA
11109	STRPTVN	25432	TCGACGCGGCCTACGGTTAAT	39755	AGCACAAGACCAACAGTCAAC
11110	STRQLQQ	25433	TCTACGCGTCAGTTGCAGCAG	39756	AGCACAAGACAACTCCAACAA
11111	STRSDMY	25434	TCTACTCGGTCTGATATGTAT	39757	AGCACAAGAAGCGACATGTAC
11112	STRSIAG	25435	TCGACGCGGTCTATTGCTGGT	39758	AGCACAAGAAGCATCGCAGGA
11113	STRSVEH	25436	TCGACTAGGTCGGTGGAGCAT	39759	AGCACAAGAAGCGTCGAACAC
11114	STRTVSN	25437	TCGACTCGTACGGTTTCTAAT	39760	AGCACAAGAACAGTCAGCAAC
11115	STRVLTT	25438	AGTACGAGGGTTTTGACTACG	39761	AGCACAAGAGTCCTCACAACA
11116	STSANLG	25439	TCTACGTCTGCGAATCTGGGT	39762	AGCACAAGCGCAAACCTCGGA
11117	STSDTWK	25440	TCTACTTCTGATACGTGGAAG	39763	AGCACAAGCGACACATGGAAA
11118	STSEGLK	25441	TCGACGTCTGAGGGTCTTAAG	39764	AGCACAAGCGAAGGACTCAAA
11119	STSEIDR	25442	TCTACTAGTGAGATTGATCGT	39765	AGCACAAGCGAAATCGACAGA
11120	STSFAVG	25443	AGTACTTCGTTTGCGGTGGGG	39766	AGCACAAGCTTCGCAGTCGGA
11121	STSKAQC	25444	TCTACTTCTAAGGCGCAGTGT	39767	AGCACAAGCAAAGCACAATGC
11122	STSKAQI	25445	AGTACGTCTAAGGCTCAGATT	39768	AGCACAAGCAAAGCACAAATC
11123	STSKYMH	25446	TCTACTTCGAAGTATATGCAT	39769	AGCACAAGCAAATACATGCAC
11124	STSLAVQ	25447	TCTACTAGTCTTGCGGTGCAG	39770	AGCACAAGCCTCGCAGTCCAA
11125	STSLGYQ	25448	TCGACTTCGTTGGGGTATCAG	39771	AGCACAAGCCTCGGATACCAA
11126	STSLPSC	25449	TCGACGTCTCTTCCGTCGTGT	39772	AGCACAAGCCTCCCAAGCTGC
11127	STSMMSA	25450	TCTACTTCTATGATGTCGGCG	39773	AGCACAAGCATGATGAGCGCA
11128	STSMSRT	25451	TCTACGTCTATGTCTCGGACT	39774	AGCACAAGCATGAGCAGAACA
11129	STSQPLP	25452	AGTACGTCGCAGCCGTTGCCT	39775	AGCACAAGCCAACCACTCCCA
11130	STSRNMS	25453	TCTACTAGTCGTAATATGAGT	39776	AGCACAAGCAGAAACATGAGC
11131	STSSLSA	25454	TCTACTTCGTCTCTGTCTGCT	39777	AGCACAAGCAGCCTCAGCGCA
11132	STSSPRH	25455	TCTACTTCGAGTCCTCGGCAT	39778	AGCACAAGCAGCCCAAGACAC
11133	STSSSLY	25456	AGTACTTCTAGTTCTCTGTAT	39779	AGCACAAGCAGCAGCCTCTAC
11134	STSSTLS	25457	TCGACGTCGTCTACGCTTTCG	39780	AGCACAAGCAGCACACTCAGC
11135	STSTGAP	25458	TCTACTTCTACTGGGGCTCCT	39781	AGCACAAGCACAGGAGCACCA
11136	STSTLPL	25459	TCGACGTCTACTCTTCCGCTT	39782	AGCACAAGCACACTCCCACTC
11137	STSTLVH	25460	TCGACGTCTACTCTTGTGCAT	39783	AGCACAAGCACACTCGTCCAC
11138	STSVPPK	25461	AGTACTAGTGTGCCGCCTAAG	39784	AGCACAAGCGTCCCACCAAAA
11139	STSVRQT	25462	TCGACTTCTGTTCGTCAGACG	39785	AGCACAAGCGTCAGACAAACA
11140	STTAKAM	25463	AGTACGACGGCTAAGGCTATG	39786	AGCACAACAGCAAAAGCAATG
11141	STTAQTK	25464	TCGACTACTGCGCAGACTAAG	39787	AGCACAACAGCACAAACAAAA
11142	STTARSH	25465	AGTACTACTGCTCGGTCGCAT	39788	AGCACAACAGCAAGAAGCCAC
11143	STTDKPS	25466	TCTACTACTGATAAGCCTTCT	39789	AGCACAACAGACAAACCAAGC
11144	STTHDGR	25467	TCTACGACTCATGATGGTCGT	39790	AGCACAACACACGACGGAAGA
11145	STTHGRD	25468	AGTACGACTCATGGGCGTGAT	39791	AGCACAACACACGGAAGAGAC
11146	STTLHYV	25469	AGTACTACTTTGCATTATGTT	39792	AGCACAACACTCCACTACGTC
11147	STTLKMP	25470	TCTACGACTCTTAAGATGCCG	39793	AGCACAACACTCAAAATGCCA
11148	STTLNGL	25471	TCTACTACTCTTAATGGGCTG	39794	AGCACAACACTCAACGGACTC
11149	STTLTPL	25472	TCGACGACGCTGACGCCGCTT	39795	AGCACAACACTCACACCACTC

11150	STTNMLL	25473	TCTACTACTAATATGTTGCTG	39796	AGCACAACAAACATGCTCCTC
11151	STTPSPM	25474	AGTACGACGCCGTCGCCGATG	39797	AGCACAACACCAAGCCCAATG
11152	STTRSLL	25475	AGTACTACGAGGTCTCTTCTT	39798	AGCACAACAAGAAGCCTCCTC
11153	STTRTGG	25476	TCTACTACTCGGACGGGGGGG	39799	AGCACAACAAGAACAGGAGGA
11154	STTRTTL	25477	TCTACTACGAGGACTACTCTT	39800	AGCACAACAAGAACAACACTC
11155	STTSPSR	25478	AGTACTACTTCTCCTTCTCGT	39801	AGCACAACAAGCCCAAGCAGA
11156	STTSRVE	25479	TCGACGACGTCTAGGGTGGAG	39802	AGCACAACAAGCAGAGTCGAA
11157	STTSTLT	25480	TCGACGACTTCTACTTTGACT	39803	AGCACAACAAGCACACTCACA
11158	STTVITP	25481	TCGACTACTGTTATTACTCCT	39804	AGCACAACAGTCATCACACCA
11159	STVIKMN	25482	AGTACGGTTATTAAGATGAAT	39805	AGCACAGTCATCAAAATGAAC
11160	STVINPT	25483	AGTACTGTTATTAATCCTACT	39806	AGCACAGTCATCAACCCAACA
11161	STVIPTP	25484	AGTACGGTTATTCCTACTCCT	39807	AGCACAGTCATCCCAACACCA
11162	STVLLTA	25485	AGTACGGTGCTGCTTACTGCT	39808	AGCACAGTCCTCCTCACAGCA
11163	STVMTKV	25486	TCTACTGTTATGACGAAGGTT	39809	AGCACAGTCATGACAAAAGTC
11164	STYMTHS	25487	AGTACGTATATGACGCATAGT	39810	AGCACATACATGACACACAGC
11165	STYNSPE	25488	TCGACGTATAATTCGCCGGAG	39811	AGCACATACAACAGCCCAGAA
11166	SVAAHQH	25489	AGTGTGGCGGCTCATCAGCAT	39812	AGCGTCGCAGCACACCAACAC
11167	SVAAIKP	25490	TCGGTGGCTGCTATTAAGCCG	39813	AGCGTCGCAGCAATCAAACCA
11168	SVAAVSL	25491	TCTGTTGCTGCGGTTAGTTTG	39814	AGCGTCGCAGCAGTCAGCCTC
11169	SVAGLIK	25492	TCTGTTGCGGGTCTTATTAAG	39815	AGCGTCGCAGGACTCATCAAA
11170	SVAHNRA	25493	AGTGTTGCGCATAATCGTGCT	39816	AGCGTCGCACACAACAGAGCA
11171	SVAHYGL	25494	AGTGTTGCGCATTATGGGCTT	39817	AGCGTCGCACACTACGGACTC
11172	SVAPATL	25495	TCTGTGGCTCCTGCTACTCTG	39818	AGCGTCGCACCAGCAACACTC
11173	SVAPVKA	25496	TCTGTTGCGCCTGTTAAGGCG	39819	AGCGTCGCACCAGTCAAAGCA
11174	SVARNSP	25497	TCTGTTGCTAGGAATTCTCCG	39820	AGCGTCGCAAGAAACAGCCCA
11175	SVASMSS	25498	TCGGTTGCTTCGATGTCGAGT	39821	AGCGTCGCAAGCATGAGCAGC
11176	SVATAQT	25499	TCGGTTGCTACGGCTCAGACG	39822	AGCGTCGCAACAGCACAAACA
11177	SVDAVTG	25500	TCTGTGGATGCGGTTACTGGT	39823	AGCGTCGACGCAGTCACAGGA
11178	SVDEGAR	25501	TCGGTTGATGAGGGTGCGCGT	39824	AGCGTCGACGAAGGAGCAAGA
11179	SVDPHNP	25502	TCGGTTGATCCTCATAATCCG	39825	AGCGTCGACCCACACAACCCA
11180	SVDSSII	25503	AGTGTTGATTCGTCTATTATT	39826	AGCGTCGACAGCAGCATCATC
11181	SVDTGHS	25504	TCGGTGGATACTGGTCATTCG	39827	AGCGTCGACACAGGACACAGC
11182	SVDYVGV	25505	AGTGTTGATTATGTGGGGGTT	39828	AGCGTCGACTACGTCGGAGTC
11183	SVEFSDA	25506	TCGGTTGAGTTTTCTGATGCG	39829	AGCGTCGAATTCAGCGACGCA
11184	SVEKDDH	25507	TCGGTGGAGAAGGATGATCAT	39830	AGCGTCGAAAAAGACGACCAC
11185	SVETGRV	25508	AGTGTTGAGACTGGTCGTGTG	39831	AGCGTCGAAACAGGAAGAGTC
11186	SVETTNY	25509	TCTGTGGAGACTACTAATTAT	39832	AGCGTCGAAACAACAAACTAC
11187	SVEVSRA	25510	TCGGTTGAGGTTAGTCGTGCT	39833	AGCGTCGAAGTCAGCAGAGCA
11188	SVFKCEP	25511	AGTGTTTTTAAGTGTGAGCCG	39834	AGCGTCTTCAAATGCGAACCA
11189	SVFPHSA	25512	TCGGTGTTTCCGCATTCTGCG	39835	AGCGTCTTCCCACACAGCGCA
11190	SVFPLPH	25513	AGTGTTTTTCCGCTTCCGCAT	39836	AGCGTCTTCCCACTCCCACAC
11191	SVGDNGS	25514	AGTGTTGGTGATAATGGTTCG	39837	AGCGTCGGAGACAACGGAAGC
11192	SVGLQLE	25515	TCGGTTGGGCTTCAGCTTGAG	39838	AGCGTCGGACTCCAACTCGAA
11193	SVGSAME	25516	AGTGTGGGTAGTGCTATGGAG	39839	AGCGTCGGAAGCGCAATGGAA
11194	SVGSYSP	25517	TCTGTGGGGAGTTATAGTCCG	39840	AGCGTCGGAAGCTACAGCCCA

11195	SVGSYVD	25518	TCGGTGGGGTCGTATGTTGAT	39841	AGCGTCGGAAGCTACGTCGAC
11196	SVGTKDD	25519	TCGGTGGGGACGAAGGATGAT	39842	AGCGTCGGAACAAAAGACGAC
11197	SVHDHRS	25520	AGTGTGCATGATCATCGTTCT	39843	AGCGTCCACGACCACAGAAGC
11198	SVHEHSM	25521	AGTGTGCATGAGCATTCTATG	39844	AGCGTCCACGAACACAGCATG
11199	SVHPNQA	25522	TCGGTTCATCCGAATCAGGCT	39845	AGCGTCCACCCAAACCAAGCA
11200	SVILRAT	25523	TCTGTGATTCTGCGGGCGACT	39846	AGCGTCATCCTCAGAGCAACA
11201	SVINSRG	25524	TCTGTGATTAATAGTCGTGGT	39847	AGCGTCATCAACAGCAGAGGA
11202	SVISRSE	25525	AGTGTGATTTCTCGGTCGGAG	39848	AGCGTCATCAGCAGAAGCGAA
11203	SVITWED	25526	AGTGTGATTACTTGGGAGGAT	39849	AGCGTCATCACATGGGAAGAC
11204	SVKPLNH	25527	TCTGTGAAGCCTCTGAATCAT	39850	AGCGTCAAACCACTCAACCAC
11205	SVKVLRP	25528	TCGGTTAAGGTGCTGCGGCCT	39851	AGCGTCAAAGTCCTCAGACCA
11206	SVLDGPP	25529	TCTGTGTTGGATGGGCCGCCG	39852	AGCGTCCTCGACGGACCACCA
11207	SVLNLPS	25530	AGTGTTCTGAATCTTCCGTCG	39853	AGCGTCCTCAACCTCCCAAGC
11208	SVLPEPS	25531	TCTGTGCTGCCTGAGCCTTCG	39854	AGCGTCCTCCCAGAACCAAGC
11209	SVLRHPT	25532	TCGGTTCTGAGGCATCCGACT	39855	AGCGTCCTCAGACACCCAACA
11210	SVLRTTP	25533	TCGGTGCTGAGGACTACTCCG	39856	AGCGTCCTCAGAACAACACCA
11211	SVLSAVP	25534	AGTGTTTTGTCTGCTGTTCCG	39857	AGCGTCCTCAGCGCAGTCCCA
11212	SVLSIDR	25535	TCGGTGCTTTCTATTGATCGG	39858	AGCGTCCTCAGCATCGACAGA
11213	SVLSSSV	25536	TCGGTTCTGAGTTCGTCTGTT	39859	AGCGTCCTCAGCAGCAGCGTC
11214	SVMANQA	25537	TCTGTTATGGCTAATCAGGCT	39860	AGCGTCATGGCAAACCAAGCA
11215	SVMPKPQ	25538	AGTGTTATGCCGAAGCCTCAG	39861	AGCGTCATGCCAAAACCACAA
11216	SVNATRG	25539	AGTGTTAATGCGACGCGTGGG	39862	AGCGTCAACGCAACAAGAGGA
11217	SVNGNDV	25540	TCTGTGAATGGTAATGATGTG	39863	AGCGTCAACGGAAACGACGTC
11218	SVNGSWK	25541	TCGGTGAATGGGAGTTGGAAG	39864	AGCGTCAACGGAAGCTGGAAA
11219	SVPEYNG	25542	TCTGTGCCGGAGTATAATGGT	39865	AGCGTCCCAGAATACAACGGA
11220	SVPGTGS	25543	TCTGTTCCGGGGACTGGGTCT	39866	AGCGTCCCAGGAACAGGAAGC
11221	SVPHTST	25544	TCTGTGCCGCATACGTCTACT	39867	AGCGTCCCACACACAAGCACA
11222	SVPQMYS	25545	AGTGTGCCGCAGATGTATAGT	39868	AGCGTCCCACAAATGTACAGC
11223	SVPSASK	25546	AGTGTGCCTAGTGCGTCGAAG	39869	AGCGTCCCAAGCGCAAGCAAA
11224	SVPSSTR	25547	AGTGTGCCGTCTTCTACTCGG	39870	AGCGTCCCAAGCAGCACAAGA
11225	SVPVTPG	25548	TCTGTTCCGGTGACGCCTGGG	39871	AGCGTCCCAGTCACACCAGGA
11226	SVPYVGT	25549	TCTGTTCCTTATGTGGGGACG	39872	AGCGTCCCATACGTCGGAACA
11227	SVQREER	25550	TCTGTTCAGAGGGAGGAGCGG	39873	AGCGTCCAAAGAGAAGAAAGA
11228	SVQRGVD	25551	TCTGTTCAGCGTGGGGTGGAT	39874	AGCGTCCAAAGAGGAGTCGAC
11229	SVQTRPE	25552	TCTGTGCAGACGCGTCCGGAG	39875	AGCGTCCAAACAAGACCAGAA
11230	SVQVGYH	25553	TCGGTGCAGGTGGGTTATCAT	39876	AGCGTCCAAGTCGGATACCAC
11231	SVRAESA	25554	AGTGTTCGTGCGGAGTCTGCG	39877	AGCGTCAGAGCAGAAAGCGCA
11232	SVRHVEP	25555	AGTGTGAGGCATGTTGAGCCT	39878	AGCGTCAGACACGTCGAACCA
11233	SVRSASQ	25556	TCGGTTAGGTCGGCTTCTCAG	39879	AGCGTCAGAAGCGCAAGCCAA
11234	SVRSLSP	25557	TCGGTGCGGAGTCTGTCTCCG	39880	AGCGTCAGAAGCCTCAGCCCA
11235	SVRSNHA	25558	AGTGTGAGGTCGAATCATGCT	39881	AGCGTCAGAAGCAACCACGCA
11236	SVRTKDS	25559	TCGGTTCGGACTAAGGATTCT	39882	AGCGTCAGAACAAAAGACAGC
11237	SVSFSSS	25560	TCTGTTTCTTTTAGTTCGTCT	39883	AGCGTCAGCTTCAGCAGCAGC
11238	SVSGAAA	25561	AGTGTTTCTGGGGCGGCTGCG	39884	AGCGTCAGCGGAGCAGCAGCA
11239	SVSHNAP	25562	TCGGTGTCTCATAATGCGCCG	39885	AGCGTCAGCCACAACGCACCA

11240	SVSKEGT	25563	TCTGTGTCTAAGGAGGGGACG	39886	AGCGTCAGCAAAGAAGGAACA
11241	SVSLADP	25564	TCTGTTTCTTTGGCTGATCCT	39887	AGCGTCAGCCTCGCAGACCCA
11242	SVSLELY	25565	TCGGTTAGTCTTGAGCTGTAT	39888	AGCGTCAGCCTCGAACTCTAC
11243	SVSLGPK	25566	TCTGTGAGTCTTGGTCCTAAG	39889	AGCGTCAGCCTCGGACCAAAA
11244	SVSPHQA	25567	TCTGTTAGTCCGCATCAGGCT	39890	AGCGTCAGCCCACACCAAGCA
11245	SVSRMVA	25568	TCGGTGTCTAGGATGGTTGCT	39891	AGCGTCAGCAGAATGGTCGCA
11246	SVSRPAL	25569	TCGGTTTCTCGGCCTGCTCTT	39892	AGCGTCAGCAGACCAGCACTC
11247	SVSRQQI	25570	TCTGTTTCGCGTCAGCAGATT	39893	AGCGTCAGCAGACAACAAATC
11248	SVSSQNT	25571	TCTGTTTCGTCTCAGAATACT	39894	AGCGTCAGCAGCCAAAACACA
11249	SVSSSQL	25572	TCTGTGAGTTCGTCGCAGCTG	39895	AGCGTCAGCAGCAGCCAACTC
11250	SVSTANP	25573	TCGGTTTCTACTGCTAATCCT	39896	AGCGTCAGCACAGCAAACCCA
11251	SVSTLPM	25574	AGTGTTAGTACGTTGCCTATG	39897	AGCGTCAGCACACTCCCAATG
11252	SVSTNKY	25575	AGTGTGTCGACTAATAAGTAT	39898	AGCGTCAGCACAAACAAATAC
11253	SVSVDYM	25576	TCTGTTAGTGTTGATTATATG	39899	AGCGTCAGCGTCGACTACATG
11254	SVTAKTY	25577	TCTGTGACTGCGAAGACGTAT	39900	AGCGTCACAGCAAAAACATAC
11255	SVTDGVL	25578	AGTGTTACGGATGGGGTGCTG	39901	AGCGTCACAGACGGAGTCCTC
11256	SVTEHVI	25579	AGTGTTACGGAGCATGTTATT	39902	AGCGTCACAGAACACGTCATC
11257	SVTGANT	25580	TCGGTTACTGGTGCGAATACT	39903	AGCGTCACAGGAGCAAACACA
11258	SVTHLFK	25581	TCGGTTACTCATTTGTTTAAG	39904	AGCGTCACACACCTCTTCAAA
11259	SVTPTRA	25582	TCGGTTACGCCTACTCGTGCT	39905	AGCGTCACACCAACAAGAGCA
11260	SVTQMFK	25583	TCTGTTACTCAGATGTTTAAG	39906	AGCGTCACACAAATGTTCAAA
11261	SVTRAPY	25584	TCGGTGACGCGGGCTCCGTAT	39907	AGCGTCACAAGAGCACCATAC
11262	SVTTRAI	25585	TCTGTGACTACTAGGGCTATT	39908	AGCGTCACAACAAGAGCAATC
11263	SVVAAVI	25586	AGTGTGGTTGCTGCGGTTATT	39909	AGCGTCGTCGCAGCAGTCATC
11264	SVVGTHA	25587	TCTGTGGTTGGGACGCATGCG	39910	AGCGTCGTCGGAACACACGCA
11265	SVVPHDL	25588	AGTGTTGTTCCTCATGATCTT	39911	AGCGTCGTCCCACACGACCTC
11266	SVVRKEA	25589	TCTGTTGTGCGGAAGGAGGCT	39912	AGCGTCGTCAGAAAAGAAGCA
11267	SVVSRLG	25590	TCTGTGGTGTCTAGGCTTGGG	39913	AGCGTCGTCAGCAGACTCGGA
11268	SVVSSQG	25591	TCGGTTGTGTCGTCTCAGGGT	39914	AGCGTCGTCAGCAGCCAAGGA
11269	SVYTQAP	25592	TCTGTTTATACGCAGGCGCCT	39915	AGCGTCTACACACAAGCACCA
11270	SWDASAL	25593	TCTTGGGATGCGAGTGCTCTT	39916	AGCTGGGACGCAAGCGCACTC
11271	SWGAKEG	25594	TCTTGGGGTGCGAAGGAGGGT	39917	AGCTGGGGAGCAAAAGAAGGA
11272	SWGETAK	25595	AGTTGGGGTGAGACGGCTAAG	39918	AGCTGGGGAGAAACAGCAAAA
11273	SWHNSQP	25596	TCTTGGCATAATAGTCAGCCT	39919	AGCTGGCACAACAGCCAACCA
11274	SWPSNGV	25597	AGTTGGCCGTCGAATGGTGTT	39920	AGCTGGCCAAGCAACGGAGTC
11275	SWQTSIA	25598	TCTTGGCAGACTTCGATTGCG	39921	AGCTGGCAAACAAGCATCGCA
11276	SWRDVPP	25599	TCTTGGCGTGATGTTCCGCCG	39922	AGCTGGAGAGACGTCCCACCA
11277	SWSHEQE	25600	TCGTGGTCGCATGAGCAGGAG	39923	AGCTGGAGCCACGAACAAGAA
11278	SYAKSLD	25601	TCGTATGCTAAGAGTCTGGAT	39924	AGCTACGCAAAAAGCCTCGAC
11279	SYARTSL	25602	TCGTATGCTAGGACGTCTTTG	39925	AGCTACGCAAGAACAAGCCTC
11280	SYASLTP	25603	TCGTATGCTTCTCTGACTCCT	39926	AGCTACGCAAGCCTCACACCA
11281	SYASRTV	25604	AGTTATGCTTCTCGGACTGTT	39927	AGCTACGCAAGCAGAACAGTC
11282	SYATSLT	25605	AGTTATGCTACGTCTTTGACT	39928	AGCTACGCAACAAGCCTCACA
11283	SYDRSPA	25606	TCTTATGATCGTTCGCCTGCG	39929	AGCTACGACAGAAGCCCAGCA
11284	SYEASKY	25607	TCTTATGAGGCTTCGAAGTAT	39930	AGCTACGAAGCAAGCAAATAC

11285	SYEDDSC	25608	TCGTATGAGGATGATAGTTGT	39931	AGCTACGAAGACGACAGCTGC
11286	SYEPNKL	25609	TCGTATGAGCCGAATAAGCTG	39932	AGCTACGAACCAAACAAACTC
11287	SYGGTLL	25610	TCGTATGGGGGTACTCTTCTT	39933	AGCTACGGAGGAACACTCCTC
11288	SYGKEYV	25611	TCGTATGGGAAGGAGTATGTG	39934	AGCTACGGAAAAGAATACGTC
11289	SYGLPAY	25612	TCGTATGGTCTTCCGGCGTAT	39935	AGCTACGGACTCCCAGCATAC
11290	SYGPIKT	25613	TCTTATGGTCCTATTAAGACT	39936	AGCTACGGACCAATCAAAACA
11291	SYGRGAE	25614	TCGTATGGGCGTGGGGCTGAG	39937	AGCTACGGAAGAGGAGCAGAA
11292	SYGSGQI	25615	AGTTATGGGTCTGGTCAGATT	39938	AGCTACGGAAGCGGACAAATC
11293	SYGSKLP	25616	TCTTATGGGTCGAAGCTTCCT	39939	AGCTACGGAAGCAAACTCCCA
11294	SYGTAPI	25617	TCGTATGGGACTGCGCCGATT	39940	AGCTACGGAACAGCACCAATC
11295	SYGVPRP	25618	TCGTATGGGGTTCCGCGTCCG	39941	AGCTACGGAGTCCCAAGACCA
11296	SYHPKLN	25619	TCGTATCATCCGAAGTTGAAT	39942	AGCTACCACCCAAAACTCAAC
11297	SYIPSTI	25620	AGTTATATTCCGTCTACGATT	39943	AGCTACATCCCAAGCACAATC
11298	SYIREDP	25621	TCGTATATTCGGGAGGATCCT	39944	AGCTACATCAGAGAAGACCCA
11299	SYKGSYM	25622	TCGTATAAGGGGTCGTATATG	39945	AGCTACAAAGGAAGCTACATG
11300	SYKHMPP	25623	TCTTATAAGCATATGCCGCCT	39946	AGCTACAAACACATGCCACCA
11301	SYKSQIA	25624	AGTTATAAGTCGCAGATTGCG	39947	AGCTACAAAAGCCAAATCGCA
11302	SYLGIAP	25625	TCGTATTTGGGGATTGCGCCT	39948	AGCTACCTCGGAATCGCACCA
11303	SYLNPMN	25626	TCTTATCTGAATCCTATGAAT	39949	AGCTACCTCAACCCAATGAAC
11304	SYLPPAP	25627	TCTTATCTTCCTCCGGCGCCG	39950	AGCTACCTCCCACCAGCACCA
11305	SYMASLP	25628	TCGTATATGGCGTCGTTGCCT	39951	AGCTACATGGCAAGCCTCCCA
11306	SYMPQTV	25629	TCGTATATGCCGCAGACGGTG	39952	AGCTACATGCCACAAACAGTC
11307	SYMSPVS	25630	AGTTATATGTCTCCGGTTTCT	39953	AGCTACATGAGCCCAGTCAGC
11308	SYMTKDL	25631	AGTTATATGACGAAGGATTTG	39954	AGCTACATGACAAAAGACCTC
11309	SYPAKPS	25632	AGTTATCCGGCGAAGCCTAGT	39955	AGCTACCCAGCAAAACCAAGC
11310	SYPASSR	25633	TCTTATCCTGCTTCGTCTCGT	39956	AGCTACCCAGCAAGCAGCAGA
11311	SYPKSYE	25634	AGTTATCCTAAGTCGTATGAG	39957	AGCTACCCAAAAAGCTACGAA
11312	SYPVSVP	25635	TCGTATCCTGTTAGTGTTCCG	39958	AGCTACCCAGTCAGCGTCCCA
11313	SYQAIST	25636	TCTTATCAGGCGATTAGTACG	39959	AGCTACCAAGCAATCAGCACA
11314	SYRPESG	25637	AGTTATCGTCCTGAGAGTGGT	39960	AGCTACAGACCAGAAAGCGGA
11315	SYRPETN	25638	TCTTATAGGCCTGAGACGAAT	39961	AGCTACAGACCAGAAACAAAC
11316	SYRVNTG	25639	AGTTATCGGGTGAATACGGGG	39962	AGCTACAGAGTCAACACAGGA
11317	SYSASEF	25640	TCGTATTCGGCTTCGGAGTTT	39963	AGCTACAGCGCAAGCGAATTC
11318	SYSATTV	25641	AGTTATTCTGCGACGACGGTT	39964	AGCTACAGCGCAACAACAGTC
11319	SYSGGCL	25642	TCTTATTCTGGGGGGTGTTTG	39965	AGCTACAGCGGAGGATGCCTC
11320	SYSHLSG	25643	TCGTATTCGCATCTTAGTGGG	39966	AGCTACAGCCACCTCAGCGGA
11321	SYSMAHP	25644	TCGTATTCTATGGCGCATCCG	39967	AGCTACAGCATGGCACACCCA
11322	SYSSDRS	25645	TCTTATAGTAGTGATCGTTCG	39968	AGCTACAGCAGCGACAGAAGC
11323	SYTDAAL	25646	TCTTATACTGATGCTGCGTTG	39969	AGCTACACAGACGCAGCACTC
11324	SYTHVSG	25647	TCGTATACTCATGTGTCTGGT	39970	AGCTACACACACGTCAGCGGA
11325	SYTKDVD	25648	TCTTATACTAAGGATGTTGAT	39971	AGCTACACAAAAGACGTCGAC
11326	SYTKSAP	25649	TCGTATACGAAGTCGGCGCCG	39972	AGCTACACAAAAAGCGCACCA
11327	SYTSPSS	25650	AGTTATACGTCTCCTTCGTCG	39973	AGCTACACAAGCCCAAGCAGC
11328	SYTVDSH	25651	AGTTATACGGTTGATTCTCAT	39974	AGCTACACAGTCGACAGCCAC
11329	SYVKPAE	25652	TCGTATGTGAAGCCTGCGGAG	39975	AGCTACGTCAAACCAGCAGAA

11330	SYVNNPG	25653	TCTTATGTGAATAATCCGGGT	39976	AGCTACGTCAACAACCCAGGA
11331	SYVRPTS	25654	TCGTATGTGCGTCCGACTTCT	39977	AGCTACGTCAGACCAACAAGC
11332	SYVSGAA	25655	AGTTATGTGAGTGGGGCGGCG	39978	AGCTACGTCAGCGGAGCAGCA
11333	TAAADRV	25656	ACGGCGGCGGCGGATCGTGTT	39979	ACAGCAGCAGCAGACAGAGTC
11334	TAAASNR	25657	ACTGCTGCTGCGTCTAATAGG	39980	ACAGCAGCAGCAAGCAACAGA
11335	TAAASVR	25658	ACGGCTGCTGCTTCGGTTCGT	39981	ACAGCAGCAGCAAGCGTCAGA
11336	TAADNDE	25659	ACTGCTGCGGATAATGATGAG	39982	ACAGCAGCAGACAACGACGAA
11337	TAAFDRV	25660	ACGGCGGCTTTTGATCGTGTG	39983	ACAGCAGCATTCGACAGAGTC
11338	TAAHLGN	25661	ACGGCGGCGCATCTTGGTAAT	39984	ACAGCAGCACACCTCGGAAAC
11339	TAAKSAG	25662	ACGGCTGCTAAGAGTGCTGGG	39985	ACAGCAGCAAAAAGCGCAGGA
11340	TAALTGH	25663	ACTGCGGCTCTGACTGGGCAT	39986	ACAGCAGCACTCACAGGACAC
11341	TAARFAA	25664	ACTGCGGCGAGGTTTGCTGCG	39987	ACAGCAGCAAGATTCGCAGCA
11342	TAARSSD	25665	ACGGCTGCTCGGAGTTCGGAT	39988	ACAGCAGCAAGAAGCAGCGAC
11343	TAASHST	25666	ACGGCTGCGTCGCATTCGACT	39989	ACAGCAGCAAGCCACAGCACA
11344	TAATNVN	25667	ACTGCTGCTACTAATGTTAAT	39990	ACAGCAGCAACAAACGTCAAC
11345	TAAVTNT	25668	ACTGCTGCGGTTACTAATACG	39991	ACAGCAGCAGTCACAAACACA
11346	TADRMMS	25669	ACTGCGGATCGGATGATGTCG	39992	ACAGCAGACAGAATGATGAGC
11347	TAEHTRF	25670	ACTGCGGAGCATACGCGGTTT	39993	ACAGCAGAACACACAAGATTC
11348	TAENLSP	25671	ACGGCGGAGAATCTGTCTCCT	39994	ACAGCAGAAAACCTCAGCCCA
11349	TAEPVRT	25672	ACTGCGGAGCCTGTTCGGACG	39995	ACAGCAGAACCAGTCAGAACA
11350	TAFQTIE	25673	ACTGCTTTTCAGACGATTGAG	39996	ACAGCATTCCAAACAATCGAA
11351	TAFRMDY	25674	ACTGCTTTTCGGATGGATTAT	39997	ACAGCATTCAGAATGGACTAC
11352	TAGGQPL	25675	ACTGCGGGGGGGCAGCCGCTT	39998	ACAGCAGGAGGACAACCACTC
11353	TAGGTTP	25676	ACTGCGGGGGGTACGACTCCT	39999	ACAGCAGGAGGAACAACACCA
11354	TAGLGVP	25677	ACTGCTGGGCTTGGGGTGCCG	40000	ACAGCAGGACTCGGAGTCCCA
11355	TAGNLIP	25678	ACGGCGGGTAATTTGATTCCG	40001	ACAGCAGGAAACCTCATCCCA
11356	TAGPHRV	25679	ACTGCGGGGCCGCATCGTGTT	40002	ACAGCAGGACCACACAGAGTC
11357	TAGVPAI	25680	ACGGCGGGTGTTCCGGCGATT	40003	ACAGCAGGAGTCCCAGCAATC
11358	TAHEERN	25681	ACGGCTCATGAGGAGAGGAAT	40004	ACAGCACACGAAGAAAGAAAC
11359	TAHFSAT	25682	ACTGCGCATTTTAGTGCGACT	40005	ACAGCACACTTCAGCGCAACA
11360	TAHPFPP	25683	ACTGCTCATCCGTTTCCTCCT	40006	ACAGCACACCCATTCCCACCA
11361	TAHQLIA	25684	ACTGCTCATCAGTTGATTGCT	40007	ACAGCACACCAACTCATCGCA
11362	TAHSLQS	25685	ACGGCTCATTCTTTGCAGTCG	40008	ACAGCACACAGCCTCCAAAGC
11363	TAHSYAH	25686	ACGGCTCATTCTTATGCTCAT	40009	ACAGCACACAGCTACGCACAC
11364	TAHVFPA	25687	ACGGCTCATGTGTTTCCTGCT	40010	ACAGCACACGTCTTCCCAGCA
11365	TAIGISP	25688	ACTGCTATTGGGATTAGTCCG	40011	ACAGCAATCGGAATCAGCCCA
11366	TAIPFPA	25689	ACGGCTATTCCTTTTCCTGCG	40012	ACAGCAATCCCATTCCCAGCA
11367	TAISSRA	25690	ACTGCTATTAGTTCTCGGGCT	40013	ACAGCAATCAGCAGCAGAGCA
11368	TAKATVE	25691	ACTGCTAAGGCTACGGTTGAG	40014	ACAGCAAAAGCAACAGTCGAA
11369	TAKSSNN	25692	ACTGCGAAGTCTTCGAATAAT	40015	ACAGCAAAAAGCAGCAACAAC
11370	TAKTSAI	25693	ACTGCGAAGACTAGTGCGATT	40016	ACAGCAAAAACAAGCGCAATC
11371	TAKYDHL	25694	ACTGCGAAGTATGATCATCTG	40017	ACAGCAAAATACGACCACCTC
11372	TALFQDA	25695	ACTGCGCTTTTTCAGGATGCT	40018	ACAGCACTCTTCCAAGACGCA
11373	TALHADV	25696	ACGGCGTTGCATGCGGATGTG	40019	ACAGCACTCCACGCAGACGTC
11374	TALHYSE	25697	ACGGCTTTGCATTATAGTGAG	40020	ACAGCACTCCACTACAGCGAA

11375	TAMPMKI	25698	ACGGCGATGCCGATGAAGATT	40021	ACAGCAATGCCAATGAAAATC
11376	TAMQMTP	25699	ACGGCGATGCAGATGACTCCG	40022	ACAGCAATGCAAATGACACCA
11377	TAMQTAM	25700	ACTGCTATGCAGACGGCTATG	40023	ACAGCAATGCAAACAGCAATG
11378	TAMTTMG	25701	ACTGCTATGACGACTATGGGG	40024	ACAGCAATGACAACAATGGGA
11379	TANPLST	25702	ACGGCTAATCCGCTTAGTACG	40025	ACAGCAAACCCACTCAGCACA
11380	TANVPAR	25703	ACTGCGAATGTGCCTGCTCGT	40026	ACAGCAAACGTCCCAGCAAGA
11381	TANVRSM	25704	ACGGCTAATGTGCGTTCGATG	40027	ACAGCAAACGTCAGAAGCATG
11382	TAPERTN	25705	ACGGCTCCTGAGAGGACTAAT	40028	ACAGCACCAGAAAGAACAAAC
11383	TAPGHAS	25706	ACGGCTCCTGGTCATGCGTCG	40029	ACAGCACCAGGACACGCAAGC
11384	TAPPTDR	25707	ACGGCTCCTCCTACGGATCGT	40030	ACAGCACCACCAACAGACAGA
11385	TAPRSSE	25708	ACGGCTCCTAGGAGTTCTGAG	40031	ACAGCACCAAGAAGCAGCGAA
11386	TAPSRMG	25709	ACGGCTCCTAGTCGGATGGGT	40032	ACAGCACCAAGCAGAATGGGA
11387	TAPTGTI	25710	ACGGCTCCTACTGGTACTATT	40033	ACAGCACCAACAGGAACAATC
11388	TAPYGDA	25711	ACTGCTCCGTATGGGGATGCT	40034	ACAGCACCATACGGAGACGCA
11389	TAQEGRT	25712	ACTGCGCAGGAGGGGCGGACT	40035	ACAGCACAAGAAGGAAGAACA
11390	TAQLTAH	25713	ACTGCGCAGTTGACTGCTCAT	40036	ACAGCACAACTCACAGCACAC
11391	TAQLTSS	25714	ACTGCTCAGCTGACTTCTTCT	40037	ACAGCACAACTCACAAGCAGC
11392	TAQRGPA	25715	ACTGCTCAGCGGGGTCCGGCT	40038	ACAGCACAAAGAGGACCAGCA
11393	TARDSSP	25716	ACGGCGCGGGATTCTAGTCCG	40039	ACAGCAAGAGACAGCAGCCCA
11394	TARGLVP	25717	ACTGCGCGTGGTCTTGTTCCT	40040	ACAGCAAGAGGACTCGTCCCA
11395	TARGNML	25718	ACTGCTCGTGGTAATATGCTG	40041	ACAGCAAGAGGAAACATGCTC
11396	TARGSPL	25719	ACTGCTCGTGGGTCTCCGTTG	40042	ACAGCAAGAGGAAGCCCACTC
11397	TARPPGV	25720	ACGGCGCGGCCGCCTGGGGTG	40043	ACAGCAAGACCACCAGGAGTC
11398	TARSSVT	25721	ACTGCTCGGTCTTCTGTGACG	40044	ACAGCAAGAAGCAGCGTCACA
11399	TARTLIS	25722	ACTGCGCGTACGTTGATTAGT	40045	ACAGCAAGAACACTCATCAGC
11400	TASAART	25723	ACTGCGTCTGCTGCGAGGACG	40046	ACAGCAAGCGCAGCAAGAACA
11401	TASATYP	25724	ACTGCTTCTGCGACTTATCCG	40047	ACAGCAAGCGCAACATACCCA
11402	TASFSST	25725	ACTGCTTCGTTTTCTTCTACG	40048	ACAGCAAGCTTCAGCAGCACA
11403	TASGSER	25726	ACGGCGAGTGGTAGTGAGCGG	40049	ACAGCAAGCGGAAGCGAAAGA
11404	TASKNDY	25727	ACGGCTTCGAAGAATGATTAT	40050	ACAGCAAGCAAAAACGACTAC
11405	TASMGER	25728	ACGGCGTCTATGGGGGAGCGT	40051	ACAGCAAGCATGGGAGAAAGA
11406	TASSMGK	25729	ACGGCGTCGTCGATGGGGAAG	40052	ACAGCAAGCAGCATGGGAAAA
11407	TASTVKM	25730	ACTGCGAGTACGGTGAAGATG	40053	ACAGCAAGCACAGTCAAAATG
11408	TASVPMK	25731	ACTGCTTCGGTTCCTATGAAG	40054	ACAGCAAGCGTCCCAATGAAA
11409	TASYSPK	25732	ACGGCTTCGTATAGTCCTAAG	40055	ACAGCAAGCTACAGCCCAAAA
11410	TATPHIG	25733	ACGGCTACTCCGCATATTGGG	40056	ACAGCAACACCACACATCGGA
11411	TATRNEV	25734	ACGGCTACTCGGAATGAGGTG	40057	ACAGCAACAAGAAACGAAGTC
11412	TATRTGP	25735	ACTGCGACTCGGACTGGTCCT	40058	ACAGCAACAAGAACAGGACCA
11413	TATYPND	25736	ACTGCTACTTATCCTAATGAT	40059	ACAGCAACATACCCAAACGAC
11414	TAVAHPA	25737	ACTGCTGTTGCTCATCCTGCG	40060	ACAGCAGTCGCACACCCAGCA
11415	TAVPEWT	25738	ACTGCGGTGCCGGAGTGGACT	40061	ACAGCAGTCCCAGAATGGACA
11416	TAVQEHT	25739	ACTGCTGTTCAGGAGCATACT	40062	ACAGCAGTCCAAGAACACACA
11417	TAVRSIS	25740	ACTGCTGTTCGTTCGATTTCG	40063	ACAGCAGTCAGAAGCATCAGC
11418	TAVVKFP	25741	ACTGCTGTGGTTAAGTTTCCG	40064	ACAGCAGTCGTCAAATTCCCA
11419	TAVYATA	25742	ACGGCGGTGTATGCGACGGCG	40065	ACAGCAGTCTACGCAACAGCA

11420	TAVYSKG	25743	ACGGCTGTGTATTCTAAGGGG	40066	ACAGCAGTCTACAGCAAAGGA
11421	TAWDPES	25744	ACTGCGTGGGATCCTGAGTCG	40067	ACAGCATGGGACCCAGAAAGC
11422	TAYCQQY	25745	ACGGCTTATTGTCAGCAGTAT	40068	ACAGCATACTGCCAACAATAC
11423	TAYPFEA	25746	ACGGCGTATCCTTTTGAGGCG	40069	ACAGCATACCCATTCGAAGCA
11424	TAYPHQI	25747	ACGGCGTATCCTCATCAGATT	40070	ACAGCATACCCACACCAAATC
11425	TDADRSP	25748	ACGGATGCTGATCGGTCTCCT	40071	ACAGACGCAGACAGAAGCCCA
11426	TDCRQGG	25749	ACGGATTGTCGTCAGGGGGGT	40072	ACAGACTGCAGACAAGGAGGA
11427	TDDIKND	25750	ACTGATGATATTAAGAATGAT	40073	ACAGACGACATCAAAAACGAC
11428	TDEYKKA	25751	ACTGATGAGTATAAGAAGGCT	40074	ACAGACGAATACAAAAAAGCA
11429	TDFRRIP	25752	ACTGATTTTCGTAGGATTCCT	40075	ACAGACTTCAGAAGAATCCCA
11430	TDGLHKL	25753	ACGGATGGGTTGCATAAGTTG	40076	ACAGACGGACTCCACAAACTC
11431	TDGPGLT	25754	ACGGATGGGCCTGGTCTGACG	40077	ACAGACGGACCAGGACTCACA
11432	TDGRLGG	25755	ACGGATGGTCGGTTGGGGGGT	40078	ACAGACGGAAGACTCGGAGGA
11433	TDGSRVP	25756	ACGGATGGGTCTAGGGTGCCT	40079	ACAGACGGAAGCAGAGTCCCA
11434	TDHVHRG	25757	ACGGATCATGTGCATCGTGGG	40080	ACAGACCACGTCCACAGAGGA
11435	TDKHGVL	25758	ACGGATAAGCATGGTGTGCTG	40081	ACAGACAAACACGGAGTCCTC
11436	TDKVRSQ	25759	ACTGATAAGGTGAGGAGTCAG	40082	ACAGACAAAGTCAGAAGCCAA
11437	TDLHLEL	25760	ACTGATCTTCATCTGGAGCTT	40083	ACAGACCTCCACCTCGAACTC
11438	TDLSHGH	25761	ACGGATTTGTCGCATGGGCAT	40084	ACAGACCTCAGCCACGGACAC
11439	TDLYSQS	25762	ACTGATCTTTATTCTCAGTCT	40085	ACAGACCTCTACAGCCAAAGC
11440	TDMQRLG	25763	ACTGATATGCAGAGGTTGGGT	40086	ACAGACATGCAAAGACTCGGA
11441	TDNRITA	25764	ACGGATAATAGGATTACGGCT	40087	ACAGACAACAGAATCACAGCA
11442	TDPHSDK	25765	ACTGATCCGCATTCGGATAAG	40088	ACAGACCCACACAGCGACAAA
11443	TDQSLMS	25766	ACGGATCAGAGTCTGATGTCT	40089	ACAGACCAAAGCCTCATGAGC
11444	TDRGGVQ	25767	ACTGATCGTGGTGGTGTTCAG	40090	ACAGACAGAGGAGGAGTCCAA
11445	TDRSALS	25768	ACTGATAGGTCGGCTTTGAGT	40091	ACAGACAGAAGCGCACTCAGC
11446	TDRSSLS	25769	ACTGATAGGAGTTCGCTTTCT	40092	ACAGACAGAAGCAGCCTCAGC
11447	TDRVPSF	25770	ACGGATCGGGTTCCGAGTTTT	40093	ACAGACAGAGTCCCAAGCTTC
11448	TDSGPTP	25771	ACGGATAGTGGTCCTACTCCT	40094	ACAGACAGCGGACCAACACCA
11449	TDSHVLY	25772	ACTGATAGTCATGTGCTGTAT	40095	ACAGACAGCCACGTCCTCTAC
11450	TDTHSSV	25773	ACGGATACGCATAGTTCGGTG	40096	ACAGACACACACAGCAGCGTC
11451	TDTSRGL	25774	ACGGATACGTCGCGGGGTCTG	40097	ACAGACACAAGCAGAGGACTC
11452	TDTTGGP	25775	ACTGATACGACGGGTGGTCCG	40098	ACAGACACAACAGGAGGACCA
11453	TDVITVA	25776	ACTGATGTTATTACTGTTGCG	40099	ACAGACGTCATCACAGTCGCA
11454	TDVPHPN	25777	ACGGATGTTCCGCATCCTAAT	40100	ACAGACGTCCCACACCCAAAC
11455	TDVRPAG	25778	ACGGATGTGCGTCCGGCTGGG	40101	ACAGACGTCAGACCAGCAGGA
11456	TDVRTKN	25779	ACGGATGTGAGGACGAAGAAT	40102	ACAGACGTCAGAACAAAAAAC
11457	TDWEHDP	25780	ACTGATTGGGAGCATGATCCG	40103	ACAGACTGGGAACACGACCCA
11458	TDYDLSS	25781	ACGGATTATGATCTTTCGAGT	40104	ACAGACTACGACCTCAGCAGC
11459	TEAASRQ	25782	ACTGAGGCTGCGAGTCGTCAG	40105	ACAGAAGCAGCAAGCAGACAA
11460	TEARNPV	25783	ACTGAGGCGCGTAATCCGGTT	40106	ACAGAAGCAAGAAACCCAGTC
11461	TEDTAPC	25784	ACTGAGGATACGGCGCCTTGT	40107	ACAGAAGACACAGCACCATGC
11462	TEFYDLE	25785	ACTGAGTTTTATGATTTGGAG	40108	ACAGAATTCTACGACCTCGAA
11463	TEGRAPT	25786	ACTGAGGGTAGGGCTCCGACG	40109	ACAGAAGGAAGAGCACCAACA
11464	TEHGTKI	25787	ACTGAGCATGGGACTAAGATT	40110	ACAGAACACGGAACAAAAATC

11465	TELNRAI	25788	ACGGAGCTGAATAGGGCGATT	40111	ACAGAACTCAACAGAGCAATC
11466	TELSHNR	25789	ACGGAGCTTTCTCATAATAGG	40112	ACAGAACTCAGCCACAACAGA
11467	TELSSPR	25790	ACGGAGCTTAGTTCGCCTAGG	40113	ACAGAACTCAGCAGCCCAAGA
11468	TELVIGK	25791	ACTGAGTTGGTTATTGGTAAG	40114	ACAGAACTCGTCATCGGAAAA
11469	TENAGTG	25792	ACGGAGAATGCGGGGACGGGT	40115	ACAGAAAACGCAGGAACAGGA
11470	TEPPHVA	25793	ACTGAGCCTCCTCATGTTGCT	40116	ACAGAACCACCACACGTCGCA
11471	TEPPYRL	25794	ACTGAGCCTCCGTATAGGTTG	40117	ACAGAACCACCATACAGACTC
11472	TEPQIGR	25795	ACGGAGCCTCAGATTGGTCGG	40118	ACAGAACCACAAATCGGAAGA
11473	TEPRMVS	25796	ACTGAGCCTCGGATGGTTTCT	40119	ACAGAACCAAGAATGGTCAGC
11474	TEPYAPD	25797	ACGGAGCCTTATGCTCCGGAT	40120	ACAGAACCATACGCACCAGAC
11475	TEPYTDF	25798	ACTGAGCCGTATACGGATTTT	40121	ACAGAACCATACACAGACTTC
11476	TERADEH	25799	ACGGAGAGGGCGGATGAGCAT	40122	ACAGAAAGAGCAGACGAACAC
11477	TERPSPT	25800	ACGGAGCGGCCTAGTCCTACG	40123	ACAGAAAGACCAAGCCCAACA
11478	TESHHPL	25801	ACTGAGTCGCATCATCCTCTT	40124	ACAGAAAGCCACCACCCACTC
11479	TESTFNM	25802	ACTGAGTCGACGTTTAATATG	40125	ACAGAAAGCACATTCAACATG
11480	TESTHQT	25803	ACGGAGTCTACGCATCAGACT	40126	ACAGAAAGCACACACCAAACA
11481	TETASSP	25804	ACGGAGACTGCGAGTAGTCCG	40127	ACAGAAACAGCAAGCAGCCCA
11482	TETGNCH	25805	ACTGAGACTGGGAATTGTCAT	40128	ACAGAAACAGGAAACTGCCAC
11483	TETLHNR	25806	ACTGAGACTCTGCATAATCGT	40129	ACAGAAACACTCCACAACAGA
11484	TETVGDL	25807	ACGGAGACGGTTGGTGATCTT	40130	ACAGAAACAGTCGGAGACCTC
11485	TEVKLLP	25808	ACGGAGGTTAAGTTGTTGCCT	40131	ACAGAAGTCAAACTCCTCCCA
11486	TEVRPGL	25809	ACTGAGGTTCGTCCGGGTTTG	40132	ACAGAAGTCAGACCAGGACTC
11487	TEVRSPL	25810	ACTGAGGTGCGGTCGCCTTTG	40133	ACAGAAGTCAGAAGCCCACTC
11488	TEVSSNK	25811	ACTGAGGTGTCGTCTAATAAG	40134	ACAGAAGTCAGCAGCAACAAA
11489	TEWSSND	25812	ACGGAGTGGAGTAGTAATGAT	40135	ACAGAATGGAGCAGCAACGAC
11490	TEYATRP	25813	ACGGAGTATGCTACGCGGCCT	40136	ACAGAATACGCAACAAGACCA
11491	TEYTLHG	25814	ACTGAGTATACGCTTCATGGT	40137	ACAGAATACACACTCCACGGA
11492	TFASGAP	25815	ACTTTTGCGTCGGGGGCGCCG	40138	ACATTCGCAAGCGGAGCACCA
11493	TFASPLL	25816	ACGTTTGCGAGTCCGCTGCTG	40139	ACATTCGCAAGCCCACTCCTC
11494	TFDPQWA	25817	ACTTTTGATCCGCAGTGGGCG	40140	ACATTCGACCCACAATGGGCA
11495	TFDTRGS	25818	ACTTTTGATACTAGGGGGAGT	40141	ACATTCGACACAAGAGGAAGC
11496	TFGAISA	25819	ACGTTTGGTGCTATTTCTGCT	40142	ACATTCGGAGCAATCAGCGCA
11497	TFGSDGT	25820	ACTTTTGGGTCGGATGGTACT	40143	ACATTCGGAAGCGACGGAACA
11498	TFGTSIK	25821	ACGTTTGGTACGTCTATTAAG	40144	ACATTCGGAACAAGCATCAAA
11499	TFHAPSS	25822	ACGTTTCATGCGCCTAGTTCT	40145	ACATTCCACGCACCAAGCAGC
11500	TFHRTDN	25823	ACGTTTCATAGGACTGATAAT	40146	ACATTCCACAGAACAGACAAC
11501	TFKDPTV	25824	ACTTTTAAGGATCCTACGGTG	40147	ACATTCAAAGACCCAACAGTC
11502	TFKITGD	25825	ACGTTTAAGATTACTGGTGAT	40148	ACATTCAAAATCACAGGAGAC
11503	TFNGMNE	25826	ACGTTTAATGGGATGAATGAG	40149	ACATTCAACGGAATGAACGAA
11504	TFPLPRT	25827	ACGTTTCCGCTTCCTCGTACT	40150	ACATTCCCACTCCCAAGAACA
11505	TFPLSDW	25828	ACTTTTCCGCTGAGTGATTGG	40151	ACATTCCCACTCAGCGACTGG
11506	TFPTSGM	25829	ACTTTTCCTACGTCTGGGATG	40152	ACATTCCCAACAAGCGGAATG
11507	TFQPTSV	25830	ACTTTTCAGCCTACTTCTGTT	40153	ACATTCCAACCAACAAGCGTC
11508	TFRGMKD	25831	ACTTTTCGGGGTATGAAGGAT	40154	ACATTCAGAGGAATGAAAGAC
11509	TFRTSVA	25832	ACTTTTCGGACGTCTGTTGCG	40155	ACATTCAGAACAAGCGTCGCA

11510	TFSIVSP	25833	ACTTTTAGTATTGTTAGTCCT	40156	ACATTCAGCATCGTCAGCCCA
11511	TFSPPNF	25834	ACTTTTTCGCCGCCTAATTTT	40157	ACATTCAGCCCACCAAACTTC
11512	TFSPTFS	25835	ACGTTTTCTCCGACTTTTTCG	40158	ACATTCAGCCCAACATTCAGC
11513	TFSSTSH	25836	ACTTTTAGTAGTACGTCGCAT	40159	ACATTCAGCAGCACAAGCCAC
11514	TFSSVAA	25837	ACTTTTAGTTCTGTGGCTGCG	40160	ACATTCAGCAGCGTCGCAGCA
11515	TFSSVTG	25838	ACTTTTTCTAGTGTTACGGGT	40161	ACATTCAGCAGCGTCACAGGA
11516	TFSTGRV	25839	ACGTTTAGTACGGGTCGTGTG	40162	ACATTCAGCACAGGAAGAGTC
11517	TFSTGSP	25840	ACTTTTTCTACTGGTTCGCCT	40163	ACATTCAGCACAGGAAGCCCA
11518	TFSTNTS	25841	ACTTTTTCGACTAATACTTCG	40164	ACATTCAGCACAAACACAAGC
11519	TFSVSQI	25842	ACGTTTTCTGTGTCGCAGATT	40165	ACATTCAGCGTCAGCCAAATC
11520	TFTNPTN	25843	ACGTTTACTAATCCTACGAAT	40166	ACATTCACAAACCCAACAAAC
11521	TFTQLAS	25844	ACTTTTACTCAGTTGGCTAGT	40167	ACATTCACACAACTCGCAAGC
11522	TFVREVV	25845	ACGTTTGTTCGTGAGGTGGTT	40168	ACATTCGTCAGAGAAGTCGTC
11523	TFVSGGD	25846	ACTTTTGTGAGTGGGGGTGAT	40169	ACATTCGTCAGCGGAGGAGAC
11524	TGAGQTL	25847	ACGGGGGCTGGTCAGACTCTG	40170	ACAGGAGCAGGACAAACACTC
11525	TGAHVGE	25848	ACGGGTGCGCATGTGGGTGAG	40171	ACAGGAGCACACGTCGGAGAA
11526	TGALATL	25849	ACGGGGGCGCTTGCTACTCTG	40172	ACAGGAGCACTCGCAACACTC
11527	TGAPPQI	25850	ACGGGGGCGCCTCCTCAGATT	40173	ACAGGAGCACCACCACAAATC
11528	TGASVLF	25851	ACTGGTGCGTCGGTGCTGTTT	40174	ACAGGAGCAAGCGTCCTCTTC
11529	TGAVFTP	25852	ACTGGTGCTGTTTTTACTCCG	40175	ACAGGAGCAGTCTTCACACCA
11530	TGDATPF	25853	ACTGGTGATGCGACTCCTTTT	40176	ACAGGAGACGCAACACCATTC
11531	TGDQKWH	25854	ACGGGTGATCAGAAGTGGCAT	40177	ACAGGAGACCAAAAATGGCAC
11532	TGDQNRY	25855	ACTGGTGATCAGAATCGGTAT	40178	ACAGGAGACCAAAACAGATAC
11533	TGDTSRT	25856	ACTGGTGATACTTCTCGTACG	40179	ACAGGAGACACAAGCAGAACA
11534	TGDVDGW	25857	ACGGGGGATGTGGATGGTTGG	40180	ACAGGAGACGTCGACGGATGG
11535	TGEQPGH	25858	ACTGGGGAGCAGCCGGGTCAT	40181	ACAGGAGAACAACCAGGACAC
11536	TGFSDQF	25859	ACTGGGTTTTCGGATCAGTTT	40182	ACAGGATTCAGCGACCAATTC
11537	TGGAQRG	25860	ACTGGGGGTGCGCAGCGTGGG	40183	ACAGGAGGAGCACAAAGAGGA
11538	TGGSPTS	25861	ACGGGTGGGTCTCCGACTTCT	40184	ACAGGAGGAAGCCCAACAAGC
11539	TGGSTRL	25862	ACTGGTGGGTCTACTCGTCTT	40185	ACAGGAGGAAGCACAAGACTC
11540	TGGYVLA	25863	ACGGGTGGGTATGTTCTGGCT	40186	ACAGGAGGATACGTCCTCGCA
11541	TGHAQNQ	25864	ACTGGGCATGCGCAGAATCAG	40187	ACAGGACACGCACAAAACCAA
11542	TGHDTVE	25865	ACTGGGCATGATACTGTTGAG	40188	ACAGGACACGACACAGTCGAA
11543	TGHTRLD	25866	ACGGGGCATACGAGGTTGGAT	40189	ACAGGACACACAAGACTCGAC
11544	TGHTSTL	25867	ACGGGGCATACGTCTACGCTT	40190	ACAGGACACACAAGCACACTC
11545	TGIAPNS	25868	ACTGGGATTGCGCCTAATTCT	40191	ACAGGAATCGCACCAAACAGC
11546	TGISSHM	25869	ACTGGTATTTCGTCGCATATG	40192	ACAGGAATCAGCAGCCACATG
11547	TGITGAP	25870	ACTGGGATTACGGGGGCTCCT	40193	ACAGGAATCACAGGAGCACCA
11548	TGKVLGF	25871	ACGGGTAAGGTTCTGGGTTTT	40194	ACAGGAAAAGTCCTCGGATTC
11549	TGLCPHP	25872	ACTGGGCTGTGTCCTCATCCT	40195	ACAGGACTCTGCCCACACCCA
11550	TGLGLLT	25873	ACTGGTCTGGGGCTTTTGACG	40196	ACAGGACTCGGACTCCTCACA
11551	TGLMGPV	25874	ACTGGTCTGATGGGTCCTGTG	40197	ACAGGACTCATGGGACCAGTC
11552	TGLNHFN	25875	ACGGGTCTTAATCATTTTAAT	40198	ACAGGACTCAACCACTTCAAC
11553	TGLNPAL	25876	ACGGGTCTGAATCCTGCGCTG	40199	ACAGGACTCAACCCAGCACTC
11554	TGLPVGF	25877	ACTGGGTTGCCTGTGGGGTTT	40200	ACAGGACTCCCAGTCGGATTC

11555	TGLRGTV	25878	ACTGGGCTTCGGGGTACGGTT	40201	ACAGGACTCAGAGGAACAGTC
11556	TGLVTDE	25879	ACGGGTCTTGTTACTGATGAG	40202	ACAGGACTCGTCACAGACGAA
11557	TGMNNFS	25880	ACGGGGATGAATAATTTTAGT	40203	ACAGGAATGAACAACTTCAGC
11558	TGMQAAL	25881	ACTGGGATGCAGGCTGCTCTG	40204	ACAGGAATGCAAGCAGCACTC
11559	TGNHIRI	25882	ACGGGGAATCATATTCGTATT	40205	ACAGGAAACCACATCAGAATC
11560	TGNHVTF	25883	ACTGGGAATCATGTTACTTTT	40206	ACAGGAAACCACGTCACATTC
11561	TGNISPL	25884	ACTGGGAATATTTCGCCGCTG	40207	ACAGGAAACATCAGCCCACTC
11562	TGNSPHA	25885	ACGGGGAATTCGCCGCATGCG	40208	ACAGGAAACAGCCCACACGCA
11563	TGPAPLD	25886	ACGGGTCCTGCTCCTTTGGAT	40209	ACAGGACCAGCACCACTCGAC
11564	TGPARGS	25887	ACTGGTCCGGCGCGTGGTTCG	40210	ACAGGACCAGCAAGAGGAAGC
11565	TGPDYPK	25888	ACTGGGCCTGATTATCCTAAG	40211	ACAGGACCAGACTACCCAAAA
11566	TGPHLKA	25889	ACTGGGCCTCATTTGAAGGCG	40212	ACAGGACCACACCTCAAAGCA
11567	TGPINAP	25890	ACTGGGCCTATTAATGCTCCG	40213	ACAGGACCAATCAACGCACCA
11568	TGPNTST	25891	ACTGGGCCGAATACGTCGACG	40214	ACAGGACCAAACACAAGCACA
11569	TGPPTTM	25892	ACGGGTCCTCCTACTACGATG	40215	ACAGGACCACCAACAACAATG
11570	TGPRLST	25893	ACGGGGCCGCGTCTTAGTACG	40216	ACAGGACCAAGACTCAGCACA
11571	TGPSARA	25894	ACTGGTCCGAGTGCGCGGGCT	40217	ACAGGACCAAGCGCAAGAGCA
11572	TGPSIHT	25895	ACGGGGCCGTCTATTCATACT	40218	ACAGGACCAAGCATCCACACA
11573	TGPSLDR	25896	ACGGGGCCTTCTTTGGATCGT	40219	ACAGGACCAAGCCTCGACAGA
11574	TGPSRTS	25897	ACTGGTCCGTCGCGGACGTCG	40220	ACAGGACCAAGCAGAACAAGC
11575	TGQGNAD	25898	ACGGGTCAGGGTAATGCGGAT	40221	ACAGGACAAGGAAACGCAGAC
11576	TGQRAGQ	25899	ACTGGTCAGAGGGCGGGTCAG	40222	ACAGGACAAAGAGCAGGACAA
11577	TGQRMDL	25900	ACTGGTCAGAGGATGGATCTG	40223	ACAGGACAAAGAATGGACCTC
11578	TGQRQNV	25901	ACGGGGCAGCGTCAGAATGTT	40224	ACAGGACAAAGACAAAACGTC
11579	TGRPVGN	25902	ACTGGGCGGCCTGTTGGTAAT	40225	ACAGGAAGACCAGTCGGAAAC
11580	TGRVAGS	25903	ACTGGTCGGGTTGCTGGGAGT	40226	ACAGGAAGAGTCGCAGGAAGC
11581	TGSAGEK	25904	ACTGGTTCTGCTGGGGAGAAG	40227	ACAGGAAGCGCAGGAGAAAAA
11582	TGSAHVS	25905	ACTGGTTCTGCGCATGTTTCG	40228	ACAGGAAGCGCACACGTCAGC
11583	TGSAMRP	25906	ACTGGTTCTGCTATGCGTCCG	40229	ACAGGAAGCGCAATGAGACCA
11584	TGSGHGP	25907	ACGGGGTCGGGGCATGGTCCT	40230	ACAGGAAGCGGACACGGACCA
11585	TGSKPGS	25908	ACTGGTTCGAAGCCTGGGTCG	40231	ACAGGAAGCAAACCAGGAAGC
11586	TGSLQYD	25909	ACGGGGTCGCTGCAGTATGAT	40232	ACAGGAAGCCTCCAATACGAC
11587	TGSSGFL	25910	ACTGGTTCGTCGGGGTTTCTT	40233	ACAGGAAGCAGCGGATTCCTC
11588	TGSSVRA	25911	ACGGGGTCTAGTGTTCGGGCG	40234	ACAGGAAGCAGCGTCAGAGCA
11589	TGTGRIH	25912	ACTGGGACTGGGCGTATTCAT	40235	ACAGGAACAGGAAGAATCCAC
11590	TGTSSWV	25913	ACGGGGACTTCGTCTTGGGTG	40236	ACAGGAACAAGCAGCTGGGTC
11591	TGTTLHP	25914	ACTGGGACGACTTTGCATCCT	40237	ACAGGAACAACACTCCACCCA
11592	TGVPRGF	25915	ACTGGGGTTCCGCGGGGTTTT	40238	ACAGGAGTCCCAAGAGGATTC
11593	TGVPRPY	25916	ACGGGTGTGCCTCGGCCTTAT	40239	ACAGGAGTCCCAAGACCATAC
11594	TGVPVDA	25917	ACTGGGGTGCCGGTGGATGCG	40240	ACAGGAGTCCCAGTCGACGCA
11595	TGYEFKL	25918	ACGGGGTATGAGTTTAAGTTG	40241	ACAGGATACGAATTCAAACTC
11596	TGYKSPN	25919	ACTGGTTATAAGAGTCCGAAT	40242	ACAGGATACAAAAGCCCAAAC
11597	THAAADF	25920	ACGCATGCTGCTGCGGATTTT	40243	ACACACGCAGCAGCAGACTTC
11598	THAIIVT	25921	ACTCATGCTATTATTGTGACG	40244	ACACACGCAATCATCGTCACA
11599	THAQTSV	25922	ACGCATGCGCAGACGTCTGTT	40245	ACACACGCACAAACAAGCGTC

11600	THDEDRR	25923	ACTCATGATGAGGATCGGAGG	40246	ACACACGACGAAGACAGAAGA
11601	THDHADS	25924	ACTCATGATCATGCTGATTCT	40247	ACACACGACCACGCAGACAGC
11602	THDLSLA	25925	ACGCATGATCTGTCGCTTGCT	40248	ACACACGACCTCAGCCTCGCA
11603	THDPRHG	25926	ACTCATGATCCGAGGCATGGG	40249	ACACACGACCCAAGACACGGA
11604	THEHYSH	25927	ACTCATGAGCATTATTCGCAT	40250	ACACACGAACACTACAGCCAC
11605	THEPRRA	25928	ACTCATGAGCCGAGGCGGGCG	40251	ACACACGAACCAAGAAGAGCA
11606	THESAAA	25929	ACGCATGAGAGTGCTGCGGCG	40252	ACACACGAAAGCGCAGCAGCA
11607	THFPGLP	25930	ACGCATTTTCCTGGTCTTCCG	40253	ACACACTTCCCAGGACTCCCA
11608	THGRLPN	25931	ACGCATGGGCGTCTTCCGAAT	40254	ACACACGGAAGACTCCCAAAC
11609	THHAALT	25932	ACTCATCATGCTGCGTTGACT	40255	ACACACCACGCAGCACTCACA
11610	THHSGSI	25933	ACGCATCATTCGGGTTCGATT	40256	ACACACCACAGCGGAAGCATC
11611	THHVTQT	25934	ACGCATCATGTGACTCAGACT	40257	ACACACCACGTCACACAAACA
11612	THIPSRP	25935	ACGCATATTCCTTCGAGGCCG	40258	ACACACATCCCAAGCAGACCA
11613	THIRSAQ	25936	ACGCATATTCGTTCGGCGCAG	40259	ACACACATCAGAAGCGCACAA
11614	THKETHM	25937	ACGCATAAGGAGACTCATATG	40260	ACACACAAAGAAACACACATG
11615	THKFPTS	25938	ACGCATAAGTTTCCGACGTCT	40261	ACACACAAATTCCCAACAAGC
11616	THKLTAE	25939	ACGCATAAGCTGACTGCTGAG	40262	ACACACAAACTCACAGCAGAA
11617	THKSISN	25940	ACTCATAAGTCTATTTCGAAT	40263	ACACACAAAAGCATCAGCAAC
11618	THLASSD	25941	ACTCATCTGGCTAGTTCGGAT	40264	ACACACCTCGCAAGCAGCGAC
11619	THLGESV	25942	ACGCATCTTGGTGAGTCGGTG	40265	ACACACCTCGGAGAAAGCGTC
11620	THLSNTL	25943	ACGCATCTGTCTAATACTCTT	40266	ACACACCTCAGCAACACACTC
11621	THLSTAK	25944	ACTCATTTGTCTACGGCTAAG	40267	ACACACCTCAGCACAGCAAAA
11622	THLSTPS	25945	ACTCATTTGTCTACGCCGTCT	40268	ACACACCTCAGCACACCAAGC
11623	THMIGNT	25946	ACTCATATGATTGGTAATACT	40269	ACACACATGATCGGAAACACA
11624	THNALTV	25947	ACGCATAATGCGCTTACTGTG	40270	ACACACAACGCACTCACAGTC
11625	THNLSIR	25948	ACTCATAATTTGTCTATTCGG	40271	ACACACAACCTCAGCATCAGA
11626	THPAVTQ	25949	ACTCATCCTGCGGTTACGCAG	40272	ACACACCCAGCAGTCACACAA
11627	THPDRGL	25950	ACTCATCCTGATCGTGGTCTG	40273	ACACACCCAGACAGAGGACTC
11628	THPKPTL	25951	ACTCATCCTAAGCCGACGTTG	40274	ACACACCCAAAACCAACACTC
11629	THPQSVD	25952	ACGCATCCGCAGAGTGTTGAT	40275	ACACACCCACAAAGCGTCGAC
11630	THPSVPV	25953	ACTCATCCTTCGGTTCCTGTT	40276	ACACACCCAAGCGTCCCAGTC
11631	THPVGIL	25954	ACGCATCCGGTTGGGATTTTG	40277	ACACACCCAGTCGGAATCCTC
11632	THPVSSV	25955	ACGCATCCTGTTAGTTCGGTT	40278	ACACACCCAGTCAGCAGCGTC
11633	THQTSVY	25956	ACTCATCAGACGTCTGTTTAT	40279	ACACACCAAACAAGCGTCTAC
11634	THQVPSV	25957	ACTCATCAGGTTCCTAGTGTG	40280	ACACACCAAGTCCCAAGCGTC
11635	THRDGIM	25958	ACTCATAGGGATGGTATTATG	40281	ACACACAGAGACGGAATCATG
11636	THRQDTS	25959	ACGCATAGGCAGGATACGTCG	40282	ACACACAGACAAGACACAAGC
11637	THRSLDV	25960	ACTCATCGGTCTCTGGATGTT	40283	ACACACAGAAGCCTCGACGTC
11638	THRSQTV	25961	ACGCATCGGAGTCAGACGGTT	40284	ACACACAGAAGCCAAACAGTC
11639	THSAYNH	25962	ACTCATTCGGCGTATAATCAT	40285	ACACACAGCGCATACAACCAC
11640	THSESSK	25963	ACTCATTCTGAGTCTTCTAAG	40286	ACACACAGCGAAAGCAGCAAA
11641	THSGANN	25964	ACTCATTCTGGTGCTAATAAT	40287	ACACACAGCGGAGCAAACAAC
11642	THSHVDD	25965	ACTCATTCGCATGTTGATGAT	40288	ACACACAGCCACGTCGACGAC
11643	THSMVMP	25966	ACGCATTCTATGGTGATGCCT	40289	ACACACAGCATGGTCATGCCA
11644	THSPLTR	25967	ACGCATAGTCCTTTGACTCGT	40290	ACACACAGCCCACTCACAAGA

11645	THTLNTR	25968	ACTCATACGTTGAATACTAGG	40291	ACACACACACTCAACACAAGA
11646	THTPLPA	25969	ACGCATACGCCTCTGCCTGCT	40292	ACACACACACCACTCCCAGCA
11647	THTRTLM	25970	ACGCATACTCGTACTCTTATG	40293	ACACACACAAGAACACTCATG
11648	THTSAAE	25971	ACTCATACGTCTGCTGCGGAG	40294	ACACACACAAGCGCAGCAGAA
11649	THTVGTQ	25972	ACGCATACGGTTGGTACTCAG	40295	ACACACACAGTCGGAACACAA
11650	THVAEVT	25973	ACTCATGTTGCTGAGGTTACG	40296	ACACACGTCGCAGAAGTCACA
11651	THVPPMR	25974	ACGCATGTTCCGCCTATGCGG	40297	ACACACGTCCCACCAATGAGA
11652	THYDVVM	25975	ACTCATTATGATGTGGTTATG	40298	ACACACTACGACGTCGTCATG
11653	TIADDQK	25976	ACTATTGCTGATGATCAGAAG	40299	ACAATCGCAGACGACCAAAAA
11654	TIADMRT	25977	ACGATTGCTGATATGCGTACG	40300	ACAATCGCAGACATGAGAACA
11655	TICNDGP	25978	ACGATTTGTAATGATGGGCCT	40301	ACAATCTGCAACGACGGACCA
11656	TIDPPLT	25979	ACGATTGATCCGCCTCTGACT	40302	ACAATCGACCCACCACTCACA
11657	TIDTTSL	25980	ACGATTGATACGACGTCGTTG	40303	ACAATCGACACAACAAGCCTC
11658	TIEQRER	25981	ACTATTGAGCAGCGGGAGCGT	40304	ACAATCGAACAAAGAGAAAGA
11659	TIESPGV	25982	ACTATTGAGTCGCCGGGTGTG	40305	ACAATCGAAAGCCCAGGAGTC
11660	TIGHESY	25983	ACGATTGGTCATGAGAGTTAT	40306	ACAATCGGACACGAAAGCTAC
11661	TIGRLMQ	25984	ACGATTGGGAGGCTTATGCAG	40307	ACAATCGGAAGACTCATGCAA
11662	TIGSVRL	25985	ACTATTGGGTCTGTTAGGCTG	40308	ACAATCGGAAGCGTCAGACTC
11663	TIHRPDM	25986	ACTATTCATCGGCCTGATATG	40309	ACAATCCACAGACCAGACATG
11664	TIIPSKL	25987	ACTATTATTCCGTCTAAGCTT	40310	ACAATCATCCCAAGCAAACTC
11665	TIIRKDS	25988	ACGATTATTCGTAAGGATTCT	40311	ACAATCATCAGAAAAGACAGC
11666	TIKAQVS	25989	ACGATTAAGGCTCAGGTGAGT	40312	ACAATCAAAGCACAAGTCAGC
11667	TIKLNVG	25990	ACTATTAAGCTTAATGTTGGG	40313	ACAATCAAACTCAACGTCGGA
11668	TIKPLSQ	25991	ACTATTAAGCCGCTTTCTCAG	40314	ACAATCAAACCACTCAGCCAA
11669	TILNPNN	25992	ACGATTCTGAATCCTAATAAT	40315	ACAATCCTCAACCCAAACAAC
11670	TILRTEE	25993	ACGATTCTTCGGACTGAGGAG	40316	ACAATCCTCAGAACAGAAGAA
11671	TILSSHG	25994	ACTATTCTTTCGAGTCATGGG	40317	ACAATCCTCAGCAGCCACGGA
11672	TILSTGS	25995	ACGATTCTGAGTACGGGGTCG	40318	ACAATCCTCAGCACAGGAAGC
11673	TINHAEQ	25996	ACTATTAATCATGCGGAGCAG	40319	ACAATCAACCACGCAGAACAA
11674	TINWVGD	25997	ACTATTAATTGGGTGGGGGAT	40320	ACAATCAACTGGGTCGGAGAC
11675	TIPSQIA	25998	ACTATTCCGTCTCAGATTGCT	40321	ACAATCCCAAGCCAAATCGCA
11676	TIQLRSA	25999	ACGATTCAGCTTCGTTCTGCT	40322	ACAATCCAACTCAGAAGCGCA
11677	TIREAFT	26000	ACGATTCGTGAGGCTTTTACT	40323	ACAATCAGAGAAGCATTCACA
11678	TIRGSFL	26001	ACTATTCGTGGGAGTTTTCTT	40324	ACAATCAGAGGAAGCTTCCTC
11679	TIRGTIS	26002	ACGATTCGTGGTACTATTAGT	40325	ACAATCAGAGGAACAATCAGC
11680	TIRVNPT	26003	ACTATTCGGGTTAATCCGACG	40326	ACAATCAGAGTCAACCCAACA
11681	TIRVSLA	26004	ACTATTAGGGTTTCTCTTGCT	40327	ACAATCAGAGTCAGCCTCGCA
11682	TISNASS	26005	ACGATTTCTAATGCGAGTTCT	40328	ACAATCAGCAACGCAAGCAGC
11683	TISSSQS	26006	ACGATTTCGTCTTCTCAGAGT	40329	ACAATCAGCAGCAGCCAAAGC
11684	TISTSKH	26007	ACTATTAGTACGTCTAAGCAT	40330	ACAATCAGCACAAGCAAACAC
11685	TITAHDP	26008	ACGATTACTGCGCATGATCCT	40331	ACAATCACAGCACACGACCCA
11686	TITPRAD	26009	ACGATTACGCCTCGTGCTGAT	40332	ACAATCACACCAAGAGCAGAC
11687	TITSPKM	26010	ACTATTACTTCTCCTAAGATG	40333	ACAATCACAAGCCCAAAAATG
11688	TITYELT	26011	ACTATTACGTATGAGCTGACG	40334	ACAATCACATACGAACTCACA
11689	TIVRELT	26012	ACTATTGTGCGTGAGCTGACG	40335	ACAATCGTCAGAGAACTCACA

11690	TIVSDPR	26013	ACGATTGTTAGTGATCCGCGG	40336	ACAATCGTCAGCGACCCAAGA
11691	TIVSGVV	26014	ACTATTGTGTCTGGTGTTGTT	40337	ACAATCGTCAGCGGAGTCGTC
11692	TIVTGAS	26015	ACGATTGTTACGGGGGCTAGT	40338	ACAATCGTCACAGGAGCAAGC
11693	TIYYDVT	26016	ACGATTTATTATGATGTGACG	40339	ACAATCTACTACGACGTCACA
11694	TKAGSFH	26017	ACGAAGGCGGGTTCTTTTCAT	40340	ACAAAAGCAGGAAGCTTCCAC
11695	TKAHCCG	26018	ACGAAGGCTCATTGTTGTGGT	40341	ACAAAAGCACACTGCTGCGGA
11696	TKALVHM	26019	ACTAAGGCTCTGGTTCATATG	40342	ACAAAAGCACTCGTCCACATG
11697	TKDQVRL	26020	ACTAAGGATCAGGTTCGTTTG	40343	ACAAAAGACCAAGTCAGACTC
11698	TKDRPFL	26021	ACTAAGGATCGGCCGTTTCTG	40344	ACAAAAGACAGACCATTCCTC
11699	TKECMLT	26022	ACTAAGGAGTGTATGTTGACT	40345	ACAAAAGAATGCATGCTCACA
11700	TKGGFND	26023	ACTAAGGGTGGTTTTAATGAT	40346	ACAAAAGGAGGATTCAACGAC
11701	TKGGKQP	26024	ACGAAGGGGGGTAAGCAGCCG	40347	ACAAAAGGAGGAAAACAACCA
11702	TKGREPV	26025	ACTAAGGGTCGGGAGCCGGTG	40348	ACAAAAGGAAGAGAACCAGTC
11703	TKGVPGY	26026	ACGAAGGGTGTTCCTGGGTAT	40349	ACAAAAGGAGTCCCAGGATAC
11704	TKHLMPA	26027	ACGAAGCATCTTATGCCGGCG	40350	ACAAAACACCTCATGCCAGCA
11705	TKIAGFS	26028	ACGAAGATTGCTGGTTTTTCG	40351	ACAAAAATCGCAGGATTCAGC
11706	TKIGSAM	26029	ACGAAGATTGGGAGTGCTATG	40352	ACAAAAATCGGAAGCGCAATG
11707	TKLNAFD	26030	ACGAAGTTGAATGCGTTTGAT	40353	ACAAAACTCAACGCATTCGAC
11708	TKLPNSS	26031	ACTAAGCTTCCGAATTCTAGT	40354	ACAAAACTCCCAAACAGCAGC
11709	TKLQASL	26032	ACTAAGCTTCAGGCTTCGCTT	40355	ACAAAACTCCAAGCAAGCCTC
11710	TKLVTES	26033	ACTAAGTTGGTGACTGAGAGT	40356	ACAAAACTCGTCACAGAAAGC
11711	TKMNASG	26034	ACGAAGATGAATGCTTCTGGG	40357	ACAAAAATGAACGCAAGCGGA
11712	TKNLDHT	26035	ACTAAGAATCTTGATCATACG	40358	ACAAAAAACCTCGACCACACA
11713	TKNLTER	26036	ACGAAGAATCTTACGGAGCGT	40359	ACAAAAAACCTCACAGAAAGA
11714	TKNRMDL	26037	ACTAAGAATAGGATGGATCTT	40360	ACAAAAAACAGAATGGACCTC
11715	TKPGSIF	26038	ACTAAGCCTGGTTCGATTTTT	40361	ACAAAACCAGGAAGCATCTTC
11716	TKPPVQS	26039	ACTAAGCCGCCTGTTCAGAGT	40362	ACAAAACCACCAGTCCAAAGC
11717	TKPQSSY	26040	ACTAAGCCGCAGAGTAGTTAT	40363	ACAAAACCACAAAGCAGCTAC
11718	TKRESHS	26041	ACTAAGCGTGAGTCGCATTCT	40364	ACAAAAAGAGAAAGCCACAGC
11719	TKSAATA	26042	ACGAAGTCGGCTGCTACGGCT	40365	ACAAAAAGCGCAGCAACAGCA
11720	TKSGLTQ	26043	ACGAAGAGTGGGTTGACGCAG	40366	ACAAAAAGCGGACTCACACAA
11721	TKSGNSL	26044	ACGAAGTCTGGTAATAGTCTG	40367	ACAAAAAGCGGAAACAGCCTC
11722	TKSQTHL	26045	ACTAAGAGTCAGACTCATCTG	40368	ACAAAAAGCCAAACACACCTC
11723	TKSSVLP	26046	ACTAAGTCGTCTGTTTTGCCT	40369	ACAAAAAGCAGCGTCCTCCCA
11724	TKSYSPN	26047	ACTAAGAGTTATTCTCCGAAT	40370	ACAAAAAGCTACAGCCCAAAC
11725	TKTGDGP	26048	ACGAAGACTGGTGATGGTCCT	40371	ACAAAAACAGGAGACGGACCA
11726	TKTSFPN	26049	ACTAAGACGTCGTTTCCTAAT	40372	ACAAAAACAAGCTTCCCAAAC
11727	TKVALDP	26050	ACTAAGGTTGCTCTGGATCCT	40373	ACAAAAGTCGCACTCGACCCA
11728	TKVAREV	26051	ACTAAGGTGGCTCGGGAGGTG	40374	ACAAAAGTCGCAAGAGAAGTC
11729	TLALYAS	26052	ACTCTTGCTTTGTATGCGTCT	40375	ACACTCGCACTCTACGCAAGC
11730	TLAPTTK	26053	ACGCTGGCTCCGACTACTAAG	40376	ACACTCGCACCAACAACAAAA
11731	TLASGRA	26054	ACTCTGGCGTCTGGGAGGGCT	40377	ACACTCGCAAGCGGAAGAGCA
11732	TLASRSV	26055	ACTCTGGCGTCTCGTAGTGTT	40378	ACACTCGCAAGCAGAAGCGTC
11733	TLATSSN	26056	ACTTTGGCTACGTCTTCTAAT	40379	ACACTCGCAACAAGCAGCAAC
11734	TLAVNSM	26057	ACTTTGGCGGTGAATTCGATG	40380	ACACTCGCAGTCAACAGCATG

11735	TLDMTSV	26058	ACGCTTGATATGACGAGTGTG	40381	ACACTCGACATGACAAGCGTC
11736	TLDNSRA	26059	ACTCTGGATAATTCTCGTGCT	40382	ACACTCGACAACAGCAGAGCA
11737	TLDVHYV	26060	ACTTTGGATGTTCATTATGTG	40383	ACACTCGACGTCCACTACGTC
11738	TLEAQTD	26061	ACTCTGGAGGCTCAGACTGAT	40384	ACACTCGAAGCACAAACAGAC
11739	TLEHTCR	26062	ACTCTGGAGCATACTTGTCGG	40385	ACACTCGAACACACATGCAGA
11740	TLEPRKD	26063	ACGCTTGAGCCTCGGAAGGAT	40386	ACACTCGAACCAAGAAAAGAC
11741	TLEQFGS	26064	ACTTTGGAGCAGTTTGGTAGT	40387	ACACTCGAACAATTCGGAAGC
11742	TLEQYKL	26065	ACGCTGGAGCAGTATAAGCTG	40388	ACACTCGAACAATACAAACTC
11743	TLERKLD	26066	ACGTTGGAGAGGAAGCTGGAT	40389	ACACTCGAAAGAAAACTCGAC
11744	TLERPFI	26067	ACTCTGGAGCGGCCGTTTATT	40390	ACACTCGAAAGACCATTCATC
11745	TLFNSEK	26068	ACGCTGTTTAATAGTGAGAAG	40391	ACACTCTTCAACAGCGAAAAA
11746	TLFQQPP	26069	ACGCTTTTTCAGCAGCCTCCT	40392	ACACTCTTCCAACAACCACCA
11747	TLFRDGS	26070	ACTCTTTTTCGGGATGGTTCG	40393	ACACTCTTCAGAGACGGAAGC
11748	TLGGSPV	26071	ACGTTGGGGGGTTCTCCGGTT	40394	ACACTCGGAGGAAGCCCAGTC
11749	TLGGSRA	26072	ACTTTGGGTGGGAGTCGGGCT	40395	ACACTCGGAGGAAGCAGAGCA
11750	TLGHAFA	26073	ACTTTGGGGCATGCTTTTGCT	40396	ACACTCGGACACGCATTCGCA
11751	TLGHVPP	26074	ACTTTGGGTCATGTTCCGCCG	40397	ACACTCGGACACGTCCCACCA
11752	TLGITAH	26075	ACGCTTGGTATTACGGCTCAT	40398	ACACTCGGAATCACAGCACAC
11753	TLGIVTQ	26076	ACGTTGGGGATTGTGACGCAG	40399	ACACTCGGAATCGTCACACAA
11754	TLGLTMP	26077	ACGCTGGGTCTGACGATGCCG	40400	ACACTCGGACTCACAATGCCA
11755	TLGPNSR	26078	ACGTTGGGTCCTAATTCTCGG	40401	ACACTCGGACCAAACAGCAGA
11756	TLGQTTG	26079	ACTCTGGGGCAGACGACGGGG	40402	ACACTCGGACAAACAACAGGA
11757	TLHQIPA	26080	ACGTTGCATCAGATTCCGGCG	40403	ACACTCCACCAAATCCCAGCA
11758	TLHSSSS	26081	ACTTTGCATAGTAGTAGTTCT	40404	ACACTCCACAGCAGCAGCAGC
11759	TLIGNDT	26082	ACGCTGATTGGTAATGATACG	40405	ACACTCATCGGAAACGACACA
11760	TLISSVT	26083	ACGCTTATTTCTTCTGTTACG	40406	ACACTCATCAGCAGCGTCACA
11761	TLKAEDL	26084	ACGTTGAAGGCTGAGGATCTT	40407	ACACTCAAAGCAGAAGACCTC
11762	TLKGPGQ	26085	ACTCTTAAGGGTCCTGGTCAG	40408	ACACTCAAAGGACCAGGACAA
11763	TLKRGLD	26086	ACGCTTAAGCGGGGTCTGGAT	40409	ACACTCAAAAGAGGACTCGAC
11764	TLKSNAK	26087	ACGTTGAAGTCGAATGCGAAG	40410	ACACTCAAAAGCAACGCAAAA
11765	TLLPASP	26088	ACGCTTCTGCCTGCGAGTCCT	40411	ACACTCCTCCCAGCAAGCCCA
11766	TLLPGDP	26089	ACGCTTTTGCCGGGTGATCCG	40412	ACACTCCTCCCAGGAGACCCA
11767	TLLPHPT	26090	ACTCTGCTTCCGCATCCTACG	40413	ACACTCCTCCCACACCCAACA
11768	TLLTDDL	26091	ACGTTGTTGACTGATGATCTT	40414	ACACTCCTCACAGACGACCTC
11769	TLMQVSG	26092	ACTTTGATGCAGGTTTCGGGG	40415	ACACTCATGCAAGTCAGCGGA
11770	TLMRGAS	26093	ACGCTGATGCGTGGTGCTTCT	40416	ACACTCATGAGAGGAGCAAGC
11771	TLNSAKK	26094	ACTCTGAATTCGGCGAAGAAG	40417	ACACTCAACAGCGCAAAAAAA
11772	TLNSERM	26095	ACGCTTAATAGTGAGCGGATG	40418	ACACTCAACAGCGAAAGAATG
11773	TLPHRVA	26096	ACTTTGCCGCATCGGGTGGCG	40419	ACACTCCCACACAGAGTCGCA
11774	TLPHSPK	26097	ACGCTTCCTCATAGTCCTAAG	40420	ACACTCCCACACAGCCCAAAA
11775	TLPKTNL	26098	ACGTTGCCGAAGACGAATCTG	40421	ACACTCCCAAAAACAAACCTC
11776	TLPLTST	26099	ACTCTTCCTTTGACTTCTACG	40422	ACACTCCCACTCACAAGCACA
11777	TLPNYLA	26100	ACTCTTCCTAATTATCTGGCT	40423	ACACTCCCAAACTACCTCGCA
11778	TLPPNSP	26101	ACGCTGCCGCCGAATTCGCCT	40424	ACACTCCCACCAAACAGCCCA
11779	TLPSERV	26102	ACGTTGCCTTCGGAGCGTGTG	40425	ACACTCCCAAGCGAAAGAGTC

11780	TLPTTLV	26103	ACGTTGCCTACGACGCTGGTT	40426	ACACTCCCAACAACACTCGTC
11781	TLPVNNL	26104	ACTTTGCCGGTGAATAATTTG	40427	ACACTCCCAGTCAACAACCTC
11782	TLQDNRA	26105	ACTTTGCAGGATAATCGTGCT	40428	ACACTCCAAGACAACAGAGCA
11783	TLQEGTG	26106	ACGCTTCAGGAGGGGACTGGG	40429	ACACTCCAAGAAGGAACAGGA
11784	TLQFGAG	26107	ACGCTTCAGTTTGGTGCTGGG	40430	ACACTCCAATTCGGAGCAGGA
11785	TLQGGSL	26108	ACTCTGCAGGGTGGGTCTCTT	40431	ACACTCCAAGGAGGAAGCCTC
11786	TLQPLRI	26109	ACGTTGCAGCCGTTGCGTATT	40432	ACACTCCAACCACTCAGAATC
11787	TLRDTAD	26110	ACGCTTCGGGATACTGCTGAT	40433	ACACTCAGAGACACAGCAGAC
11788	TLRESDT	26111	ACTCTGCGTGAGTCTGATACG	40434	ACACTCAGAGAAAGCGACACA
11789	TLRGAED	26112	ACGTTGCGTGGTGCTGAGGAT	40435	ACACTCAGAGGAGCAGAAGAC
11790	TLRLTAG	26113	ACGTTGAGGCTTACTGCTGGG	40436	ACACTCAGACTCACAGCAGGA
11791	TLRMQLN	26114	ACGCTGCGTATGCAGCTGAAT	40437	ACACTCAGAATGCAACTCAAC
11792	TLRNSPA	26115	ACTCTGCGGAATTCTCCGGCT	40438	ACACTCAGAAACAGCCCAGCA
11793	TLRPLQA	26116	ACGTTGCGGCCTTTGCAGGCT	40439	ACACTCAGACCACTCCAAGCA
11794	TLRSAGP	26117	ACGCTGCGTTCTGCGGGTCCT	40440	ACACTCAGAAGCGCAGGACCA
11795	TLRTLAE	26118	ACTCTTCGGACGCTTGCGGAG	40441	ACACTCAGAACACTCGCAGAA
11796	TLSALPP	26119	ACGCTGAGTGCGCTTCCTCCT	40442	ACACTCAGCGCACTCCCACCA
11797	TLSDRPP	26120	ACTTTGTCGGATCGTCCGCCT	40443	ACACTCAGCGACAGACCACCA
11798	TLSDSVD	26121	ACGCTGTCGGATTCTGTTGAT	40444	ACACTCAGCGACAGCGTCGAC
11799	TLSENLP	26122	ACTCTTAGTGAGAATTTGCCG	40445	ACACTCAGCGAAAACCTCCCA
11800	TLSHLPY	26123	ACGCTTTCGCATCTTCCGTAT	40446	ACACTCAGCCACCTCCCATAC
11801	TLSHNAP	26124	ACTCTGAGTCATAATGCTCCT	40447	ACACTCAGCCACAACGCACCA
11802	TLSHRLP	26125	ACGCTGTCTCATCGTCTTCCG	40448	ACACTCAGCCACAGACTCCCA
11803	TLSKHLL	26126	ACTCTGTCTAAGCATCTGCTG	40449	ACACTCAGCAAACACCTCCTC
11804	TLSKPPS	26127	ACTTTGTCTAAGCCGCCGTCG	40450	ACACTCAGCAAACCACCAAGC
11805	TLSLSAI	26128	ACGCTGTCTCTTTCTGCGATT	40451	ACACTCAGCCTCAGCGCAATC
11806	TLSLSNN	26129	ACTCTGTCTCTTAGTAATAAT	40452	ACACTCAGCCTCAGCAACAAC
11807	TLSLSTG	26130	ACTTTGAGTCTTTCGACGGGG	40453	ACACTCAGCCTCAGCACAGGA
11808	TLSNSVP	26131	ACTCTTAGTAATTCTGTTCCG	40454	ACACTCAGCAACAGCGTCCCA
11809	TLSPKSV	26132	ACTCTTTCTCCGAAGTCTGTG	40455	ACACTCAGCCCAAAAAGCGTC
11810	TLSPSGS	26133	ACGCTTTCTCCGTCTGGTAGT	40456	ACACTCAGCCCAAGCGGAAGC
11811	TLSPTTS	26134	ACTCTTTCGCCGACGACGAGT	40457	ACACTCAGCCCAACAACAAGC
11812	TLSQRPP	26135	ACTCTTAGTCAGCGTCCGCCT	40458	ACACTCAGCCAAAGACCACCA
11813	TLSQSTH	26136	ACGCTGAGTCAGTCTACTCAT	40459	ACACTCAGCCAAAGCACACAC
11814	TLSRTLE	26137	ACGCTGTCGCGTACTTTGGAG	40460	ACACTCAGCAGAACACTCGAA
11815	TLSSGQT	26138	ACTCTTTCGAGTGGTCAGACG	40461	ACACTCAGCAGCGGACAAACA
11816	TLSSRPM	26139	ACTCTTAGTTCGCGTCCTATG	40462	ACACTCAGCAGCAGACCAATG
11817	TLSSRQS	26140	ACTTTGAGTTCGCGTCAGAGT	40463	ACACTCAGCAGCAGACAAAGC
11818	TLSTVSL	26141	ACTCTTTCTACTGTGAGTCTG	40464	ACACTCAGCACAGTCAGCCTC
11819	TLSYTPA	26142	ACGTTGAGTTATACGCCGGCT	40465	ACACTCAGCTACACACCAGCA
11820	TLTFRGD	26143	ACTCTGACTTTTCGGGGGGAT	40466	ACACTCACATTCAGAGGAGAC
11821	TLTKNST	26144	ACGTTGACTAAGAATAGTACG	40467	ACACTCACAAAAAACAGCACA
11822	TLTPLYE	26145	ACGCTGACTCCGTTGTATGAG	40468	ACACTCACACCACTCTACGAA
11823	TLTPNES	26146	ACTTTGACGCCGAATGAGAGT	40469	ACACTCACACCAAACGAAAGC
11824	TLTRLSP	26147	ACGTTGACGCGTCTTTCGCCT	40470	ACACTCACAAGACTCAGCCCA

11825	TLTRMNV	26148	ACGCTGACGAGGATGAATGTG	40471	ACACTCACAAGAATGAACGTC
11826	TLTTNVS	26149	ACTCTGACTACTAATGTTTCT	40472	ACACTCACAACAAACGTCAGC
11827	TLTTPMN	26150	ACGCTGACTACTCCTATGAAT	40473	ACACTCACAACACCAATGAAC
11828	TLTVLDP	26151	ACTCTTACTGTGCTTGATCCT	40474	ACACTCACAGTCCTCGACCCA
11829	TLTYHRD	26152	ACGTTGACGTATCATCGTGAT	40475	ACACTCACATACCACAGAGAC
11830	TLVGHYY	26153	ACTTTGGTGGGTCATTATTAT	40476	ACACTCGTCGGACACTACTAC
11831	TLVGPAS	26154	ACTCTTGTGGGTCCGGCTAGT	40477	ACACTCGTCGGACCAGCAAGC
11832	TLVPRDL	26155	ACGCTGGTTCCGCGGGATCTG	40478	ACACTCGTCCCAAGAGACCTC
11833	TLVQAEM	26156	ACGTTGGTTCAGGCGGAGATG	40479	ACACTCGTCCAAGCAGAAATG
11834	TLVTREN	26157	ACTCTGGTTACTAGGGAGAAT	40480	ACACTCGTCACAAGAGAAAAC
11835	TLVVRSP	26158	ACTCTTGTTGTGCGGTCGCCT	40481	ACACTCGTCGTCAGAAGCCCA
11836	TLYGHPS	26159	ACTCTGTATGGTCATCCGTCG	40482	ACACTCTACGGACACCCAAGC
11837	TLYLHSE	26160	ACGCTGTATCTTCATTCTGAG	40483	ACACTCTACCTCCACAGCGAA
11838	TLYNTTM	26161	ACTCTTTATAATACGACTATG	40484	ACACTCTACAACACAACAATG
11839	TLYRVNP	26162	ACTCTGTATCGTGTTAATCCG	40485	ACACTCTACAGAGTCAACCCA
11840	TLYSQSE	26163	ACGTTGTATTCTCAGTCTGAG	40486	ACACTCTACAGCCAAAGCGAA
11841	TLYTNSV	26164	ACTCTGTATACGAATTCGGTT	40487	ACACTCTACACAAACAGCGTC
11842	TMAMNPR	26165	ACTATGGCTATGAATCCTCGT	40488	ACAATGGCAATGAACCCAAGA
11843	TMAPRDL	26166	ACTATGGCTCCGCGGGATTTG	40489	ACAATGGCACCAAGAGACCTC
11844	TMDNLRQ	26167	ACGATGGATAATTTGAGGCAG	40490	ACAATGGACAACCTCAGACAA
11845	TMDRTPG	26168	ACTATGGATCGTACGCCGGGG	40491	ACAATGGACAGAACACCAGGA
11846	TMDVLSF	26169	ACTATGGATGTGTTGTCTTTT	40492	ACAATGGACGTCCTCAGCTTC
11847	TMERGDS	26170	ACGATGGAGCGGGGTGATAGT	40493	ACAATGGAAAGAGGAGACAGC
11848	TMHAHPL	26171	ACGATGCATGCGCATCCGCTG	40494	ACAATGCACGCACACCCACTC
11849	TMLTRTG	26172	ACTATGCTTACTCGTACGGGG	40495	ACAATGCTCACAAGAACAGGA
11850	TMMKPLD	26173	ACTATGATGAAGCCTTTGGAT	40496	ACAATGATGAAACCACTCGAC
11851	TMNKPTL	26174	ACTATGAATAAGCCGACGCTT	40497	ACAATGAACAAACCAACACTC
11852	TMNLGEM	26175	ACTATGAATCTTGGGGAGATG	40498	ACAATGAACCTCGGAGAAATG
11853	TMNPTQN	26176	ACTATGAATCCTACGCAGAAT	40499	ACAATGAACCCAACACAAAAC
11854	TMNTLVT	26177	ACGATGAATACTTTGGTTACT	40500	ACAATGAACACACTCGTCACA
11855	TMPNHGP	26178	ACGATGCCTAATCATGGGCCT	40501	ACAATGCCAAACCACGGACCA
11856	TMPSESV	26179	ACTATGCCGAGTGAGTCGGTG	40502	ACAATGCCAAGCGAAAGCGTC
11857	TMQAPSA	26180	ACGATGCAGGCGCCGTCTGCG	40503	ACAATGCAAGCACCAAGCGCA
11858	TMQYGST	26181	ACGATGCAGTATGGGTCGACT	40504	ACAATGCAATACGGAAGCACA
11859	TMREGPA	26182	ACTATGCGGGAGGGGCCGGCT	40505	ACAATGAGAGAAGGACCAGCA
11860	TMRIDLP	26183	ACGATGCGGATTGATCTGCCT	40506	ACAATGAGAATCGACCTCCCA
11861	TMRSSEI	26184	ACTATGCGTAGTAGTGAGATT	40507	ACAATGAGAAGCAGCGAAATC
11862	TMRTNPD	26185	ACGATGCGTACGAATCCGGAT	40508	ACAATGAGAACAAACCCAGAC
11863	TMSGTSR	26186	ACTATGAGTGGGACTTCGAGG	40509	ACAATGAGCGGAACAAGCAGA
11864	TMSIALA	26187	ACGATGAGTATTGCGCTGGCT	40510	ACAATGAGCATCGCACTCGCA
11865	TMSKPSY	26188	ACGATGTCTAAGCCTTCTTAT	40511	ACAATGAGCAAACCAAGCTAC
11866	TMSMSIT	26189	ACTATGAGTATGAGTATTACT	40512	ACAATGAGCATGAGCATCACA
11867	TMSPGNN	26190	ACGATGTCTCCTGGGAATAAT	40513	ACAATGAGCCCAGGAAACAAC
11868	TMSPHSP	26191	ACTATGTCGCCTCATAGTCCG	40514	ACAATGAGCCCACACAGCCCA
11869	TMSPLNR	26192	ACGATGTCGCCGCTGAATAGG	40515	ACAATGAGCCCACTCAACAGA

11870	TMTHHQF	26193	ACGATGACGCATCATCAGTTT	40516	ACAATGACACACCACCAATTC
11871	TMTRSML	26194	ACGATGACTCGTTCTATGCTG	40517	ACAATGACAAGAAGCATGCTC
11872	TMTVLTM	26195	ACTATGACGGTTCTGACTATG	40518	ACAATGACAGTCCTCACAATG
11873	TMVASMA	26196	ACGATGGTGGCGTCGATGGCG	40519	ACAATGGTCGCAAGCATGGCA
11874	TMVKQGN	26197	ACTATGGTTAAGCAGGGTAAT	40520	ACAATGGTCAAACAAGGAAAC
11875	TMVSGGH	26198	ACGATGGTGTCGGGTGGTCAT	40521	ACAATGGTCAGCGGAGGACAC
11876	TMVVVSS	26199	ACTATGGTTGTTGTGTCTAGT	40522	ACAATGGTCGTCGTCAGCAGC
11877	TMVYTDN	26200	ACTATGGTTTATACTGATAAT	40523	ACAATGGTCTACACAGACAAC
11878	TNAALQS	26201	ACTAATGCTGCGCTGCAGTCT	40524	ACAAACGCAGCACTCCAAAGC
11879	TNAIKSG	26202	ACGAATGCTATTAAGTCTGGG	40525	ACAAACGCAATCAAAAGCGGA
11880	TNASWPP	26203	ACTAATGCGTCTTGGCCTCCG	40526	ACAAACGCAAGCTGGCCACCA
11881	TNDPMMP	26204	ACGAATGATCCTATGATGCCT	40527	ACAAACGACCCAATGATGCCA
11882	TNEHKFS	26205	ACGAATGAGCATAAGTTTTCG	40528	ACAAACGAACACAAATTCAGC
11883	TNESSGT	26206	ACGAATGAGTCTAGTGGGACG	40529	ACAAACGAAAGCAGCGGAACA
11884	TNFLPHG	26207	ACTAATTTTTTGCCTCATGGT	40530	ACAAACTTCCTCCCACACGGA
11885	TNFPQSA	26208	ACTAATTTTCCTCAGTCTGCG	40531	ACAAACTTCCCACAAAGCGCA
11886	TNFQLTV	26209	ACTAATTTTCAGCTGACTGTT	40532	ACAAACTTCCAACTCACAGTC
11887	TNGRVTA	26210	ACTAATGGGCGGGTGACGGCG	40533	ACAAACGGAAGAGTCACAGCA
11888	TNGTKPT	26211	ACTAATGGTACGAAGCCTACT	40534	ACAAACGGAACAAAACCAACA
11889	TNGVKLS	26212	ACTAATGGGGTTAAGTTGTCT	40535	ACAAACGGAGTCAAACTCAGC
11890	TNHIAAL	26213	ACGAATCATATTGCTGCTCTG	40536	ACAAACCACATCGCAGCACTC
11891	TNHSSPL	26214	ACGAATCATTCTTCTCCGCTT	40537	ACAAACCACAGCAGCCCACTC
11892	TNKTVGC	26215	ACGAATAAGACGGTGGGTTGT	40538	ACAAACAAAACAGTCGGATGC
11893	TNLAARP	26216	ACTAATTTGGCTGCGCGGCCT	40539	ACAAACCTCGCAGCAAGACCA
11894	TNLKRMD	26217	ACTAATCTTAAGCGTATGGAT	40540	ACAAACCTCAAAAGAATGGAC
11895	TNLNGND	26218	ACGAATTTGAATGGTAATGAT	40541	ACAAACCTCAACGGAAACGAC
11896	TNLNTRP	26219	ACGAATCTTAATACTCGTCCT	40542	ACAAACCTCAACACAAGACCA
11897	TNLRSEL	26220	ACGAATCTTAGGTCTGAGTTG	40543	ACAAACCTCAGAAGCGAACTC
11898	TNLRTAV	26221	ACGAATCTGCGGACTGCTGTT	40544	ACAAACCTCAGAACAGCAGTC
11899	TNMKTDS	26222	ACTAATATGAAGACTGATTCT	40545	ACAAACATGAAAACAGACAGC
11900	TNMPMNP	26223	ACTAATATGCCTATGAATCCT	40546	ACAAACATGCCAATGAACCCA
11901	TNMPPLP	26224	ACGAATATGCCGCCGCTTCCG	40547	ACAAACATGCCACCACTCCCA
11902	TNMPPLT	26225	ACGAATATGCCGCCGCTTACG	40548	ACAAACATGCCACCACTCACA
11903	TNNGGMY	26226	ACTAATAATGGTGGTATGTAT	40549	ACAAACAACGGAGGAATGTAC
11904	TNNSTNP	26227	ACTAATAATAGTACGAATCCG	40550	ACAAACAACAGCACAAACCCA
11905	TNPAPNS	26228	ACGAATCCTGCGCCGAATTCG	40551	ACAAACCCAGCACCAAACAGC
11906	TNPGPLD	26229	ACTAATCCGGGTCCTCTTGAT	40552	ACAAACCCAGGACCACTCGAC
11907	TNPHRDT	26230	ACTAATCCTCATAGGGATACG	40553	ACAAACCCACACAGAGACACA
11908	TNPLSTG	26231	ACTAATCCGTTGTCGACGGGT	40554	ACAAACCCACTCAGCACAGGA
11909	TNPNNAN	26232	ACTAATCCTAATAATGCGAAT	40555	ACAAACCCAAACAACGCAAAC
11910	TNPRSYT	26233	ACTAATCCTCGGTCGTATACT	40556	ACAAACCCAAGAAGCTACACA
11911	TNPSALG	26234	ACGAATCCGAGTGCTCTTGGG	40557	ACAAACCCAAGCGCACTCGGA
11912	TNPSMCL	26235	ACGAATCCGTCTATGTGTCTG	40558	ACAAACCCAAGCATGTGCCTC
11913	TNPTSMA	26236	ACTAATCCTACTAGTATGGCT	40559	ACAAACCCAACAAGCATGGCA
11914	TNPVLTE	26237	ACGAATCCTGTGCTTACTGAG	40560	ACAAACCCAGTCCTCACAGAA

11915	TNPVRLV	26238	ACTAATCCGGTTAGGCTTGTT	40561	ACAAACCCAGTCAGACTCGTC
11916	TNPVRTS	26239	ACGAATCCTGTTCGGACGTCT	40562	ACAAACCCAGTCAGAACAAGC
11917	TNRGWTD	26240	ACTAATCGTGGTTGGACTGAT	40563	ACAAACAGAGGATGGACAGAC
11918	TNRNSEV	26241	ACTAATCGGAATTCGGAGGTT	40564	ACAAACAGAAACAGCGAAGTC
11919	TNRPIDT	26242	ACGAATAGGCCTATTGATACT	40565	ACAAACAGACCAATCGACACA
11920	TNRQAST	26243	ACGAATAGGCAGGCTAGTACG	40566	ACAAACAGACAAGCAAGCACA
11921	TNRQDTR	26244	ACTAATCGGCAGGATACTCGG	40567	ACAAACAGACAAGACACAAGA
11922	TNSAISG	26245	ACTAATAGTGCGATTTCGGGT	40568	ACAAACAGCGCAATCAGCGGA
11923	TNSGSDA	26246	ACTAATAGTGGTTCTGATGCT	40569	ACAAACAGCGGAAGCGACGCA
11924	TNSHAML	26247	ACTAATTCTCATGCGATGCTT	40570	ACAAACAGCCACGCAATGCTC
11925	TNSLPAL	26248	ACGAATAGTTTGCCTGCTCTG	40571	ACAAACAGCCTCCCAGCACTC
11926	TNSMGVP	26249	ACTAATTCTATGGGTGTGCCG	40572	ACAAACAGCATGGGAGTCCCA
11927	TNSNHTY	26250	ACGAATAGTAATCATACGTAT	40573	ACAAACAGCAACCACACATAC
11928	TNSPSRS	26251	ACTAATTCGCCGTCGAGGTCT	40574	ACAAACAGCCCAAGCAGAAGC
11929	TNTDVTK	26252	ACTAATACTGATGTTACGAAG	40575	ACAAACACAGACGTCACAAAA
11930	TNTRTPY	26253	ACGAATACTCGTACGCCTTAT	40576	ACAAACACAAGAACACCATAC
11931	TNTSASR	26254	ACTAATACTTCTGCGTCGAGG	40577	ACAAACACAAGCGCAAGCAGA
11932	TNTSSTY	26255	ACTAATACGTCGTCGACTTAT	40578	ACAAACACAAGCAGCACATAC
11933	TNTTINL	26256	ACTAATACGACGATTAATCTG	40579	ACAAACACAACAATCAACCTC
11934	TNTVRNF	26257	ACGAATACGGTTCGGAATTTT	40580	ACAAACACAGTCAGAAACTTC
11935	TNVMKAG	26258	ACGAATGTTATGAAGGCGGGG	40581	ACAAACGTCATGAAAGCAGGA
11936	TNYNVGS	26259	ACGAATTATAATGTGGGGAGT	40582	ACAAACTACAACGTCGGAAGC
11937	TNYVLAP	26260	ACGAATTATGTTCTTGCGCCG	40583	ACAAACTACGTCCTCGCACCA
11938	TPAFKIQ	26261	ACGCCTGCTTTTAAGATTCAG	40584	ACACCAGCATTCAAAATCCAA
11939	TPAIVPT	26262	ACGCCTGCTATTGTGCCTACG	40585	ACACCAGCAATCGTCCCAACA
11940	TPALNRP	26263	ACTCCGGCTTTGAATCGGCCT	40586	ACACCAGCACTCAACAGACCA
11941	TPANDPR	26264	ACTCCGGCGAATGATCCGCGT	40587	ACACCAGCAAACGACCCAAGA
11942	TPAPNRF	26265	ACGCCTGCTCCTAATAGGTTT	40588	ACACCAGCACCAAACAGATTC
11943	TPASPSD	26266	ACGCCGGCTTCGCCTTCGGAT	40589	ACACCAGCAAGCCCAAGCGAC
11944	TPATLPS	26267	ACTCCGGCTACGCTGCCGTCT	40590	ACACCAGCAACACTCCCAAGC
11945	TPAVEKL	26268	ACGCCTGCGGTGGAGAAGCTT	40591	ACACCAGCAGTCGAAAAACTC
11946	TPAYGRI	26269	ACTCCGGCTTATGGTCGGATT	40592	ACACCAGCATACGGAAGAATC
11947	TPDMPFT	26270	ACGCCGGATATGCCTTTTACT	40593	ACACCAGACATGCCATTCACA
11948	TPDQYEF	26271	ACTCCGGATCAGTATGAGTTT	40594	ACACCAGACCAATACGAATTC
11949	TPDSMTA	26272	ACTCCGGATTCTATGACTGCG	40595	ACACCAGACAGCATGACAGCA
11950	TPEMKSN	26273	ACGCCTGAGATGAAGTCTAAT	40596	ACACCAGAAATGAAAAGCAAC
11951	TPERAMS	26274	ACTCCTGAGAGGGCGATGTCG	40597	ACACCAGAAAGAGCAATGAGC
11952	TPETNRP	26275	ACTCCTGAGACGAATCGGCCG	40598	ACACCAGAAACAAACAGACCA
11953	TPGGARP	26276	ACTCCGGGTGGTGCTCGGCCT	40599	ACACCAGGAGGAGCAAGACCA
11954	TPGHMDS	26277	ACTCCGGGGCATATGGATTCT	40600	ACACCAGGACACATGGACAGC
11955	TPGIPRC	26278	ACGCCTGGGATTCCTAGGTGT	40601	ACACCAGGAATCCCAAGATGC
11956	TPGRQFP	26279	ACGCCGGGGCGGCAGTTTCCT	40602	ACACCAGGAAGACAATTCCCA
11957	TPGTING	26280	ACTCCGGGTACTATTAATGGT	40603	ACACCAGGAACAATCAACGGA
11958	TPHGVSP	26281	ACTCCGCATGGGGTTTCGCCG	40604	ACACCACACGGAGTCAGCCCA
11959	TPHLDGH	26282	ACTCCTCATTTGGATGGGCAT	40605	ACACCACACCTCGACGGACAC

11960	TPHTGNQ	26283	ACGCCGCATACTGGGAATCAG	40606	ACACCACACACAGGAAACCAA
11961	TPHTLEV	26284	ACGCCTCATACGCTGGAGGTG	40607	ACACCACACACACTCGAAGTC
11962	TPIGLPS	26285	ACGCCGATTGGGCTTCCTTCT	40608	ACACCAATCGGACTCCCAAGC
11963	TPIRNIP	26286	ACTCCTATTAGGAATATTCCT	40609	ACACCAATCAGAAACATCCCA
11964	TPISMPS	26287	ACGCCGATTTCGATGCCTTCT	40610	ACACCAATCAGCATGCCAAGC
11965	TPIVHIN	26288	ACTCCTATTGTGCATATTAAT	40611	ACACCAATCGTCCACATCAAC
11966	TPIVHPR	26289	ACTCCTATTGTTCATCCGCGG	40612	ACACCAATCGTCCACCCAAGA
11967	TPIVKPD	26290	ACTCCTATTGTTAAGCCTGAT	40613	ACACCAATCGTCAAACCAGAC
11968	TPKDAEV	26291	ACTCCTAAGGATGCTGAGGTG	40614	ACACCAAAAGACGCAGAAGTC
11969	TPKLSEQ	26292	ACTCCTAAGCTTTCTGAGCAG	40615	ACACCAAAACTCAGCGAACAA
11970	TPKNTLA	26293	ACTCCGAAGAATACGTTGGCT	40616	ACACCAAAAAACACACTCGCA
11971	TPKSASG	26294	ACGCCTAAGTCGGCTTCTGGT	40617	ACACCAAAAAGCGCAAGCGGA
11972	TPLGGSS	26295	ACGCCTCTTGGGGGTTCTTCT	40618	ACACCACTCGGAGGAAGCAGC
11973	TPLHSPG	26296	ACGCCGCTTCATTCGCCGGGT	40619	ACACCACTCCACAGCCCAGGA
11974	TPLHSTT	26297	ACGCCGCTGCATAGTACTACG	40620	ACACCACTCCACAGCACAACA
11975	TPLLCGK	26298	ACGCCGCTTTTGTGTGGTAAG	40621	ACACCACTCCTCTGCGGAAAA
11976	TPLLSHS	26299	ACTCCGCTTCTGTCTCATAGT	40622	ACACCACTCCTCAGCCACAGC
11977	TPLQTTV	26300	ACTCCTCTTCAGACTACGGTG	40623	ACACCACTCCAAACAACAGTC
11978	TPLRSSN	26301	ACGCCGTTGAGGTCGTCTAAT	40624	ACACCACTCAGAAGCAGCAAC
11979	TPLSAIQ	26302	ACTCCGCTGTCGGCTATTCAG	40625	ACACCACTCAGCGCAATCCAA
11980	TPLTNIA	26303	ACTCCTTTGACTAATATTGCG	40626	ACACCACTCACAAACATCGCA
11981	TPLTTAG	26304	ACGCCTTTGACGACGGCGGGG	40627	ACACCACTCACAACAGCAGGA
11982	TPMAVES	26305	ACGCCTATGGCTGTTGAGAGT	40628	ACACCAATGGCAGTCGAAAGC
11983	TPMEMIP	26306	ACTCCGATGGAGATGATTCCG	40629	ACACCAATGGAAATGATCCCA
11984	TPMGSGW	26307	ACTCCTATGGGTTCGGGGTGG	40630	ACACCAATGGGAAGCGGATGG
11985	TPMQVPA	26308	ACTCCTATGCAGGTTCCGGCG	40631	ACACCAATGCAAGTCCCAGCA
11986	TPNMLSA	26309	ACGCCGAATATGCTTTCTGCT	40632	ACACCAAACATGCTCAGCGCA
11987	TPNMVTG	26310	ACTCCTAATATGGTGACGGGT	40633	ACACCAAACATGGTCACAGGA
11988	TPNSRTV	26311	ACGCCTAATTCTCGTACTGTG	40634	ACACCAAACAGCAGAACAGTC
11989	TPNVTYR	26312	ACTCCTAATGTGACTTATCGT	40635	ACACCAAACGTCACATACAGA
11990	TPNYYHE	26313	ACGCCGAATTATTATCATGAG	40636	ACACCAAACTACTACCACGAA
11991	TPPDGTR	26314	ACGCCTCCGGATGGTACTAGG	40637	ACACCACCAGACGGAACAAGA
11992	TPPDQSR	26315	ACGCCGCCGGATCAGTCTAGG	40638	ACACCACCAGACCAAAGCAGA
11993	TPPGEMR	26316	ACTCCGCCGGGTGAGATGAGG	40639	ACACCACCAGGAGAAATGAGA
11994	TPPLKAS	26317	ACGCCGCCTCTGAAGGCGTCG	40640	ACACCACCACTCAAAGCAAGC
11995	TPPPPTW	26318	ACGCCTCCGCCGCCTACTTGG	40641	ACACCACCACCACCAACATGG
11996	TPPRGIP	26319	ACGCCGCCGCGTGGTATTCCG	40642	ACACCACCAAGAGGAATCCCA
11997	TPPRTVV	26320	ACGCCTCCGCGTACTGTGGTG	40643	ACACCACCAAGAACAGTCGTC
11998	TPPSSEW	26321	ACTCCGCCTTCGTCTGAGTGG	40644	ACACCACCAAGCAGCGAATGG
11999	TPPTATR	26322	ACTCCTCCGACTGCTACGCGT	40645	ACACCACCAACAGCAACAAGA
12000	TPPTLME	26323	ACTCCTCCGACTTTGATGGAG	40646	ACACCACCAACACTCATGGAA
12001	TPPYVAQ	26324	ACTCCTCCTTATGTGGCGCAG	40647	ACACCACCATACGTCGCACAA
12002	TPQGDIA	26325	ACGCCGCAGGGTGATATTGCT	40648	ACACCACAAGGAGACATCGCA
12003	TPQHMGP	26326	ACTCCTCAGCATATGGGTCCT	40649	ACACCACAACACATGGGACCA
12004	TPQHMRG	26327	ACTCCTCAGCATATGAGGGGG	40650	ACACCACAACACATGAGAGGA

12005	TPQMPFP	26328	ACGCCTCAGATGCCGTTTCCT	40651	ACACCACAAATGCCATTCCCA
12006	TPQNIMD	26329	ACTCCGCAGAATATTATGGAT	40652	ACACCACAAAACATCATGGAC
12007	TPQRAGI	26330	ACTCCGCAGCGGGCGGGGATT	40653	ACACCACAAAGAGCAGGAATC
12008	TPRAEHT	26331	ACGCCTAGGGCTGAGCATACT	40654	ACACCAAGAGCAGAACACACA
12009	TPRGQSL	26332	ACGCCTAGGGGTCAGAGTCTT	40655	ACACCAAGAGGACAAAGCCTC
12010	TPRGSLD	26333	ACTCCGCGGGGTAGTCTTGAT	40656	ACACCAAGAGGAAGCCTCGAC
12011	TPRLTVE	26334	ACGCCTAGGCTTACTGTTGAG	40657	ACACCAAGACTCACAGTCGAA
12012	TPRPTYT	26335	ACTCCTCGGCCGACGTATACT	40658	ACACCAAGACCAACATACACA
12013	TPRTPSS	26336	ACTCCGCGTACGCCTAGTAGT	40659	ACACCAAGAACACCAAGCAGC
12014	TPSAAMI	26337	ACGCCTAGTGCTGCGATGATT	40660	ACACCAAGCGCAGCAATGATC
12015	TPSASRL	26338	ACGCCTAGTGCTTCTCGGCTT	40661	ACACCAAGCGCAAGCAGACTC
12016	TPSHLMS	26339	ACGCCGTCTCATCTGATGAGT	40662	ACACCAAGCCACCTCATGAGC
12017	TPSKGLV	26340	ACTCCTAGTAAGGGTCTTGTG	40663	ACACCAAGCAAAGGACTCGTC
12018	TPSNDIS	26341	ACTCCTTCTAATGATATTTCG	40664	ACACCAAGCAACGACATCAGC
12019	TPSNQSS	26342	ACGCCGTCGAATCAGTCTTCG	40665	ACACCAAGCAACCAAAGCAGC
12020	TPSPGDA	26343	ACTCCGTCTCCGGGTGATGCG	40666	ACACCAAGCCCAGGAGACGCA
12021	TPSPPGV	26344	ACTCCGAGTCCTCCTGGTGTG	40667	ACACCAAGCCCACCAGGAGTC
12022	TPSSAGI	26345	ACTCCTAGTTCGGCTGGGATT	40668	ACACCAAGCAGCGCAGGAATC
12023	TPSSGSR	26346	ACGCCTTCTTCTGGTTCGCGG	40669	ACACCAAGCAGCGGAAGCAGA
12024	TPSSMHP	26347	ACTCCGAGTTCTATGCATCCG	40670	ACACCAAGCAGCATGCACCCA
12025	TPSSTQL	26348	ACGCCTTCTTCTACTCAGCTT	40671	ACACCAAGCAGCACACAACTC
12026	TPSVDAC	26349	ACGCCGTCTGTTGATGCTTGT	40672	ACACCAAGCGTCGACGCATGC
12027	TPSVTLL	26350	ACGCCTTCTGTTACTCTTCTT	40673	ACACCAAGCGTCACACTCCTC
12028	TPSYVMA	26351	ACGCCGTCTTATGTGATGGCG	40674	ACACCAAGCTACGTCATGGCA
12029	TPTARNP	26352	ACTCCGACTGCGCGTAATCCG	40675	ACACCAACAGCAAGAAACCCA
12030	TPTETKY	26353	ACTCCTACTGAGACTAAGTAT	40676	ACACCAACAGAAACAAAATAC
12031	TPTGRDF	26354	ACGCCTACTGGGCGGGATTTT	40677	ACACCAACAGGAAGAGACTTC
12032	TPTLKSN	26355	ACGCCTACGCTTAAGTCGAAT	40678	ACACCAACACTCAAAAGCAAC
12033	TPTPAFR	26356	ACTCCTACTCCTGCGTTTCGG	40679	ACACCAACACCAGCATTCAGA
12034	TPTRPSA	26357	ACGCCGACTCGGCCTTCTGCT	40680	ACACCAACAAGACCAAGCGCA
12035	TPTSSEW	26358	ACGCCTACGTCTAGTGAGTGG	40681	ACACCAACAAGCAGCGAATGG
12036	TPTTSNE	26359	ACGCCTACGACTAGTAATGAG	40682	ACACCAACAACAAGCAACGAA
12037	TPTVPRD	26360	ACTCCGACGGTTCCGCGTGAT	40683	ACACCAACAGTCCCAAGAGAC
12038	TPVLNYG	26361	ACGCCGGTTTTGAATTATGGT	40684	ACACCAGTCCTCAACTACGGA
12039	TPVLSSL	26362	ACTCCTGTGCTTTCGTCTCTG	40685	ACACCAGTCCTCAGCAGCCTC
12040	TPVQAVA	26363	ACTCCTGTGCAGGCGGTTGCT	40686	ACACCAGTCCAAGCAGTCGCA
12041	TPVTINM	26364	ACGCCTGTTACTATTAATATG	40687	ACACCAGTCACAATCAACATG
12042	TPYPDTS	26365	ACGCCTTATCCGGATACTTCT	40688	ACACCATACCCAGACACAAGC
12043	TQAAAYR	26366	ACTCAGGCTGCTGCTTATCGG	40689	ACACAAGCAGCAGCATACAGA
12044	TQAGFSS	26367	ACTCAGGCTGGGTTTTCGTCT	40690	ACACAAGCAGGATTCAGCAGC
12045	TQAHFAG	26368	ACTCAGGCGCATTTTGCGGGT	40691	ACACAAGCACACTTCGCAGGA
12046	TQDSFRH	26369	ACGCAGGATTCGTTTAGGCAT	40692	ACACAAGACAGCTTCAGACAC
12047	TQELPRS	26370	ACTCAGGAGCTGCCGCGTTCG	40693	ACACAAGAACTCCCAAGAAGC
12048	TQENVER	26371	ACTCAGGAGAATGTGGAGAGG	40694	ACACAAGAAAACGTCGAAAGA
12049	TQEVERE	26372	ACTCAGGAGGTTGAGAGGGAG	40695	ACACAAGAAGTCGAAAGAGAA

12050	TQFPALG	26373	ACTCAGTTTCCGGCGTTGGGG	40696	ACACAATTCCCAGCACTCGGA
12051	TQFTHKA	26374	ACTCAGTTTACTCATAAGGCG	40697	ACACAATTCACACACAAAGCA
12052	TQGDVSS	26375	ACTCAGGGTGATGTTTCTTCT	40698	ACACAAGGAGACGTCAGCAGC
12053	TQGLDVE	26376	ACGCAGGGTCTGGATGTTGAG	40699	ACACAAGGACTCGACGTCGAA
12054	TQGQANP	26377	ACGCAGGGTCAGGCTAATCCG	40700	ACACAAGGACAAGCAAACCCA
12055	TQGRDYV	26378	ACGCAGGGTAGGGATTATGTG	40701	ACACAAGGAAGAGACTACGTC
12056	TQGTRAW	26379	ACTCAGGGTACGCGTGCTTGG	40702	ACACAAGGAACAAGAGCATGG
12057	TQHAGGF	26380	ACTCAGCATGCGGGGGGTTTT	40703	ACACAACACGCAGGAGGATTC
12058	TQISSMS	26381	ACGCAGATTAGTAGTATGAGT	40704	ACACAAATCAGCAGCATGAGC
12059	TQITVDE	26382	ACTCAGATTACTGTTGATGAG	40705	ACACAAATCACAGTCGACGAA
12060	TQKLSMS	26383	ACTCAGAAGCTTTCGATGAGT	40706	ACACAAAAACTCAGCATGAGC
12061	TQKVSDP	26384	ACTCAGAAGGTGAGTGATCCG	40707	ACACAAAAAGTCAGCGACCCA
12062	TQLNVSR	26385	ACGCAGCTGAATGTTAGTCGT	40708	ACACAACTCAACGTCAGCAGA
12063	TQLSVNP	26386	ACTCAGCTTAGTGTGAATCCG	40709	ACACAACTCAGCGTCAACCCA
12064	TQMTKAS	26387	ACTCAGATGACTAAGGCTTCG	40710	ACACAAATGACAAAAGCAAGC
12065	TQNEPHL	26388	ACGCAGAATGAGCCGCATCTG	40711	ACACAAAACGAACCACACCTC
12066	TQNLCDR	26389	ACTCAGAATCTGTGTGATCGG	40712	ACACAAAACCTCTGCGACAGA
12067	TQPPLSQ	26390	ACGCAGCCTCCGCTTTCGCAG	40713	ACACAACCACCACTCAGCCAA
12068	TQPSAAA	26391	ACTCAGCCGTCTGCTGCTGCG	40714	ACACAACCAAGCGCAGCAGCA
12069	TQPSLQA	26392	ACGCAGCCTAGTTTGCAGGCG	40715	ACACAACCAAGCCTCCAAGCA
12070	TQPSRPL	26393	ACTCAGCCTTCTAGGCCGTTG	40716	ACACAACCAAGCAGACCACTC
12071	TQPTGCE	26394	ACTCAGCCTACTGGTTGTGAG	40717	ACACAACCAACAGGATGCGAA
12072	TQPYGHA	26395	ACTCAGCCTTATGGGCATGCG	40718	ACACAACCATACGGACACGCA
12073	TQQSTIS	26396	ACGCAGCAGTCTACTATTTCT	40719	ACACAACAAAGCACAATCAGC
12074	TQQTPRG	26397	ACTCAGCAGACTCCGAGGGGT	40720	ACACAACAAACACCAAGAGGA
12075	TQQTSAY	26398	ACTCAGCAGACGAGTGCGTAT	40721	ACACAACAAACAAGCGCATAC
12076	TQRETNS	26399	ACGCAGCGGGAGACGAATTCG	40722	ACACAAAGAGAAACAAACAGC
12077	TQRGSAE	26400	ACTCAGCGTGGGTCTGCGGAG	40723	ACACAAAGAGGAAGCGCAGAA
12078	TQRPITV	26401	ACTCAGCGGCCGATTACGGTG	40724	ACACAAAGACCAATCACAGTC
12079	TQRVARD	26402	ACTCAGCGTGTTGCGCGTGAT	40725	ACACAAAGAGTCGCAAGAGAC
12080	TQSAMSV	26403	ACGCAGTCTGCGATGTCTGTT	40726	ACACAAAGCGCAATGAGCGTC
12081	TQSETVL	26404	ACGCAGTCTGAGACTGTTCTT	40727	ACACAAAGCGAAACAGTCCTC
12082	TQSFGSA	26405	ACGCAGTCTTTTGGTTCTGCG	40728	ACACAAAGCTTCGGAAGCGCA
12083	TQSLASE	26406	ACTCAGTCTCTGGCTTCTGAG	40729	ACACAAAGCCTCGCAAGCGAA
12084	TQSLMDD	26407	ACTCAGTCTTTGATGGATGAT	40730	ACACAAAGCCTCATGGACGAC
12085	TQSRDMS	26408	ACGCAGTCGCGTGATATGTCG	40731	ACACAAAGCAGAGACATGAGC
12086	TQSSALS	26409	ACGCAGTCTAGTGCTCTGTCT	40732	ACACAAAGCAGCGCACTCAGC
12087	TQSSQRI	26410	ACTCAGTCTAGTCAGCGGATT	40733	ACACAAAGCAGCCAAAGAATC
12088	TQSSTGP	26411	ACTCAGTCTTCTACTGGTCCG	40734	ACACAAAGCAGCACAGGACCA
12089	TQSSTQP	26412	ACTCAGTCGTCTACTCAGCCT	40735	ACACAAAGCAGCACACAACCA
12090	TQTRPVG	26413	ACTCAGACGCGTCCGGTTGGT	40736	ACACAAACAAGACCAGTCGGA
12091	TQTTIMP	26414	ACTCAGACGACTATTATGCCT	40737	ACACAAACAACAATCATGCCA
12092	TQTTSLY	26415	ACGCAGACTACTAGTCTGTAT	40738	ACACAAACAACAAGCCTCTAC
12093	TQTTSPV	26416	ACGCAGACGACTTCTCCGGTT	40739	ACACAAACAACAAGCCCAGTC
12094	TQVALRP	26417	ACGCAGGTTGCGCTTAGGCCG	40740	ACACAAGTCGCACTCAGACCA

12095	TQVATYQ	26418	ACGCAGGTGGCGACGTATCAG	40741	ACACAAGTCGCAACATACCAA
12096	TQWLAQG	26419	ACGCAGTGGTTGGCGCAGGGT	40742	ACACAATGGCTCGCACAAGGA
12097	TRAALGT	26420	ACGCGTGCGGCTCTGGGGACG	40743	ACAAGAGCAGCACTCGGAACA
12098	TRALQAG	26421	ACGAGGGCGTTGCAGGCTGGG	40744	ACAAGAGCACTCCAAGCAGGA
12099	TRANATN	26422	ACGCGGGCGAATGCGACGAAT	40745	ACAAGAGCAAACGCAACAAAC
12100	TRAPATM	26423	ACTAGGGCGCCGGCGACTATG	40746	ACAAGAGCACCAGCAACAATG
12101	TRASTAN	26424	ACGCGTGCTTCGACTGCGAAT	40747	ACAAGAGCAAGCACAGCAAAC
12102	TRATGDA	26425	ACGCGGGCGACGGGTGATGCT	40748	ACAAGAGCAACAGGAGACGCA
12103	TRAVDGR	26426	ACGCGGGCTGTGGATGGGCGT	40749	ACAAGAGCAGTCGACGGAAGA
12104	TRAVGGQ	26427	ACTCGGGCTGTGGGGGGTCAG	40750	ACAAGAGCAGTCGGAGGACAA
12105	TRDEWAT	26428	ACTAGGGATGAGTGGGCTACG	40751	ACAAGAGACGAATGGGCAACA
12106	TRDRGPS	26429	ACTAGGGATCGTGGGCCTTCT	40752	ACAAGAGACAGAGGACCAAGC
12107	TRDTSYT	26430	ACTCGTGATACTTCGTATACT	40753	ACAAGAGACACAAGCTACACA
12108	TREGFMV	26431	ACTCGTGAGGGTTTTATGGTT	40754	ACAAGAGAAGGATTCATGGTC
12109	TREMGPS	26432	ACTCGGGAGATGGGGCCGAGT	40755	ACAAGAGAAATGGGACCAAGC
12110	TRETVPA	26433	ACTCGTGAGACTGTGCCTGCG	40756	ACAAGAGAAACAGTCCCAGCA
12111	TRFCSSP	26434	ACGCGGTTTTGTTCGTCTCCT	40757	ACAAGATTCTGCAGCAGCCCA
12112	TRFEKYD	26435	ACTCGTTTTGAGAAGTATGAT	40758	ACAAGATTCGAAAAATACGAC
12113	TRFQVEV	26436	ACGCGTTTTCAGGTTGAGGTT	40759	ACAAGATTCCAAGTCGAAGTC
12114	TRGGDGV	26437	ACGCGGGGTGGGGATGGTGTG	40760	ACAAGAGGAGGAGACGGAGTC
12115	TRGTDLS	26438	ACTAGGGGGACGGATTTGTCG	40761	ACAAGAGGAACAGACCTCAGC
12116	TRGTSVS	26439	ACTCGTGGGACTTCGGTGTCG	40762	ACAAGAGGAACAAGCGTCAGC
12117	TRGVINA	26440	ACTCGTGGTGTGATTAATGCG	40763	ACAAGAGGAGTCATCAACGCA
12118	TRHDFLN	26441	ACGCGGCATGATTTTTTGAAT	40764	ACAAGACACGACTTCCTCAAC
12119	TRIGPSE	26442	ACTCGGATTGGTCCTAGTGAG	40765	ACAAGAATCGGACCAAGCGAA
12120	TRIHALP	26443	ACGAGGATTCATGCTTTGCCT	40766	ACAAGAATCCACGCACTCCCA
12121	TRISLSG	26444	ACGAGGATTTCTCTTAGTGGG	40767	ACAAGAATCAGCCTCAGCGGA
12122	TRKLAVD	26445	ACTCGGAAGCTGGCTGTTGAT	40768	ACAAGAAAACTCGCAGTCGAC
12123	TRLNSID	26446	ACGCGTCTTAATTCTATTGAT	40769	ACAAGACTCAACAGCATCGAC
12124	TRLPTSL	26447	ACGCGGCTGCCGACGTCGCTG	40770	ACAAGACTCCCAACAAGCCTC
12125	TRLQTSA	26448	ACTAGGCTTCAGACTAGTGCT	40771	ACAAGACTCCAAACAAGCGCA
12126	TRLSENT	26449	ACTAGGCTTAGTGAGAATACT	40772	ACAAGACTCAGCGAAAACACA
12127	TRLSSSV	26450	ACGCGTCTGTCGTCTTCTGTG	40773	ACAAGACTCAGCAGCAGCGTC
12128	TRMASDG	26451	ACTCGGATGGCTTCGGATGGG	40774	ACAAGAATGGCAAGCGACGGA
12129	TRMPSGV	26452	ACTCGGATGCCGAGTGGGGTG	40775	ACAAGAATGCCAAGCGGAGTC
12130	TRMPVIS	26453	ACTAGGATGCCTGTTATTAGT	40776	ACAAGAATGCCAGTCATCAGC
12131	TRNEYSF	26454	ACGCGTAATGAGTATTCTTTT	40777	ACAAGAAACGAATACAGCTTC
12132	TRNLDSV	26455	ACGAGGAATCTGGATTCTGTT	40778	ACAAGAAACCTCGACAGCGTC
12133	TRNMSDT	26456	ACTCGTAATATGTCTGATACT	40779	ACAAGAAACATGAGCGACACA
12134	TRNNHVT	26457	ACGAGGAATAATCATGTGACG	40780	ACAAGAAACAACCACGTCACA
12135	TRNPEPK	26458	ACGCGGAATCCTGAGCCGAAG	40781	ACAAGAAACCCAGAACCAAAA
12136	TRNPEST	26459	ACGAGGAATCCTGAGTCGACG	40782	ACAAGAAACCCAGAAAGCACA
12137	TRNPGTT	26460	ACTCGTAATCCTGGTACTACG	40783	ACAAGAAACCCAGGAACAACA
12138	TRNQLRD	26461	ACTCGTAATCAGCTTCGGGAT	40784	ACAAGAAACCAACTCAGAGAC
12139	TRNSGMA	26462	ACTCGTAATAGTGGTATGGCG	40785	ACAAGAAACAGCGGAATGGCA

12140	TRNTTEA	26463	ACGCGGAATACTACTGAGGCT	40786	ACAAGAAACACAACAGAAGCA
12141	TRPAPMA	26464	ACTCGTCCTGCTCCGATGGCT	40787	ACAAGACCAGCACCAATGGCA
12142	TRPDSLP	26465	ACTCGTCCTGATTCGCTGCCG	40788	ACAAGACCAGACAGCCTCCCA
12143	TRPGVDT	26466	ACGCGGCCGGGTGTTGATACG	40789	ACAAGACCAGGAGTCGACACA
12144	TRPLAIA	26467	ACTCGGCCTTTGGCTATTGCT	40790	ACAAGACCACTCGCAATCGCA
12145	TRPLPSN	26468	ACTAGGCCGTTGCCGTCGAAT	40791	ACAAGACCACTCCCAAGCAAC
12146	TRPLSSG	26469	ACTCGTCCTCTGAGTTCTGGG	40792	ACAAGACCACTCAGCAGCGGA
12147	TRPLSSP	26470	ACTAGGCCTTTGAGTTCGCCT	40793	ACAAGACCACTCAGCAGCCCA
12148	TRPMESA	26471	ACGCGTCCTATGGAGTCTGCG	40794	ACAAGACCAATGGAAAGCGCA
12149	TRPNLPY	26472	ACTAGGCCGAATTTGCCTTAT	40795	ACAAGACCAAACCTCCCATAC
12150	TRPSEAQ	26473	ACGAGGCCTTCTGAGGCTCAG	40796	ACAAGACCAAGCGAAGCACAA
12151	TRPSYEM	26474	ACTCGTCCTTCTTATGAGATG	40797	ACAAGACCAAGCTACGAAATG
12152	TRPTADD	26475	ACTAGGCCGACGGCTGATGAT	40798	ACAAGACCAACAGCAGACGAC
12153	TRPTPLL	26476	ACGAGGCCTACTCCGCTTTTG	40799	ACAAGACCAACACCACTCCTC
12154	TRPVGTS	26477	ACTCGTCCGGTGGGGACGTCG	40800	ACAAGACCAGTCGGAACAAGC
12155	TRPVYAD	26478	ACGCGTCCTGTTTATGCTGAT	40801	ACAAGACCAGTCTACGCAGAC
12156	TRQATSE	26479	ACTAGGCAGGCTACGTCTGAG	40802	ACAAGACAAGCAACAAGCGAA
12157	TRQLLTA	26480	ACGCGTCAGCTTCTGACTGCG	40803	ACAAGACAACTCCTCACAGCA
12158	TRQYTNS	26481	ACGCGTCAGTATACGAATAGT	40804	ACAAGACAATACACAAACAGC
12159	TRRPDIA	26482	ACGAGGCGTCCTGATATTGCG	40805	ACAAGAAGACCAGACATCGCA
12160	TRRVPSE	26483	ACGCGGCGTGTGCCGTCGGAG	40806	ACAAGAAGAGTCCCAAGCGAA
12161	TRSALEL	26484	ACTCGTTCTGCGCTTGAGTTG	40807	ACAAGAAGCGCACTCGAACTC
12162	TRSAVGS	26485	ACTCGTTCTGCGGTGGGGTCT	40808	ACAAGAAGCGCAGTCGGAAGC
12163	TRSFESS	26486	ACGAGGTCTTTTGAGAGTTCG	40809	ACAAGAAGCTTCGAAAGCAGC
12164	TRSGLIE	26487	ACTAGGTCGGGTCTTATTGAG	40810	ACAAGAAGCGGACTCATCGAA
12165	TRSGTDL	26488	ACGAGGTCTGGGACTGATCTT	40811	ACAAGAAGCGGAACAGACCTC
12166	TRSMVTL	26489	ACTCGGTCTATGGTGACTCTT	40812	ACAAGAAGCATGGTCACACTC
12167	TRSNETV	26490	ACGCGTTCTAATGAGACTGTT	40813	ACAAGAAGCAACGAAACAGTC
12168	TRSNGLT	26491	ACGCGGTCGAATGGTCTGACG	40814	ACAAGAAGCAACGGACTCACA
12169	TRSNNST	26492	ACTAGGTCTAATAATTCGACT	40815	ACAAGAAGCAACAACAGCACA
12170	TRSPSSY	26493	ACTAGGAGTCCTTCTAGTTAT	40816	ACAAGAAGCCCAAGCAGCTAC
12171	TRSQHES	26494	ACTCGTTCTCAGCATGAGTCT	40817	ACAAGAAGCCAACACGAAAGC
12172	TRSQSPM	26495	ACGAGGTCTCAGAGTCCTATG	40818	ACAAGAAGCCAAAGCCCAATG
12173	TRSSLTP	26496	ACGCGGAGTTCGTTGACGCCG	40819	ACAAGAAGCAGCCTCACACCA
12174	TRSSSIL	26497	ACTAGGTCGTCGTCGATTCTG	40820	ACAAGAAGCAGCAGCATCCTC
12175	TRSTASP	26498	ACTCGGAGTACGGCTTCTCCT	40821	ACAAGAAGCACAGCAAGCCCA
12176	TRSTPIY	26499	ACTAGGAGTACGCCTATTTAT	40822	ACAAGAAGCACACCAATCTAC
12177	TRSVELL	26500	ACGAGGTCGGTGGAGCTTCTT	40823	ACAAGAAGCGTCGAACTCCTC
12178	TRTITPL	26501	ACTAGGACTATTACGCCGCTT	40824	ACAAGAACAATCACACCACTC
12179	TRTLTSS	26502	ACGCGGACTTTGACTTCGTCG	40825	ACAAGAACACTCACAAGCAGC
12180	TRTMSMS	26503	ACTAGGACTATGTCGATGTCT	40826	ACAAGAACAATGAGCATGAGC
12181	TRTNSII	26504	ACGCGGACGAATAGTATTATT	40827	ACAAGAACAAACAGCATCATC
12182	TRTRLGD	26505	ACGCGGACGCGTCTTGGGGAT	40828	ACAAGAACAAGACTCGGAGAC
12183	TRTSDFP	26506	ACGCGTACGTCGGATTTTCCT	40829	ACAAGAACAAGCGACTTCCCA
12184	TRTSHAL	26507	ACTCGGACGTCTCATGCTCTT	40830	ACAAGAACAAGCCACGCACTC

12185	TRTSQPS	26508	ACTCGTACGTCGCAGCCTAGT	40831	ACAAGAACAAGCCAACCAAGC
12186	TRTSTGS	26509	ACTAGGACTTCTACTGGTTCT	40832	ACAAGAACAAGCACAGGAAGC
12187	TRTTGSM	26510	ACGCGGACTACTGGGTCGATG	40833	ACAAGAACAACAGGAAGCATG
12188	TRTTLES	26511	ACGAGGACTACGTTGGAGAGT	40834	ACAAGAACAACACTCGAAAGC
12189	TRTTTVT	26512	ACTCGTACTACGACGGTTACT	40835	ACAAGAACAACAACAGTCACA
12190	TRTVATY	26513	ACTAGGACGGTGGCTACTTAT	40836	ACAAGAACAGTCGCAACATAC
12191	TRTVQLG	26514	ACTCGTACGGTTCAGCTGGGT	40837	ACAAGAACAGTCCAACTCGGA
12192	TRVHGVS	26515	ACTAGGGTGCATGGTGTTAGT	40838	ACAAGAGTCCACGGAGTCAGC
12193	TRVIMND	26516	ACTAGGGTTATTATGAATGAT	40839	ACAAGAGTCATCATGAACGAC
12194	TRVSSIP	26517	ACGAGGGTGAGTAGTATTCCT	40840	ACAAGAGTCAGCAGCATCCCA
12195	TRVTAPL	26518	ACTCGTGTTACGGCTCCTTTG	40841	ACAAGAGTCACAGCACCACTC
12196	TRVYPAG	26519	ACGCGTGTGTATCCGGCGGGT	40842	ACAAGAGTCTACCCAGCAGGA
12197	TSAGLNY	26520	ACTTCTGCTGGGCTTAATTAT	40843	ACAAGCGCAGGACTCAACTAC
12198	TSAGVYK	26521	ACGTCGGCTGGGGTTTATAAG	40844	ACAAGCGCAGGAGTCTACAAA
12199	TSAKHTM	26522	ACTTCTGCGAAGCATACGATG	40845	ACAAGCGCAAAACACACAATG
12200	TSALIFE	26523	ACGTCGGCGCTGATTTTTGAG	40846	ACAAGCGCACTCATCTTCGAA
12201	TSAQSGP	26524	ACTAGTGCTCAGTCTGGGCCG	40847	ACAAGCGCACAAAGCGGACCA
12202	TSARPFL	26525	ACTTCGGCGCGTCCTTTTTTG	40848	ACAAGCGCAAGACCATTCCTC
12203	TSARPVG	26526	ACGTCTGCGAGGCCTGTGGGG	40849	ACAAGCGCAAGACCAGTCGGA
12204	TSASIPP	26527	ACTTCTGCGTCTATTCCTCCG	40850	ACAAGCGCAAGCATCCCACCA
12205	TSASSTT	26528	ACGTCTGCGAGTTCTACTACT	40851	ACAAGCGCAAGCAGCACAACA
12206	TSDLPLN	26529	ACTTCGGATCTGCCGCTTAAT	40852	ACAAGCGACCTCCCACTCAAC
12207	TSDLRGR	26530	ACGTCTGATTTGCGTGGGCGT	40853	ACAAGCGACCTCAGAGGAAGA
12208	TSDNMPH	26531	ACGAGTGATAATATGCCTCAT	40854	ACAAGCGACAACATGCCACAC
12209	TSDPCMS	26532	ACTTCGGATCCGTGTATGAGT	40855	ACAAGCGACCCATGCATGAGC
12210	TSDSAVT	26533	ACTAGTGATTCGGCTGTTACG	40856	ACAAGCGACAGCGCAGTCACA
12211	TSDVLLT	26534	ACTTCTGATGTGCTTCTTACG	40857	ACAAGCGACGTCCTCCTCACA
12212	TSESKAH	26535	ACTAGTGAGTCTAAGGCGCAT	40858	ACAAGCGAAAGCAAAGCACAC
12213	TSESWPS	26536	ACGAGTGAGTCTTGGCCTTCT	40859	ACAAGCGAAAGCTGGCCAAGC
12214	TSFGPSS	26537	ACTTCTTTTGGTCCTTCTTCG	40860	ACAAGCTTCGGACCAAGCAGC
12215	TSFLKTS	26538	ACTTCGTTTCTGAAGACGTCT	40861	ACAAGCTTCCTCAAAACAAGC
12216	TSFPSSA	26539	ACTAGTTTTCCTTCGTCGGCT	40862	ACAAGCTTCCCAAGCAGCGCA
12217	TSFRLDE	26540	ACGAGTTTTCGGCTGGATGAG	40863	ACAAGCTTCAGACTCGACGAA
12218	TSFSQST	26541	ACGTCGTTTTCTCAGTCGACG	40864	ACAAGCTTCAGCCAAAGCACA
12219	TSFSRGL	26542	ACGTCGTTTTCGCGTGGTCTG	40865	ACAAGCTTCAGCAGAGGACTC
12220	TSGHHIL	26543	ACGAGTGGTCATCATATTCTG	40866	ACAAGCGGACACCACATCCTC
12221	TSGLPEA	26544	ACGTCGGGGCTGCCTGAGGCT	40867	ACAAGCGGACTCCCAGAAGCA
12222	TSGLSEV	26545	ACTTCTGGTCTGTCGGAGGTG	40868	ACAAGCGGACTCAGCGAAGTC
12223	TSGLTLG	26546	ACTTCTGGGCTTACTCTTGGG	40869	ACAAGCGGACTCACACTCGGA
12224	TSGPSHG	26547	ACTTCGGGGCCGAGTCATGGG	40870	ACAAGCGGACCAAGCCACGGA
12225	TSGRSPT	26548	ACTTCTGGGCGGTCGCCTACG	40871	ACAAGCGGAAGAAGCCCAACA
12226	TSGSLRP	26549	ACGAGTGGGTCGCTTAGGCCT	40872	ACAAGCGGAAGCCTCAGACCA
12227	TSGSTSG	26550	ACTAGTGGGTCGACTAGTGGT	40873	ACAAGCGGAAGCACAAGCGGA
12228	TSGTLST	26551	ACGTCTGGTACGTTGTCGACT	40874	ACAAGCGGAACACTCAGCACA
12229	TSGTSTD	26552	ACGAGTGGGACGAGTACGGAT	40875	ACAAGCGGAACAAGCACAGAC

12230	TSHGPAT	26553	ACTAGTCATGGTCCGGCTACT	40876	ACAAGCCACGGACCAGCAACA
12231	TSHNGFS	26554	ACGAGTCATAATGGGTTTTCT	40877	ACAAGCCACAACGGATTCAGC
12232	TSHRPQP	26555	ACTAGTCATCGTCCTCAGCCT	40878	ACAAGCCACAGACCACAACCA
12233	TSIGPRI	26556	ACTTCGATTGGGCCTAGGATT	40879	ACAAGCATCGGACCAAGAATC
12234	TSINRLP	26557	ACGTCTATTAATCGTTTGCCT	40880	ACAAGCATCAACAGACTCCCA
12235	TSKDGHP	26558	ACTTCGAAGGATGGTCATCCT	40881	ACAAGCAAAGACGGACACCCA
12236	TSKLSCP	26559	ACTTCTAAGTTGTCGTGTCCG	40882	ACAAGCAAACTCAGCTGCCCA
12237	TSKTPSI	26560	ACGTCGAAGACGCCTTCTATT	40883	ACAAGCAAAACACCAAGCATC
12238	TSKVATI	26561	ACTAGTAAGGTTGCTACGATT	40884	ACAAGCAAAGTCGCAACAATC
12239	TSKWLTP	26562	ACTTCTAAGTGGCTGACTCCG	40885	ACAAGCAAATGGCTCACACCA
12240	TSLDARS	26563	ACGTCGCTTGATGCTCGGTCT	40886	ACAAGCCTCGACGCAAGAAGC
12241	TSLGSVS	26564	ACTTCGCTTGGGAGTGTGTCG	40887	ACAAGCCTCGGAAGCGTCAGC
12242	TSLHSGD	26565	ACGTCGCTTCATTCTGGTGAT	40888	ACAAGCCTCCACAGCGGAGAC
12243	TSLNNRL	26566	ACGAGTCTGAATAATCGGTTG	40889	ACAAGCCTCAACAACAGACTC
12244	TSLRIMP	26567	ACTTCGTTGCGGATTATGCCG	40890	ACAAGCCTCAGAATCATGCCA
12245	TSLRMNG	26568	ACTTCTCTTCGGATGAATGGT	40891	ACAAGCCTCAGAATGAACGGA
12246	TSLRSDP	26569	ACGTCGCTTCGGAGTGATCCT	40892	ACAAGCCTCAGAAGCGACCCA
12247	TSLSLAL	26570	ACTTCTTTGTCGCTTGCTTTG	40893	ACAAGCCTCAGCCTCGCACTC
12248	TSLTPVS	26571	ACGAGTTTGACTCCTGTTTCT	40894	ACAAGCCTCACACCAGTCAGC
12249	TSLVFAV	26572	ACGTCTTTGGTTTTTGCTGTG	40895	ACAAGCCTCGTCTTCGCAGTC
12250	TSMNLPD	26573	ACGTCGATGAATCTGCCTGAT	40896	ACAAGCATGAACCTCCCAGAC
12251	TSMRTEL	26574	ACGAGTATGAGGACGGAGTTG	40897	ACAAGCATGAGAACAGAACTC
12252	TSMSPRH	26575	ACGTCGATGAGTCCTAGGCAT	40898	ACAAGCATGAGCCCAAGACAC
12253	TSMSPTT	26576	ACTTCGATGTCTCCTACTACG	40899	ACAAGCATGAGCCCAACAACA
12254	TSNAVDY	26577	ACGTCGAATGCTGTTGATTAT	40900	ACAAGCAACGCAGTCGACTAC
12255	TSNGLKL	26578	ACGTCTAATGGTCTTAAGCTG	40901	ACAAGCAACGGACTCAAACTC
12256	TSNPLPR	26579	ACTAGTAATCCGTTGCCGCGG	40902	ACAAGCAACCCACTCCCAAGA
12257	TSNQSAM	26580	ACTAGTAATCAGAGTGCTATG	40903	ACAAGCAACCAAAGCGCAATG
12258	TSNTSMS	26581	ACGAGTAATACTAGTATGAGT	40904	ACAAGCAACACAAGCATGAGC
12259	TSNVRPY	26582	ACGTCTAATGTGCGTCCGTAT	40905	ACAAGCAACGTCAGACCATAC
12260	TSNYHSL	26583	ACGAGTAATTATCATTCGCTG	40906	ACAAGCAACTACCACAGCCTC
12261	TSNYLQT	26584	ACTTCGAATTATTTGCAGACG	40907	ACAAGCAACTACCTCCAAACA
12262	TSPARYS	26585	ACTAGTCCGGCTAGGTATTCT	40908	ACAAGCCCAGCAAGATACAGC
12263	TSPDFSL	26586	ACGTCTCCGGATTTTTCGTTG	40909	ACAAGCCCAGACTTCAGCCTC
12264	TSPDPNK	26587	ACTTCTCCTGATCCTAATAAG	40910	ACAAGCCCAGACCCAAACAAA
12265	TSPMHTI	26588	ACTTCTCCTATGCATACTATT	40911	ACAAGCCCAATGCACACAATC
12266	TSPPLST	26589	ACTTCGCCTCCTTTGAGTACT	40912	ACAAGCCCACCACTCAGCACA
12267	TSPTGPT	26590	ACGTCGCCGACGGGTCCGACG	40913	ACAAGCCCAACAGGACCAACA
12268	TSPVSHV	26591	ACTAGTCCTGTTTCTCATGTG	40914	ACAAGCCCAGTCAGCCACGTC
12269	TSQAVHL	26592	ACTAGTCAGGCTGTTCATCTG	40915	ACAAGCCAAGCAGTCCACCTC
12270	TSQHRQA	26593	ACTTCGCAGCATAGGCAGGCT	40916	ACAAGCCAACACAGACAAGCA
12271	TSQINRQ	26594	ACTTCGCAGATTAATCGTCAG	40917	ACAAGCCAAATCAACAGACAA
12272	TSQQLPQ	26595	ACGTCTCAGCAGCTGCCGCAG	40918	ACAAGCCAACAACTCCCACAA
12273	TSQRPML	26596	ACTTCGCAGCGTCCTATGCTT	40919	ACAAGCCAAAGACCAATGCTC
12274	TSQRYQP	26597	ACTTCGCAGCGGTATCAGCCG	40920	ACAAGCCAAAGATACCAACCA

12275	TSQVRTT	26598	ACGTCGCAGGTGCGGACGACT	40921	ACAAGCCAAGTCAGAACAACA
12276	TSRAPVL	26599	ACGTCTAGGGCGCCTGTGTTG	40922	ACAAGCAGAGCACCAGTCCTC
12277	TSRDHVR	26600	ACGTCTAGGGATCATGTTCGT	40923	ACAAGCAGAGACCACGTCAGA
12278	TSRETYT	26601	ACTTCTCGGGAGACTTATACT	40924	ACAAGCAGAGAAACATACACA
12279	TSRNEVA	26602	ACGTCGCGTAATGAGGTTGCG	40925	ACAAGCAGAAACGAAGTCGCA
12280	TSRTITT	26603	ACTAGTCGTACGATTACTACG	40926	ACAAGCAGAACAATCACAACA
12281	TSRTNDP	26604	ACGAGTCGTACTAATGATCCT	40927	ACAAGCAGAACAAACGACCCA
12282	TSRVDTS	26605	ACTTCTAGGGTTGATACTAGT	40928	ACAAGCAGAGTCGACACAAGC
12283	TSSASAV	26606	ACTAGTTCGGCGTCTGCTGTT	40929	ACAAGCAGCGCAAGCGCAGTC
12284	TSSDGLG	26607	ACTAGTTCGGATGGGTTGGGT	40930	ACAAGCAGCGACGGACTCGGA
12285	TSSGFKV	26608	ACTTCTTCTGGGTTTAAGGTT	40931	ACAAGCAGCGGATTCAAAGTC
12286	TSSGLTG	26609	ACTTCGTCGGGTCTGACGGGT	40932	ACAAGCAGCGGACTCACAGGA
12287	TSSGTNQ	26610	ACGTCTTCTGGGACTAATCAG	40933	ACAAGCAGCGGAACAAACCAA
12288	TSSHSDV	26611	ACGAGTAGTCATTCGGATGTT	40934	ACAAGCAGCCACAGCGACGTC
12289	TSSHTEH	26612	ACGAGTTCTCATACTGAGCAT	40935	ACAAGCAGCCACACAGAACAC
12290	TSSLAHI	26613	ACGAGTTCGTTGGCTCATATT	40936	ACAAGCAGCCTCGCACACATC
12291	TSSLATH	26614	ACTAGTAGTCTGGCTACTCAT	40937	ACAAGCAGCCTCGCAACACAC
12292	TSSLRLD	26615	ACGAGTAGTTTGAGGTTGGAT	40938	ACAAGCAGCCTCAGACTCGAC
12293	TSSLRPP	26616	ACTAGTTCTCTTAGGCCTCCT	40939	ACAAGCAGCCTCAGACCACCA
12294	TSSNYPS	26617	ACTTCGTCGAATTATCCGTCG	40940	ACAAGCAGCAACTACCCAAGC
12295	TSSPALT	26618	ACGTCGTCTCCGGCGCTGACT	40941	ACAAGCAGCCCAGCACTCACA
12296	TSSPLQG	26619	ACTTCTTCGCCGCTTCAGGGT	40942	ACAAGCAGCCCACTCCAAGGA
12297	TSSQHST	26620	ACTAGTTCGCAGCATTCGACT	40943	ACAAGCAGCCAACACAGCACA
12298	TSSRAYS	26621	ACGTCTAGTCGGGCTTATTCG	40944	ACAAGCAGCAGAGCATACAGC
12299	TSSRLPF	26622	ACGTCTTCGCGTCTTCCTTTT	40945	ACAAGCAGCAGACTCCCATTC
12300	TSSSARD	26623	ACGTCTTCGTCGGCGCGTGAT	40946	ACAAGCAGCAGCGCAAGAGAC
12301	TSSSGLT	26624	ACTTCGAGTTCGGGGCTTACT	40947	ACAAGCAGCAGCGGACTCACA
12302	TSSSNSP	26625	ACGTCGAGTAGTAATAGTCCT	40948	ACAAGCAGCAGCAACAGCCCA
12303	TSSTMSP	26626	ACTTCTTCGACGATGTCGCCT	40949	ACAAGCAGCACAATGAGCCCA
12304	TSSTYEE	26627	ACGTCGTCGACTTATGAGGAG	40950	ACAAGCAGCACATACGAAGAA
12305	TSSVSSI	26628	ACTAGTAGTGTTAGTTCGATT	40951	ACAAGCAGCGTCAGCAGCATC
12306	TSTAALP	26629	ACGAGTACGGCTGCTCTTCCT	40952	ACAAGCACAGCAGCACTCCCA
12307	TSTFEGM	26630	ACTTCGACTTTTGAGGGGATG	40953	ACAAGCACATTCGAAGGAATG
12308	TSTGHTV	26631	ACGAGTACTGGTCATACGGTT	40954	ACAAGCACAGGACACACAGTC
12309	TSTGVRM	26632	ACGTCGACGGGTGTGCGTATG	40955	ACAAGCACAGGAGTCAGAATG
12310	TSTLLSL	26633	ACGTCGACTTTGCTGTCTCTT	40956	ACAAGCACACTCCTCAGCCTC
12311	TSTNSLA	26634	ACTAGTACGAATAGTCTTGCT	40957	ACAAGCACAAACAGCCTCGCA
12312	TSTSMAI	26635	ACGTCTACGTCTATGGCTATT	40958	ACAAGCACAAGCATGGCAATC
12313	TSTSNRN	26636	ACGTCTACTTCGAATCGGAAT	40959	ACAAGCACAAGCAACAGAAAC
12314	TSTTMPL	26637	ACTTCTACTACGATGCCGCTT	40960	ACAAGCACAACAATGCCACTC
12315	TSTTVGN	26638	ACTTCGACTACGGTTGGGAAT	40961	ACAAGCACAACAGTCGGAAAC
12316	TSTVSPK	26639	ACTTCGACTGTGAGTCCTAAG	40962	ACAAGCACAGTCAGCCCAAAA
12317	TSVERSW	26640	ACTTCGGTTGAGCGTTCTTGG	40963	ACAAGCGTCGAAAGAAGCTGG
12318	TSVGDHF	26641	ACGTCTGTGGGTGATCATTTT	40964	ACAAGCGTCGGAGACCACTTC
12319	TSVGWQP	26642	ACGTCTGTTGGTTGGCAGCCG	40965	ACAAGCGTCGGATGGCAACCA

12320	TSVKSAS	26643	ACGTCGGTGAAGTCGGCGTCG	40966	ACAAGCGTCAAAAGCGCAAGC
12321	TSVQPPP	26644	ACTAGTGTGCAGCCGCCGCCT	40967	ACAAGCGTCCAACCACCACCA
12322	TSVSHAG	26645	ACTTCGGTTTCGCATGCTGGT	40968	ACAAGCGTCAGCCACGCAGGA
12323	TSVTMKV	26646	ACTAGTGTTACGATGAAGGTG	40969	ACAAGCGTCACAATGAAAGTC
12324	TSVTTHY	26647	ACGTCGGTGACTACTCATTAT	40970	ACAAGCGTCACAACACACTAC
12325	TSWQGAV	26648	ACGTCGTGGCAGGGTGCTGTT	40971	ACAAGCTGGCAAGGAGCAGTC
12326	TSYGPKV	26649	ACGAGTTATGGTCCGAAGGTT	40972	ACAAGCTACGGACCAAAAGTC
12327	TSYQRIE	26650	ACTAGTTATCAGCGTATTGAG	40973	ACAAGCTACCAAAGAATCGAA
12328	TTAAKVG	26651	ACTACGGCGGCGAAGGTGGGT	40974	ACAACAGCAGCAAAAGTCGGA
12329	TTAEYTR	26652	ACTACGGCTGAGTATACTAGG	40975	ACAACAGCAGAATACACAAGA
12330	TTALPQF	26653	ACGACGGCTTTGCCTCAGTTT	40976	ACAACAGCACTCCCACAATTC
12331	TTAMRGP	26654	ACGACTGCTATGAGGGGTCCT	40977	ACAACAGCAATGAGAGGACCA
12332	TTARQFQ	26655	ACTACGGCTCGTCAGTTTCAG	40978	ACAACAGCAAGACAATTCCAA
12333	TTAVSSK	26656	ACTACGGCGGTTTCGTCTAAG	40979	ACAACAGCAGTCAGCAGCAAA
12334	TTDAARP	26657	ACTACTGATGCTGCGAGGCCT	40980	ACAACAGACGCAGCAAGACCA
12335	TTDCCAA	26658	ACGACGGATTGTTGTGCTGCT	40981	ACAACAGACTGCTGCGCAGCA
12336	TTDVYVR	26659	ACGACTGATGTTTATGTGCGT	40982	ACAACAGACGTCTACGTCAGA
12337	TTDYPLS	26660	ACTACTGATTATCCTCTGAGT	40983	ACAACAGACTACCCACTCAGC
12338	TTEHGYV	26661	ACTACGGAGCATGGTTATGTT	40984	ACAACAGAACACGGATACGTC
12339	TTFLQNG	26662	ACGACTTTTCTTCAGAATGGT	40985	ACAACATTCCTCCAAAACGGA
12340	TTGAIDI	26663	ACTACTGGTGCTATTGATATT	40986	ACAACAGGAGCAATCGACATC
12341	TTGHLSV	26664	ACTACGGGTCATCTTTCTGTT	40987	ACAACAGGACACCTCAGCGTC
12342	TTGHTLI	26665	ACTACGGGTCATACGCTTATT	40988	ACAACAGGACACACACTCATC
12343	TTGLSLG	26666	ACTACTGGGCTTAGTCTGGGT	40989	ACAACAGGACTCAGCCTCGGA
12344	TTGNSLP	26667	ACGACTGGGAATTCTCTTCCT	40990	ACAACAGGAAACAGCCTCCCA
12345	TTGNTLS	26668	ACTACTGGTAATACGTTGTCT	40991	ACAACAGGAAACACACTCAGC
12346	TTGSIPH	26669	ACTACTGGTTCGATTCCTCAT	40992	ACAACAGGAAGCATCCCACAC
12347	TTHAPLS	26670	ACTACTCATGCTCCTCTTTCG	40993	ACAACACACGCACCACTCAGC
12348	TTHASCT	26671	ACTACGCATGCTTCGTGTACG	40994	ACAACACACGCAAGCTGCACA
12349	TTHDVYR	26672	ACTACTCATGATGTTTATCGG	40995	ACAACACACGACGTCTACAGA
12350	TTHSTAA	26673	ACTACTCATTCGACGGCGGCG	40996	ACAACACACAGCACAGCAGCA
12351	TTHTQYR	26674	ACTACGCATACGCAGTATCGT	40997	ACAACACACACACAATACAGA
12352	TTILGPM	26675	ACTACGATTCTTGGTCCTATG	40998	ACAACAATCCTCGGACCAATG
12353	TTKIGDD	26676	ACGACGAAGATTGGTGATGAT	40999	ACAACAAAAATCGGAGACGAC
12354	TTKSADT	26677	ACTACTAAGAGTGCTGATACT	41000	ACAACAAAAAGCGCAGACACA
12355	TTKVGSP	26678	ACGACGAAGGTTGGTTCTCCG	41001	ACAACAAAAGTCGGAAGCCCA
12356	TTLDPSL	26679	ACTACGTTGGATCCTTCTTTG	41002	ACAACACTCGACCCAAGCCTC
12357	TTLGPSR	26680	ACTACGCTTGGTCCGTCGCGT	41003	ACAACACTCGGACCAAGCAGA
12358	TTLGSAV	26681	ACGACGCTTGGGTCTGCTGTG	41004	ACAACACTCGGAAGCGCAGTC
12359	TTLSGGT	26682	ACGACGTTGAGTGGGGGTACT	41005	ACAACACTCAGCGGAGGAACA
12360	TTLSPNK	26683	ACTACTCTGTCGCCGAATAAG	41006	ACAACACTCAGCCCAAACAAA
12361	TTLSPRG	26684	ACGACGCTGTCTCCGAGGGGT	41007	ACAACACTCAGCCCAAGAGGA
12362	TTLSSLA	26685	ACTACGTTGTCTAGTCTGGCT	41008	ACAACACTCAGCAGCCTCGCA
12363	TTMALGA	26686	ACTACTATGGCTCTTGGGGCG	41009	ACAACAATGGCACTCGGAGCA
12364	TTMKPEA	26687	ACGACTATGAAGCCGGAGGCT	41010	ACAACAATGAAACCAGAAGCA

12365	TTMTLVS	26688	ACTACTATGACTTTGGTTTCG	41011	ACAACAATGACACTCGTCAGC
12366	TTMYTTT	26689	ACTACGATGTATACGACTACT	41012	ACAACAATGTACACAACAACA
12367	TTNAQGG	26690	ACGACTAATGCTCAGGGTGGT	41013	ACAACAAACGCACAAGGAGGA
12368	TTNIVRQ	26691	ACTACGAATATTGTGCGGCAG	41014	ACAACAAACATCGTCAGACAA
12369	TTNLAMM	26692	ACTACTAATTTGGCTATGATG	41015	ACAACAAACCTCGCAATGATG
12370	TTPGYAP	26693	ACGACGCCGGGTTATGCTCCG	41016	ACAACACCAGGATACGCACCA
12371	TTPIRDG	26694	ACGACGCCTATTAGGGATGGT	41017	ACAACACCAATCAGAGACGGA
12372	TTPLTKG	26695	ACTACTCCTTTGACGAAGGGG	41018	ACAACACCACTCACAAAAGGA
12373	TTPPMHL	26696	ACTACTCCTCCGATGCATCTT	41019	ACAACACCACCAATGCACCTC
12374	TTPQLNL	26697	ACTACTCCTCAGCTGAATTTG	41020	ACAACACCACAACTCAACCTC
12375	TTPRLLS	26698	ACGACGCCTAGGTTGTTGTCT	41021	ACAACACCAAGACTCCTCAGC
12376	TTPTDGA	26699	ACGACTCCTACTGATGGGGCG	41022	ACAACACCAACAGACGGAGCA
12377	TTPTNRP	26700	ACGACGCCGACGAATCGTCCT	41023	ACAACACCAACAAACAGACCA
12378	TTQEHLP	26701	ACTACGCAGGAGCATCTGCCG	41024	ACAACACAAGAACACCTCCCA
12379	TTQNVNQ	26702	ACGACGCAGAATGTGAATCAG	41025	ACAACACAAAACGTCAACCAA
12380	TTQSTYE	26703	ACGACGCAGTCTACTTATGAG	41026	ACAACACAAAGCACATACGAA
12381	TTQTAET	26704	ACGACGCAGACGGCTGAGACG	41027	ACAACACAAACAGCAGAAACA
12382	TTRDPPA	26705	ACGACGAGGGATCCTCCGGCT	41028	ACAACAAGAGACCCACCAGCA
12383	TTRGDEP	26706	ACTACGAGGGGTGATGAGCCT	41029	ACAACAAGAGGAGACGAACCA
12384	TTRIAAE	26707	ACGACTAGGATTGCGGCTGAG	41030	ACAACAAGAATCGCAGCAGAA
12385	TTRLALA	26708	ACGACTCGGCTGGCTCTTGCT	41031	ACAACAAGACTCGCACTCGCA
12386	TTRLVSP	26709	ACTACGCGGCTGGTGAGTCCG	41032	ACAACAAGACTCGTCAGCCCA
12387	TTRPPHY	26710	ACGACGCGTCCTCCGCATTAT	41033	ACAACAAGACCACCACACTAC
12388	TTRPSEP	26711	ACTACGCGTCCGTCTGAGCCG	41034	ACAACAAGACCAAGCGAACCA
12389	TTRQSDN	26712	ACTACGAGGCAGTCTGATAAT	41035	ACAACAAGACAAAGCGACAAC
12390	TTRSAAS	26713	ACTACTCGTTCGGCTGCGTCT	41036	ACAACAAGAAGCGCAGCAAGC
12391	TTRSESG	26714	ACTACGAGGAGTGAGTCTGGT	41037	ACAACAAGAAGCGAAAGCGGA
12392	TTRSVLQ	26715	ACGACTCGGTCTGTGCTGCAG	41038	ACAACAAGAAGCGTCCTCCAA
12393	TTRVEMA	26716	ACTACTAGGGTTGAGATGGCT	41039	ACAACAAGAGTCGAAATGGCA
12394	TTRVGLV	26717	ACGACTCGGGTTGGGTTGGTG	41040	ACAACAAGAGTCGGACTCGTC
12395	TTSADHS	26718	ACTACTAGTGCGGATCATTCT	41041	ACAACAAGCGCAGACCACAGC
12396	TTSAREL	26719	ACGACTAGTGCGCGTGAGCTT	41042	ACAACAAGCGCAAGAGAACTC
12397	TTSGDRL	26720	ACGACGTCGGGGTGATCGTCTG	41043	ACAACAAGCGGAGACAGACTC
12398	TTSGFSP	26721	ACGACTTCTGGGTTTAGTCCT	41044	ACAACAAGCGGATTCAGCCCA
12399	TTSHAPS	26722	ACTACGTCGCATGCTCCGTCT	41045	ACAACAAGCCACGCACCAAGC
12400	TTSHPLM	26723	ACTACTAGTCATCCTCTTATG	41046	ACAACAAGCCACCCACTCATG
12401	TTSIGSA	26724	ACGACGAGTATTGGGTCGGCG	41047	ACAACAAGCATCGGAAGCGCA
12402	TTSLGRV	26725	ACTACGTCTCTGGGTCGTGTT	41048	ACAACAAGCCTCGGAAGAGTC
12403	TTSLMEA	26726	ACTACGTCTTTGATGGAGGCT	41049	ACAACAAGCCTCATGGAAGCA
12404	TTSNVHT	26727	ACGACGAGTAATGTTCATACT	41050	ACAACAAGCAACGTCCACACA
12405	TTSPLRT	26728	ACTACTTCTCCGTTGCGTACT	41051	ACAACAAGCCCACTCAGAACA
12406	TTSPQRS	26729	ACGACTAGTCCGCAGAGGTCT	41052	ACAACAAGCCCACAAAGAAGC
12407	TTSRLSA	26730	ACGACTTCGCGTCTGTCTGCT	41053	ACAACAAGCAGACTCAGCGCA
12408	TTSSSPS	26731	ACGACTTCGAGTAGTCCGTCT	41054	ACAACAAGCAGCAGCCCAAGC
12409	TTTAMIV	26732	ACGACTACTGCTATGATTGTG	41055	ACAACAACAGCAATGATCGTC

12410	TTTASFE	26733	ACTACTACGGCGAGTTTTGAG	41056	ACAACAACAGCAAGCTTCGAA
12411	TTTDKPL	26734	ACGACTACTGATAAGCCGCTT	41057	ACAACAACAGACAAACCACTC
12412	TTTDVAR	26735	ACGACGACGGATGTGGCGCGT	41058	ACAACAACAGACGTCGCAAGA
12413	TTTERTR	26736	ACGACTACGGAGAGGACTAGG	41059	ACAACAACAGAAAGAACAAGA
12414	TTTKHVY	26737	ACTACGACGAAGCATGTGTAT	41060	ACAACAACAAAACACGTCTAC
12415	TTTPITN	26738	ACGACGACGCCTATTACTAAT	41061	ACAACAACACCAATCACAAAC
12416	TTTRVNA	26739	ACTACGACTCGTGTGAATGCG	41062	ACAACAACAAGAGTCAACGCA
12417	TTTVPIF	26740	ACGACTACGGTTCCGATTTTT	41063	ACAACAACAGTCCCAATCTTC
12418	TTTVTYL	26741	ACTACTACTGTGACTTATCTT	41064	ACAACAACAGTCACATACCTC
12419	TTVDVVH	26742	ACTACTGTGGATGTGGTGCAT	41065	ACAACAGTCGACGTCGTCCAC
12420	TTVPDSV	26743	ACGACTGTTCCTGATAGTGTT	41066	ACAACAGTCCCAGACAGCGTC
12421	TTVPNTS	26744	ACTACTGTTCCGAATACGTCG	41067	ACAACAGTCCCAAACACAAGC
12422	TTVRVHP	26745	ACGACTGTGAGGGTTCATCCG	41068	ACAACAGTCAGAGTCCACCCA
12423	TTVVSDL	26746	ACGACGGTGGTGTCGGATTTG	41069	ACAACAGTCGTCAGCGACCTC
12424	TTVVYTA	26747	ACGACTGTGGTTTATACTGCG	41070	ACAACAGTCGTCTACACAGCA
12425	TTYPIHA	26748	ACGACGTATCCTATTCATGCT	41071	ACAACATACCCAATCCACGCA
12426	TTYSNSA	26749	ACTACTTATTCTAATTCGGCT	41072	ACAACATACAGCAACAGCGCA
12427	TVAGNIA	26750	ACGGTGGCTGGGAATATTGCG	41073	ACAGTCGCAGGAAACATCGCA
12428	TVAHRIP	26751	ACTGTTGCTCATAGGATTCCT	41074	ACAGTCGCACACAGAATCCCA
12429	TVAIHEP	26752	ACTGTGGCTATTCATGAGCCT	41075	ACAGTCGCAATCCACGAACCA
12430	TVAPDLN	26753	ACTGTTGCTCCGGATCTGAAT	41076	ACAGTCGCACCAGACCTCAAC
12431	TVCVSRT	26754	ACTGTTTGTGTGTCGAGGACT	41077	ACAGTCTGCGTCAGCAGAACA
12432	TVDEWAG	26755	ACGGTGGATGAGTGGGCTGGG	41078	ACAGTCGACGAATGGGCAGGA
12433	TVDGSHQ	26756	ACGGTTGATGGTTCGCATCAG	41079	ACAGTCGACGGAAGCCACCAA
12434	TVDSSGV	26757	ACGGTTGATTCTAGTGGGGTT	41080	ACAGTCGACAGCAGCGGAGTC
12435	TVDTKHS	26758	ACGGTTGATACTAAGCATTCT	41081	ACAGTCGACACAAAACACAGC
12436	TVEGDRL	26759	ACTGTGGAGGGTGATCGTCTT	41082	ACAGTCGAAGGAGACAGACTC
12437	TVFSESE	26760	ACGGTTTTTTCGGAGTCTGAG	41083	ACAGTCTTCAGCGAAAGCGAA
12438	TVGHLNV	26761	ACGGTGGGTCATCTTAATGTT	41084	ACAGTCGGACACCTCAACGTC
12439	TVGNYRD	26762	ACTGTTGGTAATTATCGTGAT	41085	ACAGTCGGAAACTACAGAGAC
12440	TVGSLSD	26763	ACGGTTGGTTCTCTTTCTGAT	41086	ACAGTCGGAAGCCTCAGCGAC
12441	TVGTLML	26764	ACGGTGGGTACGCTGATGTTG	41087	ACAGTCGGAACACTCATGCTC
12442	TVGTPPT	26765	ACGGTTGGTACTCCGCCGACT	41088	ACAGTCGGAACACCACCAACA
12443	TVGTRAM	26766	ACGGTGGGTACGCGGGCTATG	41089	ACAGTCGGAACAAGAGCAATG
12444	TVGVEGS	26767	ACTGTGGGGGTGGAGGGGTCG	41090	ACAGTCGGAGTCGAAGGAAGC
12445	TVGVNAS	26768	ACGGTTGGTGTTAATGCTTCT	41091	ACAGTCGGAGTCAACGCAAGC
12446	TVHFSQA	26769	ACGGTTCATTTTAGTCAGGCG	41092	ACAGTCCACTTCAGCCAAGCA
12447	TVHILTP	26770	ACTGTTCATATTTTGACGCCT	41093	ACAGTCCACATCCTCACACCA
12448	TVHNVQF	26771	ACGGTTCATAATGTTCAGTTT	41094	ACAGTCCACAACGTCCAATTC
12449	TVHRQVD	26772	ACGGTTCATCGGCAGGTTGAT	41095	ACAGTCCACAGACAAGTCGAC
12450	TVHTFRE	26773	ACTGTGCATACGTTTAGGGAG	41096	ACAGTCCACACATTCAGAGAA
12451	TVKISEG	26774	ACTGTTAAGATTTCTGAGGGG	41097	ACAGTCAAAATCAGCGAAGGA
12452	TVKQSQV	26775	ACTGTGAAGCAGTCTCAGGTT	41098	ACAGTCAAACAAAGCCAAGTC
12453	TVKVSKP	26776	ACTGTTAAGGTGAGTAAGCCG	41099	ACAGTCAAAGTCAGCAAACCA
12454	TVLAARG	26777	ACGGTGCTTGCGGCTAGGGGG	41100	ACAGTCCTCGCAGCAAGAGGA

12455	TVLASPV	26778	ACGGTGCTGGCTTCGCCTGTG	41101	ACAGTCCTCGCAAGCCCAGTC
12456	TVLESQS	26779	ACGGTTCTTGAGTCGCAGTCG	41102	ACAGTCCTCGAAAGCCAAAGC
12457	TVLKTSI	26780	ACTGTTTTGAAGACTTCGATT	41103	ACAGTCCTCAAAACAAGCATC
12458	TVMRTLA	26781	ACTGTTATGCGGACTTTGGCT	41104	ACAGTCATGAGAACACTCGCA
12459	TVMRVTG	26782	ACTGTGATGCGTGTTACTGGT	41105	ACAGTCATGAGAGTCACAGGA
12460	TVNGLRA	26783	ACGGTTAATGGTCTTCGGGCT	41106	ACAGTCAACGGACTCAGAGCA
12461	TVNHQSL	26784	ACTGTGAATCATCAGTCGTTG	41107	ACAGTCAACCACCAAAGCCTC
12462	TVNIETN	26785	ACTGTTAATATTGAGACTAAT	41108	ACAGTCAACATCGAAACAAAC
12463	TVNKVCL	26786	ACTGTTAATAAGGTGTGTCTG	41109	ACAGTCAACAAAGTCTGCCTC
12464	TVNYNDI	26787	ACTGTTAATTATAATGATATT	41110	ACAGTCAACTACAACGACATC
12465	TVPAGHE	26788	ACTGTGCCTGCTGGGCATGAG	41111	ACAGTCCCAGCAGGACACGAA
12466	TVPARTM	26789	ACTGTTCCTGCGCGGACGATG	41112	ACAGTCCCAGCAAGAACAATG
12467	TVPQSVL	26790	ACTGTGCCTCAGAGTGTGCTT	41113	ACAGTCCCACAAAGCGTCCTC
12468	TVPTAVA	26791	ACTGTTCCGACTGCGGTTGCT	41114	ACAGTCCCAACAGCAGTCGCA
12469	TVPVAIV	26792	ACTGTTCCGGTTGCGATTGTT	41115	ACAGTCCCAGTCGCAATCGTC
12470	TVQDTFR	26793	ACGGTGCAGGATACTTTTCGT	41116	ACAGTCCAAGACACATTCAGA
12471	TVQGIDR	26794	ACGGTGCAGGGGATTGATCGT	41117	ACAGTCCAAGGAATCGACAGA
12472	TVQQQAN	26795	ACTGTTCAGCAGCAGGCGAAT	41118	ACAGTCCAACAACAAGCAAAC
12473	TVQSPLL	26796	ACTGTTCAGAGTCCTCTTTTG	41119	ACAGTCCAAAGCCCACTCCTC
12474	TVQSSAT	26797	ACTGTTCAGTCGAGTGCGACT	41120	ACAGTCCAAAGCAGCGCAACA
12475	TVQTTST	26798	ACGGTTCAGACTACGTCTACG	41121	ACAGTCCAAACAACAAGCACA
12476	TVQVRLP	26799	ACGGTGCAGGTGCGGCTGCCT	41122	ACAGTCCAAGTCAGACTCCCA
12477	TVRGISL	26800	ACGGTTAGGGGGATTTCGTTG	41123	ACAGTCAGAGGAATCAGCCTC
12478	TVRGLDT	26801	ACTGTTCGTGGGTTGGATACG	41124	ACAGTCAGAGGACTCGACACA
12479	TVRGSPL	26802	ACTGTTCGTGGTAGTCCTTTG	41125	ACAGTCAGAGGAAGCCCACTC
12480	TVRLDGV	26803	ACGGTTCGGCTGGATGGGGTT	41126	ACAGTCAGACTCGACGGAGTC
12481	TVRPVSS	26804	ACTGTTCGTCCGGTTTCTTCT	41127	ACAGTCAGACCAGTCAGCAGC
12482	TVRSPSI	26805	ACTGTGCGTTCTCCTTCGATT	41128	ACAGTCAGAAGCCCAAGCATC
12483	TVSAQPR	26806	ACTGTTTCTGCTCAGCCGCGG	41129	ACAGTCAGCGCACAACCAAGA
12484	TVSDTSF	26807	ACTGTTTCTGATACTTCGTTT	41130	ACAGTCAGCGACACAAGCTTC
12485	TVSGKHT	26808	ACTGTGTCTGGGAAGCATACG	41131	ACAGTCAGCGGAAAACACACA
12486	TVSHGQR	26809	ACTGTGAGTCATGGTCAGCGT	41132	ACAGTCAGCCACGGACAAAGA
12487	TVSKMGG	26810	ACGGTGTCTAAGATGGGTGGG	41133	ACAGTCAGCAAAATGGGAGGA
12488	TVSRNDA	26811	ACGGTGTCTCGGAATGATGCT	41134	ACAGTCAGCAGAAACGACGCA
12489	TVSRQVC	26812	ACTGTTAGTCGGCAGGTGTGT	41135	ACAGTCAGCAGACAAGTCTGC
12490	TVSTTCA	26813	ACGGTGAGTACGACTTGTGCT	41136	ACAGTCAGCACAACATGCGCA
12491	TVSVTKP	26814	ACGGTGTCGGTGACTAAGCCG	41137	ACAGTCAGCGTCACAAAACCA
12492	TVSVVDK	26815	ACTGTTAGTGTGGTGGATAAG	41138	ACAGTCAGCGTCGTCGACAAA
12493	TVTEARN	26816	ACGGTGACGGAGGCGAGGAAT	41139	ACAGTCACAGAAGCAAGAAAC
12494	TVTGNGF	26817	ACGGTTACGGGTAATGGTTTT	41140	ACAGTCACAGGAAACGGATTC
12495	TVTHNME	26818	ACGGTGACTCATAATATGGAG	41141	ACAGTCACACACAACATGGAA
12496	TVTNPRN	26819	ACTGTGACTAATCCGCGGAAT	41142	ACAGTCACAAACCCAAGAAAC
12497	TVTPAVN	26820	ACTGTGACGCCTGCGGTGAAT	41143	ACAGTCACACCAGCAGTCAAC
12498	TVTRHPS	26821	ACTGTGACTCGGCATCCGTCT	41144	ACAGTCACAAGACACCCAAGC
12499	TVTTAER	26822	ACGGTGACTACGGCTGAGCGT	41145	ACAGTCACAACAGCAGAAAGA

12500	TVTTGRW	26823	ACGGTGACGACGGGTCGGTGG	41146	ACAGTCACAACAGGAAGATGG
12501	TVTTRQA	26824	ACGGTGACTACTCGTCAGGCG	41147	ACAGTCACAACAAGACAAGCA
12502	TVVKSGD	26825	ACGGTTGTGAAGTCTGGTGAT	41148	ACAGTCGTCAAAAGCGGAGAC
12503	TVVLTSG	26826	ACGGTTGTTCTGACTAGTGGG	41149	ACAGTCGTCCTCACAAGCGGA
12504	TVVPSGR	26827	ACTGTTGTGCCTTCTGGGCGT	41150	ACAGTCGTCCCAAGCGGAAGA
12505	TVVPVPG	26828	ACGGTGGTGCCGGTTCCTGGG	41151	ACAGTCGTCCCAGTCCCAGGA
12506	TVYSGRP	26829	ACTGTGTATTCGGGTAGGCCT	41152	ACAGTCTACAGCGGAAGACCA
12507	TVYSPNT	26830	ACTGTTTATAGTCCTAATACT	41153	ACAGTCTACAGCCCAAACACA
12508	TWNATMN	26831	ACTTGGAATGCTACTATGAAT	41154	ACATGGAACGCAACAATGAAC
12509	TWQDNRA	26832	ACGTGGCAGGATAATAGGGCT	41155	ACATGGCAAGACAACAGAGCA
12510	TWSATQG	26833	ACGTGGAGTGCGACTCAGGGG	41156	ACATGGAGCGCAACACAAGGA
12511	TWSSGTD	26834	ACTTGGAGTTCGGGTACGGAT	41157	ACATGGAGCAGCGGAACAGAC
12512	TWSTNVS	26835	ACGTGGTCTACTAATGTGAGT	41158	ACATGGAGCACAAACGTCAGC
12513	TYAIIPD	26836	ACTTATGCTATTATTCCGGAT	41159	ACATACGCAATCATCCCAGAC
12514	TYANSAF	26837	ACTTATGCTAATTCGGCGTTT	41160	ACATACGCAAACAGCGCATTC
12515	TYANVSS	26838	ACTTATGCTAATGTTTCTAGT	41161	ACATACGCAAACGTCAGCAGC
12516	TYAPSRG	26839	ACGTATGCTCCTTCTCGGGGT	41162	ACATACGCACCAAGCAGAGGA
12517	TYAPVET	26840	ACTTATGCGCCGGTGGAGACG	41163	ACATACGCACCAGTCGAAACA
12518	TYARSQA	26841	ACTTATGCTCGGTCGCAGGCG	41164	ACATACGCAAGAAGCCAAGCA
12519	TYEARQL	26842	ACGTATGAGGCTAGGCAGCTG	41165	ACATACGAAGCAAGACAACTC
12520	TYEGRLR	26843	ACTTATGAGGGTAGGCTGCGG	41166	ACATACGAAGGAAGACTCAGA
12521	TYELSPP	26844	ACTTATGAGCTTTCTCCGCCT	41167	ACATACGAACTCAGCCCACCA
12522	TYEVRQL	26845	ACGTATGAGGTTCGTCAGCTT	41168	ACATACGAAGTCAGACAACTC
12523	TYGAAVQ	26846	ACGTATGGGGCTGCGGTGCAG	41169	ACATACGGAGCAGCAGTCCAA
12524	TYGGPMI	26847	ACGTATGGGGGTCCGATGATT	41170	ACATACGGAGGACCAATGATC
12525	TYGIQAP	26848	ACGTATGGTATTCAGGCTCCT	41171	ACATACGGAATCCAAGCACCA
12526	TYGLSVP	26849	ACTTATGGTCTTTCGGTGCCT	41172	ACATACGGACTCAGCGTCCCA
12527	TYGMTGA	26850	ACTTATGGTATGACGGGTGCT	41173	ACATACGGAATGACAGGAGCA
12528	TYHTGDG	26851	ACTTATCATACTGGTGATGGG	41174	ACATACCACACAGGAGACGGA
12529	TYINTNP	26852	ACGTATATTAATACGAATCCG	41175	ACATACATCAACACAAACCCA
12530	TYKDEQP	26853	ACTTATAAGGATGAGCAGCCT	41176	ACATACAAAGACGAACAACCA
12531	TYKGAPP	26854	ACTTATAAGGGTGCTCCGCCG	41177	ACATACAAAGGAGCACCACCA
12532	TYKNQTH	26855	ACTTATAAGAATCAGACGCAT	41178	ACATACAAAAACCAAACACAC
12533	TYLIATP	26856	ACGTATTTGATTGCTACGCCG	41179	ACATACCTCATCGCAACACCA
12534	TYLSGAY	26857	ACTTATCTGTCTGGGGCTTAT	41180	ACATACCTCAGCGGAGCATAC
12535	TYPLPNE	26858	ACTTATCCGCTGCCGAATGAG	41181	ACATACCCACTCCCAAACGAA
12536	TYPPAAL	26859	ACGTATCCTCCTGCGGCTTTG	41182	ACATACCCACCAGCAGCACTC
12537	TYPTEPR	26860	ACTTATCCGACGGAGCCTCGG	41183	ACATACCCAACAGAACCAAGA
12538	TYPTLLD	26861	ACGTATCCTACGTTGCTTGAT	41184	ACATACCCAACACTCCTCGAC
12539	TYQASLI	26862	ACGTATCAGGCTTCTCTTATT	41185	ACATACCAAGCAAGCCTCATC
12540	TYQSQSG	26863	ACGTATCAGTCGCAGAGTGGG	41186	ACATACCAAAGCCAAAGCGGA
12541	TYSAETM	26864	ACTTATTCTGCGGAGACTATG	41187	ACATACAGCGCAGAAACAATG
12542	TYSAVLA	26865	ACGTATTCTGCGGTGCTGGCT	41188	ACATACAGCGCAGTCCTCGCA
12543	TYSHARA	26866	ACGTATTCGCATGCTCGGGCT	41189	ACATACAGCCACGCAAGAGCA
12544	TYSPTAT	26867	ACGTATTCGCCTACTGCTACG	41190	ACATACAGCCCAACAGCAACA

12545	TYSTAIY	26868	ACGTATTCTACGGCGATTTAT	41191	ACATACAGCACAGCAATCTAC
12546	TYSVSLA	26869	ACGTATTCTGTTTCGCTTGCG	41192	ACATACAGCGTCAGCCTCGCA
12547	TYSYSSA	26870	ACGTATAGTTATTCGAGTGCT	41193	ACATACAGCTACAGCAGCGCA
12548	TYTGLAA	26871	ACGTATACTGGGCTGGCGGCG	41194	ACATACACAGGACTCGCAGCA
12549	TYTHHSV	26872	ACGTATACGCATCATAGTGTG	41195	ACATACACACACCACAGCGTC
12550	TYTSTYA	26873	ACGTATACGTCTACTTATGCT	41196	ACATACACAAGCACATACGCA
12551	TYVDVLH	26874	ACTTATGTTGATGTTCTTCAT	41197	ACATACGTCGACGTCCTCCAC
12552	TYVGRGA	26875	ACGTATGTTGGTAGGGGGGCG	41198	ACATACGTCGGAAGAGGAGCA
12553	TYVMTPK	26876	ACTTATGTGATGACTCCTAAG	41199	ACATACGTCATGACACCAAAA
12554	TYYAAEI	26877	ACTTATTATGCGGCTGAGATT	41200	ACATACTACGCAGCAGAAATC
12555	TYYKNTG	26878	ACTTATTATAAGAATACGGGT	41201	ACATACTACAAAAACACAGGA
12556	VAAGQSP	26879	GTTGCTGCGGGGCAGTCGCCT	41202	GTCGCAGCAGGACAAAGCCCA
12557	VAARSAQ	26880	GTGGCGGCGCGTTCGGCGCAG	41203	GTCGCAGCAAGAAGCGCACAA
12558	VADATKP	26881	GTTGCGGATGCGACGAAGCCT	41204	GTCGCAGACGCAACAAAACCA
12559	VADFVRC	26882	GTGGCTGATTTTGTTCGTTGT	41205	GTCGCAGACTTCGTCAGATGC
12560	VADKALV	26883	GTTGCGGATAAGGCGTTGGTT	41206	GTCGCAGACAAAGCACTCGTC
12561	VADLRPE	26884	GTGGCGGATCTGCGGCCGGAG	41207	GTCGCAGACCTCAGACCAGAA
12562	VADPPRS	26885	GTTGCTGATCCTCCTAGGTCG	41208	GTCGCAGACCCACCAAGAAGC
12563	VADRLTT	26886	GTTGCTGATCGTTTGACTACT	41209	GTCGCAGACAGACTCACAACA
12564	VAEHPKR	26887	GTTGCTGAGCATCCTAAGCGG	41210	GTCGCAGAACACCCAAAAAGA
12565	VAEQHSL	26888	GTGGCTGAGCAGCATTCTCTG	41211	GTCGCAGAACAACACAGCCTC
12566	VAGAGTT	26889	GTTGCTGGGGCGGGTACGACT	41212	GTCGCAGGAGCAGGAACAACA
12567	VAGAHAT	26890	GTTGCTGGTGCTCATGCGACT	41213	GTCGCAGGAGCACACGCAACA
12568	VAGDAKN	26891	GTGGCTGGTGATGCGAAGAAT	41214	GTCGCAGGAGACGCAAAAAAC
12569	VAGIRSQ	26892	GTTGCGGGTATTCGGAGTCAG	41215	GTCGCAGGAATCAGAAGCCAA
12570	VAGLNHR	26893	GTTGCTGGGTTGAATCATCGT	41216	GTCGCAGGACTCAACCACAGA
12571	VAGPTGP	26894	GTGGCGGGGCCGACTGGTCCT	41217	GTCGCAGGACCAACAGGACCA
12572	VAGQRSG	26895	GTGGCTGGTCAGAGGAGTGGT	41218	GTCGCAGGACAAAGAAGCGGA
12573	VAGQSPP	26896	GTGGCGGGGCAGTCGCCTCCT	41219	GTCGCAGGACAAAGCCCACCA
12574	VAGRDQP	26897	GTTGCTGGGCGGGATCAGCCG	41220	GTCGCAGGAAGAGACCAACCA
12575	VAGRDVR	26898	GTGGCGGGGCGTGATGTGCGG	41221	GTCGCAGGAAGAGACGTCAGA
12576	VAGRDYQ	26899	GTTGCGGGGCGGGATTATCAG	41222	GTCGCAGGAAGAGACTACCAA
12577	VAGSATV	26900	GTGGCTGGGAGTGCGACGGTT	41223	GTCGCAGGAAGCGCAACAGTC
12578	VAGTVER	26901	GTTGCTGGTACTGTTGAGCGT	41224	GTCGCAGGAACAGTCGAAAGA
12579	VAGVRTA	26902	GTGGCGGGTGTGAGGACTGCT	41225	GTCGCAGGAGTCAGAACAGCA
12580	VAGVSEM	26903	GTTGCTGGTGTTTCGGAGATG	41226	GTCGCAGGAGTCAGCGAAATG
12581	VAHLSMS	26904	GTTGCGCATCTTAGTATGTCG	41227	GTCGCACACCTCAGCATGAGC
12582	VAHSLPA	26905	GTGGCTCATTCGTTGCCTGCT	41228	GTCGCACACAGCCTCCCAGCA
12583	VAHSTNA	26906	GTGGCGCATTCTACTAATGCT	41229	GTCGCACACAGCACAAACGCA
12584	VAHTGAR	26907	GTTGCTCATACTGGGGCTCGG	41230	GTCGCACACACAGGAGCAAGA
12585	VAHTVYS	26908	GTTGCTCATACGGTGTATTCG	41231	GTCGCACACACAGTCTACAGC
12586	VAHVQSD	26909	GTTGCTCATGTGCAGAGTGAT	41232	GTCGCACACGTCCAAAGCGAC
12587	VAHYPAS	26910	GTTGCGCATTATCCGGCTAGT	41233	GTCGCACACTACCCAGCAAGC
12588	VAIHGAV	26911	GTTGCGATTCATGGTGCTGTT	41234	GTCGCAATCCACGGAGCAGTC
12589	VAIPRGS	26912	GTTGCGATTCCGCGTGGGTCT	41235	GTCGCAATCCCAAGAGGAAGC

12590	VAIRSPA	26913	GTGGCGATTCGTAGTCCTGCT	41236	GTCGCAATCAGAAGCCCAGCA
12591	VALAGQY	26914	GTGGCGCTTGCGGGGCAGTAT	41237	GTCGCACTCGCAGGACAATAC
12592	VALHPLN	26915	GTGGCTCTGCATCCTTTGAAT	41238	GTCGCACTCCACCCACTCAAC
12593	VALIKYS	26916	GTGGCGCTGATTAAGTATAGT	41239	GTCGCACTCATCAAATACAGC
12594	VALSAAK	26917	GTGGCTTTGTCTGCGGCTAAG	41240	GTCGCACTCAGCGCAGCAAAA
12595	VANETHY	26918	GTTGCGAATGAGACGCATTAT	41241	GTCGCAAACGAAACACACTAC
12596	VANGKSH	26919	GTGGCTAATGGTAAGTCTCAT	41242	GTCGCAAACGGAAAAAGCCAC
12597	VANHIEV	26920	GTTGCTAATCATATTGAGGTT	41243	GTCGCAAACCACATCGAAGTC
12598	VANQQGT	26921	GTGGCTAATCAGCAGGGGACG	41244	GTCGCAAACCAACAAGGAACA
12599	VANRDVQ	26922	GTGGCGAATAGGGATGTGCAG	41245	GTCGCAAACAGAGACGTCCAA
12600	VANVLTN	26923	GTTGCTAATGTGCTTACGAAT	41246	GTCGCAAACGTCCTCACAAAC
12601	VAPAIPG	26924	GTTGCGCCGGCGATTCCTGGT	41247	GTCGCACCAGCAATCCCAGGA
12602	VAPIGSE	26925	GTTGCTCCTATTGGGTCTGAG	41248	GTCGCACCAATCGGAAGCGAA
12603	VAPLIPK	26926	GTTGCGCCGCTTATTCCGAAG	41249	GTCGCACCACTCATCCCAAAA
12604	VAPPPQK	26927	GTTGCTCCTCCTCCTCAGAAG	41250	GTCGCACCACCACCACAAAAA
12605	VAPPPRH	26928	GTTGCTCCTCCGCCTAGGCAT	41251	GTCGCACCACCACCAAGACAC
12606	VAPPYSG	26929	GTTGCGCCGCCGTATTCTGGT	41252	GTCGCACCACCATACAGCGGA
12607	VAPSEGS	26930	GTGGCGCCGTCTGAGGGTAGT	41253	GTCGCACCAAGCGAAGGAAGC
12608	VAPSQRL	26931	GTTGCGCCGTCGCAGCGGTTG	41254	GTCGCACCAAGCCAAAGACTC
12609	VAQRSGP	26932	GTTGCGCAGCGTTCGGGTCCG	41255	GTCGCACAAAGAAGCGGACCA
12610	VAQSRSI	26933	GTGGCTCAGAGTCGGAGTATT	41256	GTCGCACAAAGCAGAAGCATC
12611	VARAHIV	26934	GTTGCGCGGGCTCATATTGTG	41257	GTCGCAAGAGCACACATCGTC
12612	VARGPTT	26935	GTTGCGAGGGGGCCGACTACT	41258	GTCGCAAGAGGACCAACAACA
12613	VARHSNE	26936	GTGGCGAGGCATTCTAATGAG	41259	GTCGCAAGACACAGCAACGAA
12614	VARIDGM	26937	GTTGCTAGGATTGATGGGATG	41260	GTCGCAAGAATCGACGGAATG
12615	VARLPQV	26938	GTTGCGCGGCTGCCTCAGGTT	41261	GTCGCAAGACTCCCACAAGTC
12616	VARPLSM	26939	GTTGCTCGGCCGCTTTCGATG	41262	GTCGCAAGACCACTCAGCATG
12617	VARSGTT	26940	GTTGCGAGGAGTGGTACGACT	41263	GTCGCAAGAAGCGGAACAACA
12618	VARSLQA	26941	GTTGCTAGGTCGCTTCAGGCT	41264	GTCGCAAGAAGCCTCCAAGCA
12619	VARSNLD	26942	GTGGCGCGGTCTAATTTGGAT	41265	GTCGCAAGAAGCAACCTCGAC
12620	VASALGG	26943	GTTGCGTCGGCGTTGGGTGGT	41266	GTCGCAAGCGCACTCGGAGGA
12621	VASASPA	26944	GTGGCGAGTGCGTCGCCGGCG	41267	GTCGCAAGCGCAAGCCCAGCA
12622	VASGVVF	26945	GTTGCGAGTGGTGTGGTTTTT	41268	GTCGCAAGCGGAGTCGTCTTC
12623	VASHITP	26946	GTGGCGTCGCATATTACTCCT	41269	GTCGCAAGCCACATCACACCA
12624	VASKIID	26947	GTTGCGTCGAAGATTATTGAT	41270	GTCGCAAGCAAAATCATCGAC
12625	VASLQVG	26948	GTGGCTTCGTTGCAGGTTGGG	41271	GTCGCAAGCCTCCAAGTCGGA
12626	VASLTHD	26949	GTGGCTTCGTTGACGCATGAT	41272	GTCGCAAGCCTCACACACGAC
12627	VASNNKA	26950	GTTGCTAGTAATAATAAGGCG	41273	GTCGCAAGCAACAACAAAGCA
12628	VASRAPT	26951	GTGGCTTCGAGGGCTCCTACT	41274	GTCGCAAGCAGAGCACCAACA
12629	VASSKTP	26952	GTGGCTAGTTCTAAGACTCCT	41275	GTCGCAAGCAGCAAAACACCA
12630	VASSSGI	26953	GTTGCTAGTTCTTCTGGGATT	41276	GTCGCAAGCAGCAGCGGAATC
12631	VASTGSP	26954	GTTGCGAGTACGGGGTCTCCG	41277	GTCGCAAGCACAGGAAGCCCA
12632	VASVKML	26955	GTGGCTTCGGTGAAGATGTTG	41278	GTCGCAAGCGTCAAAATGCTC
12633	VASVRTN	26956	GTGGCGTCTGTGAGGACGAAT	41279	GTCGCAAGCGTCAGAACAAAC
12634	VASYSGF	26957	GTTGCTTCTTATTCGGGTTTT	41280	GTCGCAAGCTACAGCGGATTC

12635	VASYSRE	26958	GTGGCTAGTTATTCGCGGGAG	41281	GTCGCAAGCTACAGCAGAGAA
12636	VATASVT	26959	GTTGCGACTGCTTCTGTTACG	41282	GTCGCAACAGCAAGCGTCACA
12637	VATELAG	26960	GTTGCGACGGAGCTGGCTGGG	41283	GTCGCAACAGAACTCGCAGGA
12638	VATLNYV	26961	GTGGCTACTCTGAATTATGTT	41284	GTCGCAACACTCAACTACGTC
12639	VATLRGN	26962	GTTGCGACGCTGCGTGGTAAT	41285	GTCGCAACACTCAGAGGAAAC
12640	VATMVVP	26963	GTTGCTACTATGGTTGTGCCG	41286	GTCGCAACAATGGTCGTCCCA
12641	VATNNDV	26964	GTGGCTACTAATAATGATGTG	41287	GTCGCAACAAACAACGACGTC
12642	VATNSIS	26965	GTTGCGACGAATAGTATTTCT	41288	GTCGCAACAAACAGCATCAGC
12643	VATNTYL	26966	GTTGCTACTAATACGTATCTT	41289	GTCGCAACAAACACATACCTC
12644	VATPTVL	26967	GTTGCTACTCCGACGGTTTTG	41290	GTCGCAACACCAACAGTCCTC
12645	VATRDSY	26968	GTGGCGACGCGGGATTCGTAT	41291	GTCGCAACAAGAGACAGCTAC
12646	VATRVVE	26969	GTTGCGACGCGGGTTGTGGAG	41292	GTCGCAACAAGAGTCGTCGAA
12647	VATSVRP	26970	GTGGCGACGTCTGTTCGGCCG	41293	GTCGCAACAAGCGTCAGACCA
12648	VAVMMPS	26971	GTTGCTGTGATGATGCCTTCG	41294	GTCGCAGTCATGATGCCAAGC
12649	VAVNSRS	26972	GTTGCTGTTAATTCTCGTAGT	41295	GTCGCAGTCAACAGCAGAAGC
12650	VAVRTSD	26973	GTTGCGGTTAGGACGTCTGAT	41296	GTCGCAGTCAGAACAAGCGAC
12651	VAVSAPL	26974	GTTGCTGTGTCGGCGCCTCTT	41297	GTCGCAGTCAGCGCACCACTC
12652	VAVSTVT	26975	GTGGCTGTGAGTACTGTTACG	41298	GTCGCAGTCAGCACAGTCACA
12653	VAYDTAV	26976	GTGGCTTATGATACTGCGGTG	41299	GTCGCATACGACACAGCAGTC
12654	VAYPARS	26977	GTTGCTTATCCGGCTCGTAGT	41300	GTCGCATACCCAGCAAGAAGC
12655	VCGPPFH	26978	GTTTGTGGTCCTCCTTTTCAT	41301	GTCTGCGGACCACCATTCCAC
12656	VCNSVGY	26979	GTTTGTAATAGTGTTGGTTAT	41302	GTCTGCAACAGCGTCGGATAC
12657	VDAKAND	26980	GTTGATGCGAAGGCGAATGAT	41303	GTCGACGCAAAAGCAAACGAC
12658	VDDFPRC	26981	GTGGATGATTTTCCTAGGTGT	41304	GTCGACGACTTCCCAAGATGC
12659	VDDLRAR	26982	GTTGATGATTTGCGGGCTCGG	41305	GTCGACGACCTCAGAGCAAGA
12660	VDEIRRP	26983	GTTGATGAGATTCGTCGTCCG	41306	GTCGACGAAATCAGAAGACCA
12661	VDFEHSQ	26984	GTTGATTTTGAGCATTCTCAG	41307	GTCGACTTCGAACACAGCCAA
12662	VDGARQP	26985	GTTGATGGTGCGCGGCAGCCT	41308	GTCGACGGAGCAAGACAACCA
12663	VDGLGSK	26986	GTGGATGGTCTGGGTTCTAAG	41309	GTCGACGGACTCGGAAGCAAA
12664	VDGVRGA	26987	GTGGATGGTGTGCGTGGGGCT	41310	GTCGACGGAGTCAGAGGAGCA
12665	VDKLSHT	26988	GTGGATAAGCTTTCTCATACT	41311	GTCGACAAACTCAGCCACACA
12666	VDKPHLA	26989	GTGGATAAGCCTCATCTTGCG	41312	GTCGACAAACCACACCTCGCA
12667	VDLQCAP	26990	GTTGATCTGCAGTGTGCGCCG	41313	GTCGACCTCCAATGCGCACCA
12668	VDLRPYA	26991	GTTGATCTTCGGCCTTATGCG	41314	GTCGACCTCAGACCATACGCA
12669	VDNAAQS	26992	GTGGATAATGCTGCGCAGAGT	41315	GTCGACAACGCAGCACAAAGC
12670	VDNLARA	26993	GTGGATAATCTTGCTCGTGCT	41316	GTCGACAACCTCGCAAGAGCA
12671	VDNTLTD	26994	GTGGATAATACTTTGACTGAT	41317	GTCGACAACACACTCACAGAC
12672	VDPGRHH	26995	GTTGATCCTGGGCGTCATCAT	41318	GTCGACCCAGGAAGACACCAC
12673	VDPMPAL	26996	GTTGATCCGATGCCTGCTCTT	41319	GTCGACCCAATGCCAGCACTC
12674	VDPRWHP	26997	GTGGATCCGCGGTGGCATCCG	41320	GTCGACCCAAGATGGCACCCA
12675	VDQHTIA	26998	GTGGATCAGCATACTATTGCG	41321	GTCGACCAACACACAATCGCA
12676	VDQVNNP	26999	GTTGATCAGGTGAATAATCCG	41322	GTCGACCAAGTCAACAACCCA
12677	VDRHHSP	27000	GTGGATAGGCATCATTCGCCG	41323	GTCGACAGACACCACAGCCCA
12678	VDRRPDS	27001	GTGGATCGTAGGCCTGATTCG	41324	GTCGACAGAAGACCAGACAGC
12679	VDRRTTT	27002	GTGGATAGGCGGACTACGACG	41325	GTCGACAGAAGAACAACAACA

12680	VDSLTPY	27003	GTGGATTCTTTGACGCCGTAT	41326	GTCGACAGCCTCACACCATAC
12681	VDSPSAP	27004	GTGGATTCTCCGTCGGCTCCT	41327	GTCGACAGCCCAAGCGCACCA
12682	VDSSTNL	27005	GTGGATAGTTCGACTAATCTG	41328	GTCGACAGCAGCACAAACCTC
12683	VDTLMNR	27006	GTTGATACTCTTATGAATCGT	41329	GTCGACACACTCATGAACAGA
12684	VDTPGNR	27007	GTTGATACTCCTGGGAATAGG	41330	GTCGACACACCAGGAAACAGA
12685	VDTRRES	27008	GTTGATACGAGGAGGGAGTCT	41331	GTCGACACAAGAAGAGAAAGC
12686	VDTSLEC	27009	GTTGATACTTCGCTGGAGTGT	41332	GTCGACACAAGCCTCGAATGC
12687	VDTTKFQ	27010	GTGGATACTACGAAGTTTCAG	41333	GTCGACACAACAAAATTCCAA
12688	VDVRKHP	27011	GTTGATGTTCGTAAGCATCCT	41334	GTCGACGTCAGAAAACACCCA
12689	VDYAVSM	27012	GTTGATTATGCGGTTAGTATG	41335	GTCGACTACGCAGTCAGCATG
12690	VEATSRV	27013	GTGGAGGCGACGAGTCGGGTG	41336	GTCGAAGCAACAAGCAGAGTC
12691	VEGVRSA	27014	GTTGAGGGGGTGCGGTCTGCG	41337	GTCGAAGGAGTCAGAAGCGCA
12692	VEHNSLN	27015	GTGGAGCATAATTCGCTTAAT	41338	GTCGAACACAACAGCCTCAAC
12693	VEHNTPF	27016	GTTGAGCATAATACTCCTTTT	41339	GTCGAACACAACACACCATTC
12694	VEHRVST	27017	GTGGAGCATAGGGTTAGTACT	41340	GTCGAACACAGAGTCAGCACA
12695	VEHSTNV	27018	GTTGAGCATTCTACTAATGTT	41341	GTCGAACACAGCACAAACGTC
12696	VEIKTRS	27019	GTTGAGATTAAGACTCGTAGT	41342	GTCGAAATCAAAACAAGAAGC
12697	VEISSVS	27020	GTTGAGATTTCGTCTGTGTCG	41343	GTCGAAATCAGCAGCGTCAGC
12698	VEKEMNS	27021	GTTGAGAAGGAGATGAATTCG	41344	GTCGAAAAAGAAATGAACAGC
12699	VEKTPME	27022	GTGGAGAAGACGCCGATGGAG	41345	GTCGAAAAAACACCAATGGAA
12700	VEKVSML	27023	GTTGAGAAGGTTTCTATGTTG	41346	GTCGAAAAAGTCAGCATGCTC
12701	VEKYKNL	27024	GTTGAGAAGTATAAGAATTTG	41347	GTCGAAAAATACAAAAACCTC
12702	VELNQGD	27025	GTTGAGTTGAATCAGGGTGAT	41348	GTCGAACTCAACCAAGGAGAC
12703	VENARPQ	27026	GTGGAGAATGCTAGGCCTCAG	41349	GTCGAAAACGCAAGACCACAA
12704	VEPAFTD	27027	GTGGAGCCGGCGTTTACTGAT	41350	GTCGAACCAGCATTCACAGAC
12705	VEPRKSA	27028	GTGGAGCCGAGGAAGTCGGCT	41351	GTCGAACCAAGAAAAAGCGCA
12706	VEPRSMY	27029	GTTGAGCCGCGGTCGATGTAT	41352	GTCGAACCAAGAAGCATGTAC
12707	VEPTLTR	27030	GTTGAGCCTACTTTGACGCGT	41353	GTCGAACCAACACTCACAAGA
12708	VEPVLHT	27031	GTGGAGCCTGTTCTGCATACG	41354	GTCGAACCAGTCCTCCACACA
12709	VERDDRT	27032	GTTGAGCGGGATGATCGGACG	41355	GTCGAAAGAGACGACAGAACA
12710	VERDIDS	27033	GTGGAGCGTGATATTGATTCT	41356	GTCGAAAGAGACATCGACAGC
12711	VERPVNK	27034	GTTGAGAGGCCTGTGAATAAG	41357	GTCGAAAGACCAGTCAACAAA
12712	VERVRTL	27035	GTTGAGCGTGTTAGGACGCTT	41358	GTCGAAAGAGTCAGAACACTC
12713	VESDTSW	27036	GTTGAGTCTGATACGTCGTGG	41359	GTCGAAAGCGACACAAGCTGG
12714	VESNSPM	27037	GTTGAGTCGAATTCGCCTATG	41360	GTCGAAAGCAACAGCCCAATG
12715	VESNSSF	27038	GTTGAGTCGAATAGTTCTTTT	41361	GTCGAAAGCAACAGCAGCTTC
12716	VESSPLP	27039	GTTGAGAGTAGTCCTTTGCCG	41362	GTCGAAAGCAGCCCACTCCCA
12717	VETGHNK	27040	GTTGAGACGGGGCATAATAAG	41363	GTCGAAACAGGACACAACAAA
12718	VETNRNR	27041	GTGGAGACGAATCGGAATCGT	41364	GTCGAAACAAACAGAAACAGA
12719	VETNVKL	27042	GTTGAGACTAATGTGAAGTTG	41365	GTCGAAACAAACGTCAAACTC
12720	VETPLRK	27043	GTGGAGACTCCGTTGCGTAAG	41366	GTCGAAACACCACTCAGAAAA
12721	VEVNTLH	27044	GTTGAGGTGAATACGCTGCAT	41367	GTCGAAGTCAACACACTCCAC
12722	VFDNTVR	27045	GTGTTTGATAATACTGTGCGT	41368	GTCTTCGACAACACAGTCAGA
12723	VFGANVA	27046	GTTTTTGGTGCTAATGTGGCG	41369	GTCTTCGGAGCAAACGTCGCA
12724	VFGDTLL	27047	GTTTTTGGGGATACGTTGTTG	41370	GTCTTCGGAGACACACTCCTC

12725	VFGIPSP	27048	GTGTTTGGGATTCCGTCGCCG	41371	GTCTTCGGAATCCCAAGCCCA
12726	VFHKGFD	27049	GTTTTTCATAAGGGGTTTGAT	41372	GTCTTCCACAAAGGATTCGAC
12727	VFHKSET	27050	GTGTTTCATAAGTCTGAGACT	41373	GTCTTCCACAAAAGCGAAACA
12728	VFHTPEP	27051	GTTTTTCATACTCCGGAGCCT	41374	GTCTTCCACACACCAGAACCA
12729	VFLEPSS	27052	GTTTTTTTGGAGCCTAGTTCT	41375	GTCTTCCTCGAACCAAGCAGC
12730	VFPQSTP	27053	GTTTTTCCGCAGTCTACGCCG	41376	GTCTTCCCACAAAGCACACCA
12731	VFQDSIP	27054	GTGTTTCAGGATAGTATTCCG	41377	GTCTTCCAAGACAGCATCCCA
12732	VFQGQIV	27055	GTGTTTCAGGGGCAGATTGTG	41378	GTCTTCCAAGGACAAATCGTC
12733	VFQTNNA	27056	GTGTTTCAGACTAATAATGCT	41379	GTCTTCCAAACAAACAACGCA
12734	VFRTTSP	27057	GTTTTTCGTACTACTTCGCCT	41380	GTCTTCAGAACAACAAGCCCA
12735	VFSGRQA	27058	GTTTTTAGTGGGCGTCAGGCG	41381	GTCTTCAGCGGAAGACAAGCA
12736	VFSNSAV	27059	GTGTTTTCGAATTCTGCTGTT	41382	GTCTTCAGCAACAGCGCAGTC
12737	VFTHERT	27060	GTGTTTACTCATGAGCGGACG	41383	GTCTTCACACACGAAAGAACA
12738	VFTHSDP	27061	GTTTTTACGCATTCTGATCCT	41384	GTCTTCACACACAGCGACCCA
12739	VFTNPRL	27062	GTTTTTACGAATCCGCGTTTG	41385	GTCTTCACAAACCCAAGACTC
12740	VFTPEER	27063	GTTTTTACTCCGGAGGAGCGT	41386	GTCTTCACACCAGAAGAAAGA
12741	VFTSVTT	27064	GTGTTTACGTCGGTGACTACG	41387	GTCTTCACAAGCGTCACAACA
12742	VFTTGSP	27065	GTTTTTACTACGGGGAGTCCG	41388	GTCTTCACAACAGGAAGCCCA
12743	VFVGLKP	27066	GTTTTTGTGGGTCTGAAGCCG	41389	GTCTTCGTCGGACTCAAACCA
12744	VGAASER	27067	GTTGGTGCGGCTAGTGAGAGG	41390	GTCGGAGCAGCAAGCGAAAGA
12745	VGADTRD	27068	GTTGGGGCTGATACGCGTGAT	41391	GTCGGAGCAGACACAAGAGAC
12746	VGAPNRT	27069	GTTGGTGCGCCTAATCGGACT	41392	GTCGGAGCACCAAACAGAACA
12747	VGAPVER	27070	GTTGGGGCGCCTGTTGAGCGT	41393	GTCGGAGCACCAGTCGAAAGA
12748	VGARAPA	27071	GTGGGTGCTAGGGCGCCGGCT	41394	GTCGGAGCAAGAGCACCAGCA
12749	VGASHAK	27072	GTGGGTGCTAGTCATGCGAAG	41395	GTCGGAGCAAGCCACGCAAAA
12750	VGAVYSQ	27073	GTTGGGGCTGTGTATAGTCAG	41396	GTCGGAGCAGTCTACAGCCAA
12751	VGDDSVL	27074	GTTGGTGATGATAGTGTGCTT	41397	GTCGGAGACGACAGCGTCCTC
12752	VGEIMAM	27075	GTGGGTGAGATTATGGCTATG	41398	GTCGGAGAAATCATGGCAATG
12753	VGERSSR	27076	GTTGGGGAGCGTAGTAGTCGT	41399	GTCGGAGAAAGAAGCAGCAGA
12754	VGGDDDM	27077	GTGGGTGGTGATGATGATATG	41400	GTCGGAGGAGACGACGACATG
12755	VGGDLCD	27078	GTTGGTGGTGATCTTTGTGAT	41401	GTCGGAGGAGACCTCTGCGAC
12756	VGGDSVP	27079	GTTGGGGGTGATAGTGTGCCT	41402	GTCGGAGGAGACAGCGTCCCA
12757	VGGGHGT	27080	GTGGGGGGTGGTCATGGGACG	41403	GTCGGAGGAGGACACGGAACA
12758	VGGGTGP	27081	GTGGGTGGTGGTACTGGGCCG	41404	GTCGGAGGAGGAACAGGACCA
12759	VGGMDLT	27082	GTTGGTGGGATGGATCTTACG	41405	GTCGGAGGAATGGACCTCACA
12760	VGGPIGY	27083	GTGGGGGGGCCGATTGGTTAT	41406	GTCGGAGGACCAATCGGATAC
12761	VGHPLKP	27084	GTGGGGCATCCTTTGAAGCCT	41407	GTCGGACACCCACTCAAACCA
12762	VGHSLMP	27085	GTTGGTCATTCTTTGATGCCT	41408	GTCGGACACAGCCTCATGCCA
12763	VGHSMPP	27086	GTGGGGCATAGTATGCCTCCT	41409	GTCGGACACAGCATGCCACCA
12764	VGHSVTL	27087	GTTGGTCATAGTGTGACTCTT	41410	GTCGGACACAGCGTCACACTC
12765	VGKDMSV	27088	GTGGGTAAGGATATGAGTGTG	41411	GTCGGAAAAGACATGAGCGTC
12766	VGKGEAS	27089	GTTGGTAAGGGTGAGGCTTCT	41412	GTCGGAAAAGGAGAAGCAAGC
12767	VGKLVNC	27090	GTTGGTAAGCTGGTTAATTGT	41413	GTCGGAAAACTCGTCAACTGC
12768	VGLPPAP	27091	GTGGGTTTGCCTCCGGCGCCG	41414	GTCGGACTCCCACCAGCACCA
12769	VGLQHNL	27092	GTTGGGCTTCAGCATAATCTT	41415	GTCGGACTCCAACACAACCTC

12770	VGLTSTV	27093	GTTGGTTTGACTTCGACGGTG	41416	GTCGGACTCACAAGCACAGTC
12771	VGMRIPA	27094	GTTGGGATGAGGATTCCGGCG	41417	GTCGGAATGAGAATCCCAGCA
12772	VGNKGIS	27095	GTGGGTAATAAGGGGATTAGT	41418	GTCGGAAACAAAGGAATCAGC
12773	VGNLQAF	27096	GTTGGTAATTTGCAGGCTTTT	41419	GTCGGAAACCTCCAAGCATTC
12774	VGNRAFI	27097	GTGGGGAATCGGGCGTTTATT	41420	GTCGGAAACAGAGCATTCATC
12775	VGNSLHA	27098	GTTGGTAATTCTTTGCATGCT	41421	GTCGGAAACAGCCTCCACGCA
12776	VGNYVGR	27099	GTTGGGAATTATGTGGGTAGG	41422	GTCGGAAACTACGTCGGAAGA
12777	VGPTGSA	27100	GTGGGTCCTACTGGTTCGGCT	41423	GTCGGACCAACAGGAAGCGCA
12778	VGQNAEW	27101	GTTGGTCAGAATGCTGAGTGG	41424	GTCGGACAAAACGCAGAATGG
12779	VGRLTMP	27102	GTTGGTCGTCTGACGATGCCT	41425	GTCGGAAGACTCACAATGCCA
12780	VGRSVLD	27103	GTGGGGAGGTCGGTGCTTGAT	41426	GTCGGAAGAAGCGTCCTCGAC
12781	VGSFIPT	27104	GTGGGTTCGTTTATTCCGACT	41427	GTCGGAAGCTTCATCCCAACA
12782	VGSGAPE	27105	GTTGGTAGTGGTGCGCCTGAG	41428	GTCGGAAGCGGAGCACCAGAA
12783	VGSGLDN	27106	GTTGGGTCTGGTCTTGATAAT	41429	GTCGGAAGCGGACTCGACAAC
12784	VGSIDLP	27107	GTGGGGTCGATTGATTTGCCT	41430	GTCGGAAGCATCGACCTCCCA
12785	VGSKALL	27108	GTTGGTTCGAAGGCTCTGTTG	41431	GTCGGAAGCAAAGCACTCCTC
12786	VGSLWLD	27109	GTTGGTTCTCTTTGGCTTGAT	41432	GTCGGAAGCCTCTGGCTCGAC
12787	VGSPKPT	27110	GTGGGGTCGCCGAAGCCTACG	41433	GTCGGAAGCCCAAAACCAACA
12788	VGSQYLP	27111	GTTGGGAGTCAGTATCTGCCG	41434	GTCGGAAGCCAATACCTCCCA
12789	VGSRATS	27112	GTTGGGTCTCGTGCTACGAGT	41435	GTCGGAAGCAGAGCAACAAGC
12790	VGSSKGA	27113	GTTGGGTCGTCTAAGGGGGCT	41436	GTCGGAAGCAGCAAAGGAGCA
12791	VGSSVDA	27114	GTGGGGAGTTCTGTGGATGCT	41437	GTCGGAAGCAGCGTCGACGCA
12792	VGSTGRT	27115	GTGGGTTCGACTGGGAGGACT	41438	GTCGGAAGCACAGGAAGAACA
12793	VGSTREL	27116	GTTGGTAGTACTCGTGAGCTT	41439	GTCGGAAGCACAAGAGAACTC
12794	VGSYITV	27117	GTTGGTTCTTATATTACTGTT	41440	GTCGGAAGCTACATCACAGTC
12795	VGTVTRP	27118	GTTGGGACGGTTACTAGGCCG	41441	GTCGGAACAGTCACAAGACCA
12796	VGVTMPY	27119	GTTGGTGTGACGATGCCGTAT	41442	GTCGGAGTCACAATGCCATAC
12797	VGYEAHA	27120	GTGGGGTATGAGGCGCATGCG	41443	GTCGGATACGAAGCACACGCA
12798	VGYPANP	27121	GTTGGTTATCCGGCGAATCCG	41444	GTCGGATACCCAGCAAACCCA
12799	VHAELMR	27122	GTTCATGCGGAGCTTATGCGT	41445	GTCCACGCAGAACTCATGAGA
12800	VHASTAV	27123	GTTCATGCTTCGACTGCTGTG	41446	GTCCACGCAAGCACAGCAGTC
12801	VHDGGRH	27124	GTGCATGATGGTGGGCGTCAT	41447	GTCCACGACGGAGGAAGACAC
12802	VHDGKIR	27125	GTTCATGATGGGAAGATTCGT	41448	GTCCACGACGGAAAAATCAGA
12803	VHENGSV	27126	GTTCATGAGAATGGGTCGGTT	41449	GTCCACGAAAACGGAAGCGTC
12804	VHGAAQT	27127	GTGCATGGGGCTGCTCAGACG	41450	GTCCACGGAGCAGCACAAACA
12805	VHGPMQH	27128	GTTCATGGTCCTATGCAGCAT	41451	GTCCACGGACCAATGCAACAC
12806	VHGTDPD	27129	GTTCATGGTACGGATCCGGAT	41452	GTCCACGGAACAGACCCAGAC
12807	VHHNLTP	27130	GTTCATCATAATTTGACGCCG	41453	GTCCACCACAACCTCACACCA
12808	VHKSADY	27131	GTGCATAAGAGTGCTGATTAT	41454	GTCCACAAAAGCGCAGACTAC
12809	VHLPSMP	27132	GTTCATCTTCCTAGTATGCCG	41455	GTCCACCTCCCAAGCATGCCA
12810	VHLPTLA	27133	GTTCATCTGCCTACTCTTGCT	41456	GTCCACCTCCCAACACTCGCA
12811	VHNGGRS	27134	GTTCATAATGGGGGGCGTTCT	41457	GTCCACAACGGAGGAAGAAGC
12812	VHNGLTP	27135	GTGCATAATGGTTTGACGCCT	41458	GTCCACAACGGACTCACACCA
12813	VHNMLKA	27136	GTTCATAATATGCTGAAGGCT	41459	GTCCACAACATGCTCAAAGCA
12814	VHPHSVN	27137	GTGCATCCTCATTCTGTTAAT	41460	GTCCACCCACACAGCGTCAAC

12815	VHPRMLT	27138	GTGCATCCTCGTATGCTGACG	41461	GTCCACCCAAGAATGCTCACA
12816	VHPSSVT	27139	GTGCATCCGAGTTCGGTGACT	41462	GTCCACCCAAGCAGCGTCACA
12817	VHPVLAS	27140	GTGCATCCGGTGCTGGCGTCG	41463	GTCCACCCAGTCCTCGCAAGC
12818	VHQARFA	27141	GTGCATCAGGCTCGTTTTGCG	41464	GTCCACCAAGCAAGATTCGCA
12819	VHQERSW	27142	GTGCATCAGGAGCGGTCGTGG	41465	GTCCACCAAGAAAGAAGCTGG
12820	VHRQLED	27143	GTTCATCGTCAGCTGGAGGAT	41466	GTCCACAGACAACTCGAAGAC
12821	VHRTQDS	27144	GTTCATAGGACGCAGGATTCT	41467	GTCCACAGAACACAAGACAGC
12822	VHSFKLG	27145	GTGCATTCGTTTAAGTTGGGG	41468	GTCCACAGCTTCAAACTCGGA
12823	VHSNSPS	27146	GTGCATAGTAATTCTCCTTCT	41469	GTCCACAGCAACAGCCCAAGC
12824	VHSPQQS	27147	GTTCATTCGCCGCAGCAGAGT	41470	GTCCACAGCCCACAACAAAGC
12825	VHSSINA	27148	GTGCATTCGAGTATTAATGCT	41471	GTCCACAGCAGCATCAACGCA
12826	VHTPIGT	27149	GTGCATACTCCGATTGGGACT	41472	GTCCACACACCAATCGGAACA
12827	VHTSTIS	27150	GTGCATACGTCTACGATTTCT	41473	GTCCACACAAGCACAATCAGC
12828	VHTTGML	27151	GTGCATACGACTGGGATGCTG	41474	GTCCACACAACAGGAATGCTC
12829	VHVSTMP	27152	GTGCATGTTTCTACGATGCCG	41475	GTCCACGTCAGCACAATGCCA
12830	VHVTGNL	27153	GTTCATGTTACTGGTAATCTG	41476	GTCCACGTCACAGGAAACCTC
12831	VIASDIS	27154	GTGATTGCTTCTGATATTTCT	41477	GTCATCGCAAGCGACATCAGC
12832	VIATDRL	27155	GTTATTGCGACGGATAGGCTT	41478	GTCATCGCAACAGACAGACTC
12833	VIAVDRM	27156	GTGATTGCTGTTGATCGGATG	41479	GTCATCGCAGTCGACAGAATG
12834	VIDSELD	27157	GTTATTGATTCGGAGCTTGAT	41480	GTCATCGACAGCGAACTCGAC
12835	VIDSQKK	27158	GTGATTGATTCGCAGAAGAAG	41481	GTCATCGACAGCCAAAAAAAA
12836	VIEASRN	27159	GTTATTGAGGCTAGTAGGAAT	41482	GTCATCGAAGCAAGCAGAAAC
12837	VIGKGTH	27160	GTTATTGGTAAGGGGACTCAT	41483	GTCATCGGAAAAGGAACACAC
12838	VIHTMGA	27161	GTTATTCATACTATGGGGGCG	41484	GTCATCCACACAATGGGAGCA
12839	VIIETSA	27162	GTGATTATTGAGACTTCTGCT	41485	GTCATCATCGAAACAAGCGCA
12840	VILDKAV	27163	GTGATTTTGGATAAGGCTGTT	41486	GTCATCCTCGACAAAGCAGTC
12841	VILKGAP	27164	GTTATTTTGAAGGGTGCTCCG	41487	GTCATCCTCAAAGGAGCACCA
12842	VILTSAV	27165	GTTATTCTTACGTCTGCGGTG	41488	GTCATCCTCACAAGCGCAGTC
12843	VINGLAS	27166	GTTATTAATGGTCTTGCGTCT	41489	GTCATCAACGGACTCGCAAGC
12844	VINGLGV	27167	GTTATTAATGGGTTGGGTGTG	41490	GTCATCAACGGACTCGGAGTC
12845	VINNTGN	27168	GTTATTAATAATACTGGTAAT	41491	GTCATCAACAACACAGGAAAC
12846	VIPPMRS	27169	GTTATTCCTCCTATGCGTAGT	41492	GTCATCCCACCAATGAGAAGC
12847	VIPPWDI	27170	GTGATTCCTCCTTGGGATATT	41493	GTCATCCCACCATGGGACATC
12848	VIPRTLQ	27171	GTGATTCCGCGGACTTTGCAG	41494	GTCATCCCAAGAACACTCCAA
12849	VIQLRGA	27172	GTTATTCAGTTGCGTGGGGCG	41495	GTCATCCAACTCAGAGGAGCA
12850	VIRPSTH	27173	GTTATTCGGCCGTCGACGCAT	41496	GTCATCAGACCAAGCACACAC
12851	VISGLNM	27174	GTTATTAGTGGGTTGAATATG	41497	GTCATCAGCGGACTCAACATG
12852	VISHKTN	27175	GTGATTTCTCATAAGACTAAT	41498	GTCATCAGCCACAAAACAAAC
12853	VISLSEL	27176	GTTATTTCGCTTAGTGAGCTG	41499	GTCATCAGCCTCAGCGAACTC
12854	VISNTRD	27177	GTTATTAGTAATACGCGTGAT	41500	GTCATCAGCAACACAAGAGAC
12855	VISRKGP	27178	GTTATTTCTCGTAAGGGGCCG	41501	GTCATCAGCAGAAAAGGACCA
12856	VISSADL	27179	GTGATTTCTTCTGCGGATCTT	41502	GTCATCAGCAGCGCAGACCTC
12857	VISSFAE	27180	GTTATTAGTTCTTTTGCGGAG	41503	GTCATCAGCAGCTTCGCAGAA
12858	VISTSLP	27181	GTTATTAGTACTAGTCTGCCG	41504	GTCATCAGCACAAGCCTCCCA
12859	VISVPAS	27182	GTGATTTCTGTGCCGGCTTCG	41505	GTCATCAGCGTCCCAGCAAGC

12860	VITEKSA	27183	GTTATTACGGAGAAGTCTGCT	41506	GTCATCACAGAAAAAAGCGCA
12861	VITRSGT	27184	GTGATTACGAGGTCTGGTACT	41507	GTCATCACAAGAAGCGGAACA
12862	VITSLGP	27185	GTTATTACGAGTTTGGGTCCG	41508	GTCATCACAAGCCTCGGACCA
12863	VITSTGA	27186	GTTATTACTTCTACGGGTGCG	41509	GTCATCACAAGCACAGGAGCA
12864	VIVLGPV	27187	GTGATTGTTCTGGGTCCTGTT	41510	GTCATCGTCCTCGGACCAGTC
12865	VIVPDVW	27188	GTTATTGTTCCTGATGTTTGG	41511	GTCATCGTCCCAGACGTCTGG
12866	VKDAFAP	27189	GTTAAGGATGCTTTTGCGCCG	41512	GTCAAAGACGCATTCGCACCA
12867	VKDDHRC	27190	GTTAAGGATGATCATAGGTGT	41513	GTCAAAGACGACCACAGATGC
12868	VKDLPQA	27191	GTTAAGGATCTTCCTCAGGCG	41514	GTCAAAGACCTCCCACAAGCA
12869	VKDPRMS	27192	GTTAAGGATCCTCGGATGTCG	41515	GTCAAAGACCCAAGAATGAGC
12870	VKDSTIG	27193	GTGAAGGATTCGACTATTGGT	41516	GTCAAAGACAGCACAATCGGA
12871	VKFQPSL	27194	GTGAAGTTTCAGCCGTCTCTT	41517	GTCAAATTCCAACCAAGCCTC
12872	VKGQLCC	27195	GTTAAGGGGCAGCTTTGTTGT	41518	GTCAAAGGACAACTCTGCTGC
12873	VKGYSNY	27196	GTTAAGGGTTATTCGAATTAT	41519	GTCAAAGGATACAGCAACTAC
12874	VKLAMED	27197	GTGAAGCTTGCGATGGAGGAT	41520	GTCAAACTCGCAATGGAAGAC
12875	VKLGIQA	27198	GTTAAGCTTGGTATTCAGGCG	41521	GTCAAACTCGGAATCCAAGCA
12876	VKNAVTP	27199	GTGAAGAATGCGGTTACGCCT	41522	GTCAAAAACGCAGTCACACCA
12877	VKNCMVE	27200	GTGAAGAATTGTATGGTGGAG	41523	GTCAAAAACTGCATGGTCGAA
12878	VKNPISY	27201	GTTAAGAATCCGATTTCGTAT	41524	GTCAAAAACCCAATCAGCTAC
12879	VKNTNVS	27202	GTGAAGAATACTAATGTGTCG	41525	GTCAAAAACACAAACGTCAGC
12880	VKNTYPE	27203	GTGAAGAATACTTATCCTGAG	41526	GTCAAAAACACATACCCAGAA
12881	VKNYEPQ	27204	GTGAAGAATTATGAGCCTCAG	41527	GTCAAAAACTACGAACCACAA
12882	VKPDACF	27205	GTTAAGCCTGATGCTTGTTTT	41528	GTCAAACCAGACGCATGCTTC
12883	VKPGMMP	27206	GTGAAGCCGGGGATGATGCCT	41529	GTCAAACCAGGAATGATGCCA
12884	VKPLGMP	27207	GTGAAGCCGTTGGGGATGCCT	41530	GTCAAACCACTCGGAATGCCA
12885	VKPMASS	27208	GTTAAGCCGATGGCGAGTTCG	41531	GTCAAACCAATGGCAAGCAGC
12886	VKPSPIL	27209	GTGAAGCCGTCGCCGATTTTG	41532	GTCAAACCAAGCCCAATCCTC
12887	VKPTPDA	27210	GTGAAGCCTACTCCTGATGCG	41533	GTCAAACCAACACCAGACGCA
12888	VKPYSLH	27211	GTGAAGCCTTATTCGCTTCAT	41534	GTCAAACCATACAGCCTCCAC
12889	VKPYVTM	27212	GTTAAGCCGTATGTTACGATG	41535	GTCAAACCATACGTCACAATG
12890	VKQRAMV	27213	GTGAAGCAGCGTGCGATGGTT	41536	GTCAAACAAAGAGCAATGGTC
12891	VKSAETI	27214	GTGAAGTCTGCTGAGACGATT	41537	GTCAAAAGCGCAGAAACAATC
12892	VKSDILA	27215	GTGAAGTCGGATATTCTTGCT	41538	GTCAAAAGCGACATCCTCGCA
12893	VKSEFPK	27216	GTGAAGAGTGAGTTTCCTAAG	41539	GTCAAAAGCGAATTCCCAAAA
12894	VKSETGV	27217	GTGAAGTCGGAGACTGGGGTG	41540	GTCAAAAGCGAAACAGGAGTC
12895	VKSRAET	27218	GTTAAGAGTCGTGCTGAGACT	41541	GTCAAAAGCAGAGCAGAAACA
12896	VKSSDST	27219	GTGAAGTCTAGTGATAGTACT	41542	GTCAAAAGCAGCGACAGCACA
12897	VKTNATL	27220	GTGAAGACTAATGCGACGCTG	41543	GTCAAAACAAACGCAACACTC
12898	VKTPPLT	27221	GTTAAGACTCCTCCTCTGACG	41544	GTCAAAACACCACCACTCACA
12899	VKTPSLN	27222	GTTAAGACGCCTTCGTTGAAT	41545	GTCAAAACACCAAGCCTCAAC
12900	VKTPWGP	27223	GTGAAGACTCCTTGGGGGCCT	41546	GTCAAAACACCATGGGGACCA
12901	VKTQSDL	27224	GTTAAGACGCAGTCGGATCTG	41547	GTCAAAACACAAAGCGACCTC
12902	VKVPGAF	27225	GTTAAGGTGCCGGGTGCTTTT	41548	GTCAAAGTCCCAGGAGCATTC
12903	VLAHSDS	27226	GTTTTGGCGCATAGTGATAGT	41549	GTCCTCGCACACAGCGACAGC
12904	VLAHSTY	27227	GTTTTGGCTCATTCGACGTAT	41550	GTCCTCGCACACAGCACATAC

12905	VLAPLVS	27228	GTTTTGGCGCCGTTGGTTTCT	41551	GTCCTCGCACCACTCGTCAGC
12906	VLARQYP	27229	GTTTTGGCGCGGCAGTATCCT	41552	GTCCTCGCAAGACAATACCCA
12907	VLASTVS	27230	GTGTTGGCTTCTACGGTTTCT	41553	GTCCTCGCAAGCACAGTCAGC
12908	VLATTVG	27231	GTGCTTGCTACGACTGTGGGT	41554	GTCCTCGCAACAACAGTCGGA
12909	VLATVTK	27232	GTGCTTGCGACGGTGACTAAG	41555	GTCCTCGCAACAGTCACAAAA
12910	VLAVRTN	27233	GTTTTGGCGGTTCGTACGAAT	41556	GTCCTCGCAGTCAGAACAAAC
12911	VLDWEGD	27234	GTTCTTGATTGGGAGGGGGAT	41557	GTCCTCGACTGGGAAGGAGAC
12912	VLEHLHP	27235	GTTCTTGAGCATCTTCATCCG	41558	GTCCTCGAACACCTCCACCCA
12913	VLEKLKT	27236	GTGCTGGAGAAGTTGAAGACT	41559	GTCCTCGAAAAACTCAAAACA
12914	VLELEHR	27237	GTTTTGGAGCTTGAGCATCGG	41560	GTCCTCGAACTCGAACACAGA
12915	VLEPLSK	27238	GTGCTTGAGCCTCTGTCTAAG	41561	GTCCTCGAACCACTCAGCAAA
12916	VLETRTL	27239	GTTTTGGAGACTCGTACTCTT	41562	GTCCTCGAAACAAGAACACTC
12917	VLGGLAS	27240	GTTCTTGGGGGGCTGGCTTCT	41563	GTCCTCGGAGGACTCGCAAGC
12918	VLGLAPA	27241	GTTCTTGGTCTGGCGCCTGCT	41564	GTCCTCGGACTCGCACCAGCA
12919	VLGLGGP	27242	GTGCTTGGGCTTGGGGGGCCT	41565	GTCCTCGGACTCGGAGGACCA
12920	VLGMGEW	27243	GTGTTGGGGATGGGTGAGTGG	41566	GTCCTCGGAATGGGAGAATGG
12921	VLGRGYS	27244	GTTCTGGGTCGTGGTTATTCG	41567	GTCCTCGGAAGAGGATACAGC
12922	VLGSLQH	27245	GTGCTGGGTTCGCTGCAGCAT	41568	GTCCTCGGAAGCCTCCAACAC
12923	VLGSVGS	27246	GTGTTGGGGTCTGTGGGTTCT	41569	GTCCTCGGAAGCGTCGGAAGC
12924	VLGYSKP	27247	GTGCTTGGTTATAGTAAGCCT	41570	GTCCTCGGATACAGCAAACCA
12925	VLHAASA	27248	GTGCTGCATGCTGCTTCGGCT	41571	GTCCTCCACGCAGCAAGCGCA
12926	VLHQRGA	27249	GTTCTTCATCAGAGGGGTGCT	41572	GTCCTCCACCAAAGAGGAGCA
12927	VLKAHPD	27250	GTGTTGAAGGCGCATCCTGAT	41573	GTCCTCAAAGCACACCCAGAC
12928	VLKPGVT	27251	GTTTTGAAGCCTGGGGTGACG	41574	GTCCTCAAACCAGGAGTCACA
12929	VLKPSVP	27252	GTTCTTAAGCCTTCTGTTCCG	41575	GTCCTCAAACCAAGCGTCCCA
12930	VLKPYIN	27253	GTGCTTAAGCCTTATATTAAT	41576	GTCCTCAAACCATACATCAAC
12931	VLKSHSA	27254	GTGCTTAAGTCTCATTCTGCG	41577	GTCCTCAAAAGCCACAGCGCA
12932	VLKSSAS	27255	GTTCTGAAGTCTTCGGCTAGT	41578	GTCCTCAAAAGCAGCGCAAGC
12933	VLLPSHP	27256	GTGCTGCTTCCTAGTCATCCT	41579	GTCCTCCTCCCAAGCCACCCA
12934	VLLTKTC	27257	GTTCTGTTGACTAAGACGTGT	41580	GTCCTCCTCACAAAAACATGC
12935	VLMPSTI	27258	GTGTTGATGCCTTCTACGATT	41581	GTCCTCATGCCAAGCACAATC
12936	VLMPTEA	27259	GTTCTGATGCCTACTGAGGCT	41582	GTCCTCATGCCAACAGAAGCA
12937	VLNGRSS	27260	GTGTTGAATGGTAGGAGTTCT	41583	GTCCTCAACGGAAGAAGCAGC
12938	VLNHPTF	27261	GTTCTGAATCATCCTACTTTT	41584	GTCCTCAACCACCCAACATTC
12939	VLNHQSS	27262	GTGTTGAATCATCAGTCGAGT	41585	GTCCTCAACCACCAAAGCAGC
12940	VLNLTQG	27263	GTTCTTAATTTGACGCAGGGG	41586	GTCCTCAACCTCACACAAGGA
12941	VLNPLNS	27264	GTTCTTAATCCGCTTAATTCT	41587	GTCCTCAACCCACTCAACAGC
12942	VLNTDVT	27265	GTGCTTAATACTGATGTTACT	41588	GTCCTCAACACAGACGTCACA
12943	VLNTGVG	27266	GTGCTGAATACTGGGGTTGGG	41589	GTCCTCAACACAGGAGTCGGA
12944	VLPKTSA	27267	GTGTTGCCTAAGACTTCGGCT	41590	GTCCTCCCAAAAACAAGCGCA
12945	VLPNSKN	27268	GTTCTGCCGAATTCTAAGAAT	41591	GTCCTCCCAAACAGCAAAAAC
12946	VLPPLAA	27269	GTTCTGCCTCCGCTTGCGGCG	41592	GTCCTCCCACCACTCGCAGCA
12947	VLPPNNK	27270	GTGTTGCCGCCTAATAATAAG	41593	GTCCTCCCACCAAACAACAAA
12948	VLPVPRA	27271	GTTCTTCCTGTTCCTAGGGCT	41594	GTCCTCCCAGTCCCAAGAGCA
12949	VLQGSSA	27272	GTGCTGCAGGGTTCTTCTGCT	41595	GTCCTCCAAGGAAGCAGCGCA

12950	VLQTTRP	27273	GTTTTGCAGACGACTAGGCCG	41596	GTCCTCCAAACAACAAGACCA
12951	VLRGHLA	27274	GTTTTGCGTGGTCATTTGGCT	41597	GTCCTCAGAGGACACCTCGCA
12952	VLRLGTA	27275	GTTCTTCGTCTTGGGACTGCT	41598	GTCCTCAGACTCGGAACAGCA
12953	VLRNGAE	27276	GTGCTTCGTAATGGTGCGGAG	41599	GTCCTCAGAAACGGAGCAGAA
12954	VLRQSVP	27277	GTTCTTAGGCAGAGTGTGCCT	41600	GTCCTCAGACAAAGCGTCCCA
12955	VLRSDAA	27278	GTTCTGCGTTCGGATGCGGCT	41601	GTCCTCAGAAGCGACGCAGCA
12956	VLRTGEF	27279	GTTTTGCGTACTGGTGAGTTT	41602	GTCCTCAGAACAGGAGAATTC
12957	VLRTSSG	27280	GTGTTGCGGACTAGTTCTGGT	41603	GTCCTCAGAACAAGCAGCGGA
12958	VLSHDVV	27281	GTGCTTTCTCATGATGTTGTT	41604	GTCCTCAGCCACGACGTCGTC
12959	VLSHGGA	27282	GTTTTGTCTCATGGGGGTGCT	41605	GTCCTCAGCCACGGAGGAGCA
12960	VLSPNTA	27283	GTTTTGTCGCCGAATACGGCT	41606	GTCCTCAGCCCAAACACAGCA
12961	VLSPTGM	27284	GTTTTGAGTCCGACTGGTATG	41607	GTCCTCAGCCCAACAGGAATG
12962	VLSRGNT	27285	GTGCTTAGTAGGGGGAATACG	41608	GTCCTCAGCAGAGGAAACACA
12963	VLSSNSY	27286	GTTTTGAGTTCTAATTCGTAT	41609	GTCCTCAGCAGCAACAGCTAC
12964	VLSTISS	27287	GTTCTTTCGACGATTAGTTCG	41610	GTCCTCAGCACAATCAGCAGC
12965	VLSTMSP	27288	GTGCTGTCGACTATGAGTCCT	41611	GTCCTCAGCACAATGAGCCCA
12966	VLSVSGR	27289	GTTCTTTCGGTTTCGGGTCGT	41612	GTCCTCAGCGTCAGCGGAAGA
12967	VLSYHTG	27290	GTGTTGTCGTATCATACTGGG	41613	GTCCTCAGCTACCACACAGGA
12968	VLTATMS	27291	GTTCTTACTGCTACGATGAGT	41614	GTCCTCACAGCAACAATGAGC
12969	VLTGQRL	27292	GTTCTTACGGGTCAGCGGCTG	41615	GTCCTCACAGGACAAAGACTC
12970	VLTQQPV	27293	GTTCTGACTCAGCAGCCTGTT	41616	GTCCTCACACAACAACCAGTC
12971	VLTRAGI	27294	GTGTTGACGCGTGCGGGGATT	41617	GTCCTCACAAGAGCAGGAATC
12972	VLTSNTP	27295	GTTTTGACGAGTAATACTCCG	41618	GTCCTCACAAGCAACACACCA
12973	VLVAASM	27296	GTTTTGGTGGCGGCTAGTATG	41619	GTCCTCGTCGCAGCAAGCATG
12974	VLVRSGS	27297	GTGTTGGTTAGGAGTGGTAGT	41620	GTCCTCGTCAGAAGCGGAAGC
12975	VLVVPNH	27298	GTTTTGGTGGTGCCTAATCAT	41621	GTCCTCGTCGTCCCAAACCAC
12976	VLVVRGT	27299	GTTTTGGTGGTGAGGGGGACG	41622	GTCCTCGTCGTCAGAGGAACA
12977	VLYSGLS	27300	GTTCTGTATTCTGGTTTGTCT	41623	GTCCTCTACAGCGGACTCAGC
12978	VLYTNLE	27301	GTTTTGTATACTAATTTGGAG	41624	GTCCTCTACACAAACCTCGAA
12979	VMDGLEP	27302	GTGATGGATGGGCTGGAGCCG	41625	GTCATGGACGGACTCGAACCA
12980	VMDGVRP	27303	GTGATGGATGGGGTTCGTCCG	41626	GTCATGGACGGAGTCAGACCA
12981	VMGAKGL	27304	GTGATGGGTGCTAAGGGTTTG	41627	GTCATGGGAGCAAAAGGACTC
12982	VMGGNPS	27305	GTTATGGGGGGTAATCCTAGT	41628	GTCATGGGAGGAAACCCAAGC
12983	VMHLADD	27306	GTTATGCATCTGGCTGATGAT	41629	GTCATGCACCTCGCAGACGAC
12984	VMNLLKH	27307	GTTATGAATCTGTTGAAGCAT	41630	GTCATGAACCTCCTCAAACAC
12985	VMNLSTM	27308	GTTATGAATCTTTCTACTATG	41631	GTCATGAACCTCAGCACAATG
12986	VMNSPRS	27309	GTTATGAATAGTCCTCGTTCG	41632	GTCATGAACAGCCCAAGAAGC
12987	VMPFTHD	27310	GTTATGCCTTTTACGCATGAT	41633	GTCATGCCATTCACACACGAC
12988	VMPNTPS	27311	GTGATGCCGAATACTCCTTCT	41634	GTCATGCCAAACACACCAAGC
12989	VMPQRLS	27312	GTTATGCCGCAGCGGTTGTCG	41635	GTCATGCCACAAAGACTCAGC
12990	VMPSASA	27313	GTTATGCCTTCTGCTTCTGCG	41636	GTCATGCCAAGCGCAAGCGCA
12991	VMPSLVS	27314	GTTATGCCTAGTCTGGTGAGT	41637	GTCATGCCAAGCCTCGTCAGC
12992	VMQASNS	27315	GTGATGCAGGCGTCGAATAGT	41638	GTCATGCAAGCAAGCAACAGC
12993	VMQENCP	27316	GTGATGCAGGAGAATTGTCCG	41639	GTCATGCAAGAAAACTGCCCA
12994	VMQLGES	27317	GTGATGCAGCTTGGTGAGAGT	41640	GTCATGCAACTCGGAGAAAGC

12995	VMQSILA	27318	GTGATGCAGTCGATTTTGGCT	41641	GTCATGCAAAGCATCCTCGCA
12996	VMRLDKQ	27319	GTGATGCGGCTGGATAAGCAG	41642	GTCATGAGACTCGACAAACAA
12997	VMRPDRS	27320	GTTATGCGGCCTGATAGGTCG	41643	GTCATGAGACCAGACAGAAGC
12998	VMSAVDL	27321	GTGATGAGTGCGGTTGATTTG	41644	GTCATGAGCGCAGTCGACCTC
12999	VMSDSKV	27322	GTTATGTCTGATTCGAAGGTG	41645	GTCATGAGCGACAGCAAAGTC
13000	VMSMPRL	27323	GTTATGAGTATGCCTCGTTTG	41646	GTCATGAGCATGCCAAGACTC
13001	VMSPDSM	27324	GTGATGTCTCCGGATTCTATG	41647	GTCATGAGCCCAGACAGCATG
13002	VMSSRTT	27325	GTTATGAGTAGTAGGACTACG	41648	GTCATGAGCAGCAGAACAACA
13003	VMTDALH	27326	GTGATGACGGATGCGCTGCAT	41649	GTCATGACAGACGCACTCCAC
13004	VMTSHPM	27327	GTGATGACTAGTCATCCTATG	41650	GTCATGACAAGCCACCCAATG
13005	VMTSQAM	27328	GTTATGACGAGTCAGGCTATG	41651	GTCATGACAAGCCAAGCAATG
13006	VMTTTGH	27329	GTTATGACTACGACTGGTCAT	41652	GTCATGACAACAACAGGACAC
13007	VMTVASL	27330	GTGATGACTGTGGCTTCTCTG	41653	GTCATGACAGTCGCAAGCCTC
13008	VMVESGP	27331	GTTATGGTTGAGTCTGGGCCG	41654	GTCATGGTCGAAAGCGGACCA
13009	VNAKSST	27332	GTTAATGCGAAGTCGTCGACT	41655	GTCAACGCAAAAAGCAGCACA
13010	VNALSSA	27333	GTGAATGCGTTGTCTAGTGCT	41656	GTCAACGCACTCAGCAGCGCA
13011	VNAVGAP	27334	GTTAATGCGGTTGGGGCGCCT	41657	GTCAACGCAGTCGGAGCACCA
13012	VNDVLPT	27335	GTTAATGATGTGTTGCCTACT	41658	GTCAACGACGTCCTCCCAACA
13013	VNDYAHS	27336	GTTAATGATTATGCGCATAGT	41659	GTCAACGACTACGCACACAGC
13014	VNELGRT	27337	GTGAATGAGCTGGGTAGGACG	41660	GTCAACGAACTCGGAAGAACA
13015	VNELVRT	27338	GTGAATGAGTTGGTTCGGACT	41661	GTCAACGAACTCGTCAGAACA
13016	VNFNPIS	27339	GTTAATTTTAATCCGATTTCG	41662	GTCAACTTCAACCCAATCAGC
13017	VNGHALT	27340	GTTAATGGGCATGCGCTGACT	41663	GTCAACGGACACGCACTCACA
13018	VNGLNVV	27341	GTTAATGGGCTTAATGTTGTT	41664	GTCAACGGACTCAACGTCGTC
13019	VNGNEHG	27342	GTGAATGGGAATGAGCATGGT	41665	GTCAACGGAAACGAACACGGA
13020	VNGSAFS	27343	GTTAATGGGTCTGCTTTTTCG	41666	GTCAACGGAAGCGCATTCAGC
13021	VNHMSSP	27344	GTGAATCATATGTCGTCTCCT	41667	GTCAACCACATGAGCAGCCCA
13022	VNHRSAP	27345	GTGAATCATAGGTCTGCTCCG	41668	GTCAACCACAGAAGCGCACCA
13023	VNKDPLA	27346	GTGAATAAGGATCCTTTGGCG	41669	GTCAACAAAGACCCACTCGCA
13024	VNKGVSA	27347	GTTAATAAGGGTGTGTCTGCT	41670	GTCAACAAAGGAGTCAGCGCA
13025	VNKSGYP	27348	GTTAATAAGTCTGGTTATCCT	41671	GTCAACAAAAGCGGATACCCA
13026	VNKSTVS	27349	GTGAATAAGTCTACGGTGTCT	41672	GTCAACAAAAGCACAGTCAGC
13027	VNKSYSM	27350	GTTAATAAGAGTTATTCGATG	41673	GTCAACAAAAGCTACAGCATG
13028	VNLASSV	27351	GTTAATTTGGCGTCTAGTGTG	41674	GTCAACCTCGCAAGCAGCGTC
13029	VNLGSNN	27352	GTTAATCTTGGGTCTAATAAT	41675	GTCAACCTCGGAAGCAACAAC
13030	VNLRLGS	27353	GTTAATTTGCGGCTGGGTTCG	41676	GTCAACCTCAGACTCGGAAGC
13031	VNLSSVC	27354	GTTAATCTGTCGAGTGTTTGT	41677	GTCAACCTCAGCAGCGTCTGC
13032	VNLVHGV	27355	GTGAATCTGGTGCATGGTGTT	41678	GTCAACCTCGTCCACGGAGTC
13033	VNLYLTE	27356	GTTAATCTGTATCTTACGGAG	41679	GTCAACCTCTACCTCACAGAA
13034	VNNTRNV	27357	GTGAATAATACTAGGAATGTT	41680	GTCAACAACACAAGAAACGTC
13035	VNPPNVG	27358	GTTAATCCTCCGAATGTTGGT	41681	GTCAACCCACCAAACGTCGGA
13036	VNPPSRP	27359	GTTAATCCGCCTTCGCGTCCG	41682	GTCAACCCACCAAGCAGACCA
13037	VNPPTHV	27360	GTTAATCCTCCTACGCATGTT	41683	GTCAACCCACCAACACACGTC
13038	VNPRVVQ	27361	GTTAATCCGCGTGTGGTTCAG	41684	GTCAACCCAAGAGTCGTCCAA
13039	VNPSASS	27362	GTTAATCCTTCGGCTTCGTCT	41685	GTCAACCCAAGCGCAAGCAGC

13040	VNPSSPS	27363	GTTAATCCTAGTAGTCCTTCG	41686	GTCAACCCAAGCAGCCCAAGC
13041	VNRSVSP	27364	GTGAATCGGTCTGTTAGTCCG	41687	GTCAACAGAAGCGTCAGCCCA
13042	VNRTTLY	27365	GTGAATCGTACGACGTTGTAT	41688	GTCAACAGAACAACACTCTAC
13043	VNSASKS	27366	GTGAATAGTGCGTCTAAGTCG	41689	GTCAACAGCGCAAGCAAAAGC
13044	VNSFERS	27367	GTTAATTCTTTTGAGCGTTCT	41690	GTCAACAGCTTCGAAAGAAGC
13045	VNSGATT	27368	GTGAATTCGGGGGCGACTACT	41691	GTCAACAGCGGAGCAACAACA
13046	VNSMERP	27369	GTTAATTCGATGGAGAGGCCG	41692	GTCAACAGCATGGAAAGACCA
13047	VNSRLIA	27370	GTGAATTCTAGGCTGATTGCT	41693	GTCAACAGCAGACTCATCGCA
13048	VNSSLHG	27371	GTGAATTCTTCTCTGCATGGT	41694	GTCAACAGCAGCCTCCACGGA
13049	VNSSNSR	27372	GTGAATTCGTCGAATAGTCGG	41695	GTCAACAGCAGCAACAGCAGA
13050	VNSSVWA	27373	GTTAATTCGAGTGTTTGGGCT	41696	GTCAACAGCAGCGTCTGGGCA
13051	VNSTAFH	27374	GTGAATAGTACTGCGTTTCAT	41697	GTCAACAGCACAGCATTCCAC
13052	VNTKVGP	27375	GTGAATACGAAGGTTGGGCCG	41698	GTCAACACAAAAGTCGGACCA
13053	VNTLTGD	27376	GTGAATACTCTGACTGGTGAT	41699	GTCAACACACTCACAGGAGAC
13054	VNTNLAS	27377	GTGAATACTAATCTTGCGAGT	41700	GTCAACACAAACCTCGCAAGC
13055	VNTSGWQ	27378	GTTAATACTTCTGGTTGGCAG	41701	GTCAACACAAGCGGATGGCAA
13056	VNTVPYG	27379	GTTAATACGGTTCCTTATGGT	41702	GTCAACACAGTCCCATACGGA
13057	VNTVTSS	27380	GTGAATACTGTGACGTCGTCG	41703	GTCAACACAGTCACAAGCAGC
13058	VNVGTLY	27381	GTGAATGTTGGTACTCTTTAT	41704	GTCAACGTCGGAACACTCTAC
13059	VNVKREV	27382	GTTAATGTGAAGAGGGAGGTT	41705	GTCAACGTCAAAAGAGAAGTC
13060	VNVRETT	27383	GTGAATGTTAGGGAGACTACG	41706	GTCAACGTCAGAGAAACAACA
13061	VNVSHYS	27384	GTGAATGTGTCTCATTATTCG	41707	GTCAACGTCAGCCACTACAGC
13062	VNVSQTG	27385	GTTAATGTTTCTCAGACTGGG	41708	GTCAACGTCAGCCAAACAGGA
13063	VNYAPAV	27386	GTTAATTATGCTCCGGCTGTG	41709	GTCAACTACGCACCAGCAGTC
13064	VNYPEST	27387	GTGAATTATCCTGAGTCGACG	41710	GTCAACTACCCAGAAAGCACA
13065	VPAMTQG	27388	GTTCCTGCGATGACTCAGGGT	41711	GTCCCAGCAATGACACAAGGA
13066	VPAPGYN	27389	GTTCCGGCTCCTGGTTATAAT	41712	GTCCCAGCACCAGGATACAAC
13067	VPAQSRE	27390	GTTCCTGCGCAGTCGCGTGAG	41713	GTCCCAGCACAAAGCAGAGAA
13068	VPARSPG	27391	GTTCCTGCGAGGTCTCCTGGT	41714	GTCCCAGCAAGAAGCCCAGGA
13069	VPASSTS	27392	GTTCCTGCGTCGTCGACTAGT	41715	GTCCCAGCAAGCAGCACAAGC
13070	VPATDFR	27393	GTGCCTGCTACGGATTTTCGG	41716	GTCCCAGCAACAGACTTCAGA
13071	VPAVTSR	27394	GTTCCGGCGGTGACGTCGCGT	41717	GTCCCAGCAGTCACAAGCAGA
13072	VPCPSHT	27395	GTGCCGTGTCCTTCGCATACT	41718	GTCCCATGCCCAAGCCACACA
13073	VPDASDF	27396	GTTCCGGATGCGAGTGATTTT	41719	GTCCCAGACGCAAGCGACTTC
13074	VPDSWDR	27397	GTTCCGGATTCTTGGGATCGG	41720	GTCCCAGACAGCTGGGACAGA
13075	VPERATI	27398	GTTCCGGAGCGTGCGACTATT	41721	GTCCCAGAAAGAGCAACAATC
13076	VPEYIIT	27399	GTTCCGGAGTATATTATTACG	41722	GTCCCAGAATACATCATCACA
13077	VPFASMT	27400	GTTCCGTTTGCGAGTATGACG	41723	GTCCCATTCGCAAGCATGACA
13078	VPFQFEG	27401	GTTCCTTTTCAGTTTGAGGGG	41724	GTCCCATTCCAATTCGAAGGA
13079	VPGANRI	27402	GTTCCGGGGGCGAATCGGATT	41725	GTCCCAGGAGCAAACAGAATC
13080	VPGDLRV	27403	GTGCCGGGTGATCTGAGGGTT	41726	GTCCCAGGAGACCTCAGAGTC
13081	VPGKPGD	27404	GTTCCTGGTAAGCCGGGTGAT	41727	GTCCCAGGAAAACCAGGAGAC
13082	VPGMTTL	27405	GTTCCGGGTATGACGACTTTG	41728	GTCCCAGGAATGACAACACTC
13083	VPGNPAT	27406	GTGCCTGGGAATCCGGCGACT	41729	GTCCCAGGAAACCCAGCAACA
13084	VPGPVVA	27407	GTTCCGGGGCCTGTGGTGGCG	41730	GTCCCAGGACCAGTCGTCGCA

13085	VPGRTTP	27408	GTTCCGGGTCGGACGACGCCG	41731	GTCCCAGGAAGAACAACACCA
13086	VPGSRST	27409	GTGCCTGGTTCTCGGAGTACT	41732	GTCCCAGGAAGCAGAAGCACA
13087	VPGSSRL	27410	GTGCCTGGTTCGAGTCGGTTG	41733	GTCCCAGGAAGCAGCAGACTC
13088	VPGSSSH	27411	GTGCCGGGGTCGTCTTCTCAT	41734	GTCCCAGGAAGCAGCAGCCAC
13089	VPHEKTP	27412	GTGCCGCATGAGAAGACTCCG	41735	GTCCCACACGAAAAAACACCA
13090	VPHIVST	27413	GTTCCGCATATTGTTTCTACG	41736	GTCCCACACATCGTCAGCACA
13091	VPHLTST	27414	GTGCCGCATTTGACGTCGACG	41737	GTCCCACACCTCACAAGCACA
13092	VPHLTVV	27415	GTTCCTCATCTGACGGTGGTT	41738	GTCCCACACCTCACAGTCGTC
13093	VPHYSSS	27416	GTTCCGCATTATTCTTCGAGT	41739	GTCCCACACTACAGCAGCAGC
13094	VPIISDQ	27417	GTGCCTATTATTAGTGATCAG	41740	GTCCCAATCATCAGCGACCAA
13095	VPKFPLE	27418	GTTCCTAAGTTTCCTCTGGAG	41741	GTCCCAAAATTCCCACTCGAA
13096	VPKLSYP	27419	GTGCCTAAGTTGTCGTATCCG	41742	GTCCCAAAACTCAGCTACCCA
13097	VPKNEMG	27420	GTTCCGAAGAATGAGATGGGT	41743	GTCCCAAAAAACGAAATGGGA
13098	VPKQSMQ	27421	GTTCCGAAGCAGTCTATGCAG	41744	GTCCCAAAACAAAGCATGCAA
13099	VPKQSVN	27422	GTGCCGAAGCAGTCTGTGAAT	41745	GTCCCAAAACAAAGCGTCAAC
13100	VPKQVSF	27423	GTTCCGAAGCAGGTGTCGTTT	41746	GTCCCAAAACAAGTCAGCTTC
13101	VPLDHAD	27424	GTTCCGCTGGATCATGCTGAT	41747	GTCCCACTCGACCACGCAGAC
13102	VPLDRIH	27425	GTGCCTCTTGATCGGATTCAT	41748	GTCCCACTCGACAGAATCCAC
13103	VPLDSES	27426	GTTCCGCTTGATTCGGAGAGT	41749	GTCCCACTCGACAGCGAAAGC
13104	VPLGTDV	27427	GTTCCGCTTGGGACTGATGTT	41750	GTCCCACTCGGAACAGACGTC
13105	VPLHTSL	27428	GTGCCGTTGCATACGAGTCTT	41751	GTCCCACTCCACACAAGCCTC
13106	VPLISMD	27429	GTGCCGCTTATTTCTATGGAT	41752	GTCCCACTCATCAGCATGGAC
13107	VPLNKAA	27430	GTTCCTCTTAATAAGGCGGCG	41753	GTCCCACTCAACAAAGCAGCA
13108	VPLQETF	27431	GTTCCGCTTCAGGAGACGTTT	41754	GTCCCACTCCAAGAAACATTC
13109	VPLSGGF	27432	GTGCCTTTGAGTGGGGGGTTT	41755	GTCCCACTCAGCGGAGGATTC
13110	VPLSNMS	27433	GTGCCGCTTTCTAATATGTCG	41756	GTCCCACTCAGCAACATGAGC
13111	VPLSQLN	27434	GTGCCGTTGTCGCAGTTGAAT	41757	GTCCCACTCAGCCAACTCAAC
13112	VPLSVTV	27435	GTGCCTTTGTCTGTGACTGTT	41758	GTCCCACTCAGCGTCACAGTC
13113	VPLYSGS	27436	GTGCCTCTTTATTCTGGGTCG	41759	GTCCCACTCTACAGCGGAAGC
13114	VPMQTVL	27437	GTGCCTATGCAGACGGTGCTT	41760	GTCCCAATGCAAACAGTCCTC
13115	VPMSGAP	27438	GTGCCTATGTCGGGTGCTCCG	41761	GTCCCAATGAGCGGAGCACCA
13116	VPMSRPS	27439	GTTCCTATGTCTAGGCCTTCG	41762	GTCCCAATGAGCAGACCAAGC
13117	VPNDRLQ	27440	GTGCCTAATGATAGGCTTCAG	41763	GTCCCAAACGACAGACTCCAA
13118	VPNHSTG	27441	GTTCCGAATCATTCGACTGGT	41764	GTCCCAAACCACAGCACAGGA
13119	VPNLEDD	27442	GTTCCTAATCTTGAGGATGAT	41765	GTCCCAAACCTCGAAGACGAC
13120	VPPAARS	27443	GTTCCGCCTGCTGCTCGTTCG	41766	GTCCCACCAGCAGCAAGAAGC
13121	VPPAIHA	27444	GTGCCTCCGGCGATTCATGCG	41767	GTCCCACCAGCAATCCACGCA
13122	VPPISPS	27445	GTTCCTCCGATTTCTCCTAGT	41768	GTCCCACCAATCAGCCCAAGC
13123	VPPLRQE	27446	GTGCCGCCTCTTAGGCAGGAG	41769	GTCCCACCACTCAGACAAGAA
13124	VPPLTSS	27447	GTGCCTCCTCTGACTTCGTCT	41770	GTCCCACCACTCACAAGCAGC
13125	VPPRHIN	27448	GTGCCGCCTAGGCATATTAAT	41771	GTCCCACCAAGACACATCAAC
13126	VPPRQTH	27449	GTTCCGCCGCGTCAGACTCAT	41772	GTCCCACCAAGACAAACACAC
13127	VPPSRQS	27450	GTGCCTCCGTCTAGGCAGTCT	41773	GTCCCACCAAGCAGACAAAGC
13128	VPPSVSR	27451	GTTCCTCCTTCTGTGAGTAGG	41774	GTCCCACCAAGCGTCAGCAGA
13129	VPPVQTP	27452	GTTCCTCCGGTGCAGACGCCT	41775	GTCCCACCAGTCCAAACACCA

13130	VPPYSVP	27453	GTGCCGCCTTATAGTGTTCCG	41776	GTCCCACCATACAGCGTCCCA
13131	VPQKVTV	27454	GTTCCTCAGAAGGTGACGGTG	41777	GTCCCACAAAAAGTCACAGTC
13132	VPRDYRY	27455	GTGCCGCGTGATTATCGGTAT	41778	GTCCCAAGAGACTACAGATAC
13133	VPRERVN	27456	GTGCCTCGGGAGCGGGTGAAT	41779	GTCCCAAGAGAAAGAGTCAAC
13134	VPRGDAA	27457	GTGCCTAGGGGTGATGCGGCT	41780	GTCCCAAGAGGAGACGCAGCA
13135	VPRNAPD	27458	GTTCCTCGTAATGCGCCGGAT	41781	GTCCCAAGAAACGCACCAGAC
13136	VPRNVTM	27459	GTGCCTCGTAATGTGACGATG	41782	GTCCCAAGAAACGTCACAATG
13137	VPRSDTL	27460	GTGCCTCGTTCTGATACGCTG	41783	GTCCCAAGAAGCGACACACTC
13138	VPRSNVS	27461	GTGCCGCGTAGTAATGTGAGT	41784	GTCCCAAGAAGCAACGTCAGC
13139	VPRSQLT	27462	GTGCCGAGGAGTCAGCTGACG	41785	GTCCCAAGAAGCCAACTCACA
13140	VPRSTNL	27463	GTTCCTCGGTCTACGAATTTG	41786	GTCCCAAGAAGCACAAACCTC
13141	VPRTGSN	27464	GTTCCTCGGACGGGGTCGAAT	41787	GTCCCAAGAACAGGAAGCAAC
13142	VPRTLTP	27465	GTTCCGAGGACTCTGACTCCT	41788	GTCCCAAGAACACTCACACCA
13143	VPSATKI	27466	GTTCCTAGTGCGACTAAGATT	41789	GTCCCAAGCGCAACAAAAATC
13144	VPSHIGA	27467	GTGCCTAGTCATATTGGTGCG	41790	GTCCCAAGCCACATCGGAGCA
13145	VPSKPSY	27468	GTGCCTTCTAAGCCTTCTTAT	41791	GTCCCAAGCAAACCAAGCTAC
13146	VPSKTPF	27469	GTTCCTTCTAAGACGCCTTTT	41792	GTCCCAAGCAAAACACCATTC
13147	VPSPSSS	27470	GTGCCTTCTCCTTCGTCTTCG	41793	GTCCCAAGCCCAAGCAGCAGC
13148	VPSRSQN	27471	GTGCCTTCTCGGTCTCAGAAT	41794	GTCCCAAGCAGAAGCCAAAAC
13149	VPSSISS	27472	GTTCCTAGTTCTATTTCTAGT	41795	GTCCCAAGCAGCATCAGCAGC
13150	VPSVPGA	27473	GTGCCGAGTGTGCCGGGGGCG	41796	GTCCCAAGCGTCCCAGGAGCA
13151	VPSVVRS	27474	GTTCCTTCGGTTGTTCGTAGT	41797	GTCCCAAGCGTCGTCAGAAGC
13152	VPTALMS	27475	GTTCCGACTGCTTTGATGAGT	41798	GTCCCAACAGCACTCATGAGC
13153	VPTDYLS	27476	GTGCCGACGGATTATCTGTCT	41799	GTCCCAACAGACTACCTCAGC
13154	VPTHYDP	27477	GTTCCGACGCATTATGATCCT	41800	GTCCCAACACACTACGACCCA
13155	VPTRGEF	27478	GTGCCGACGCGGGGGGAGTTT	41801	GTCCCAACAAGAGGAGAATTC
13156	VPTSAVK	27479	GTTCCTACGTCGGCTGTTAAG	41802	GTCCCAACAAGCGCAGTCAAA
13157	VPTTSDF	27480	GTGCCGACGACTTCGGATTTT	41803	GTCCCAACAACAAGCGACTTC
13158	VPTVSNI	27481	GTGCCTACGGTTTCTAATATT	41804	GTCCCAACAGTCAGCAACATC
13159	VPVDILS	27482	GTGCCGGTGGATATTCTTAGT	41805	GTCCCAGTCGACATCCTCAGC
13160	VPVKTSP	27483	GTTCCTGTTAAGACTAGTCCG	41806	GTCCCAGTCAAAACAAGCCCA
13161	VPVKTTY	27484	GTGCCGGTTAAGACGACTTAT	41807	GTCCCAGTCAAAACAACATAC
13162	VPVNPRA	27485	GTGCCTGTGAATCCTAGGGCG	41808	GTCCCAGTCAACCCAAGAGCA
13163	VPVSRAF	27486	GTTCCGGTGTCGCGTGCTTTT	41809	GTCCCAGTCAGCAGAGCATTC
13164	VPWDSPV	27487	GTTCCGTGGGATTCTCCGGTT	41810	GTCCCATGGGACAGCCCAGTC
13165	VPYGQVH	27488	GTTCCTTATGGGCAGGTTCAT	41811	GTCCCATACGGACAAGTCCAC
13166	VPYSSLP	27489	GTTCCTTATTCTTCTCTGCCG	41812	GTCCCATACAGCAGCCTCCCA
13167	VPYTGMT	27490	GTTCCTTATACTGGTATGACT	41813	GTCCCATACACAGGAATGACA
13168	VPYTSTD	27491	GTGCCGTATACGTCTACGGAT	41814	GTCCCATACACAAGCACAGAC
13169	VQAGLRS	27492	GTTCAGGCTGGTCTTCGGTCT	41815	GTCCAAGCAGGACTCAGAAGC
13170	VQASSMK	27493	GTTCAGGCTTCGAGTATGAAG	41816	GTCCAAGCAAGCAGCATGAAA
13171	VQDTDST	27494	GTTCAGGATACGGATTCGACT	41817	GTCCAAGACACAGACAGCACA
13172	VQEPVVM	27495	GTGCAGGAGCCTGTTGTTATG	41818	GTCCAAGAACCAGTCGTCATG
13173	VQGGSNT	27496	GTTCAGGGTGGTTCGAATACT	41819	GTCCAAGGAGGAAGCAACACA
13174	VQGRLAG	27497	GTTCAGGGTAGGCTTGCTGGT	41820	GTCCAAGGAAGACTCGCAGGA

13175	VQGRSGM	27498	GTTCAGGGGCGTTCGGGGATG	41821	GTCCAAGGAAGAAGCGGAATG
13176	VQGSKPE	27499	GTGCAGGGGTCTAAGCCTGAG	41822	GTCCAAGGAAGCAAACCAGAA
13177	VQGTLPS	27500	GTTCAGGGTACGTTGCCGAGT	41823	GTCCAAGGAACACTCCCAAGC
13178	VQHLRAT	27501	GTTCAGCATCTTAGGGCTACG	41824	GTCCAACACCTCAGAGCAACA
13179	VQHPTRA	27502	GTTCAGCATCCGACGCGTGCG	41825	GTCCAACACCCAACAAGAGCA
13180	VQHRMEV	27503	GTTCAGCATCGTATGGAGGTT	41826	GTCCAACACAGAATGGAAGTC
13181	VQHVAEL	27504	GTGCAGCATGTTGCTGAGCTG	41827	GTCCAACACGTCGCAGAACTC
13182	VQLASNS	27505	GTTCAGCTTGCTTCGAATTCG	41828	GTCCAACTCGCAAGCAACAGC
13183	VQLGGHV	27506	GTGCAGTTGGGTGGGCATGTG	41829	GTCCAACTCGGAGGACACGTC
13184	VQMERHS	27507	GTTCAGATGGAGAGGCATAGT	41830	GTCCAAATGGAAAGACACAGC
13185	VQMMRDA	27508	GTGCAGATGATGCGTGATGCG	41831	GTCCAAATGATGAGAGACGCA
13186	VQNVIGP	27509	GTGCAGAATGTTATTGGTCCG	41832	GTCCAAAACGTCATCGGACCA
13187	VQPEILA	27510	GTGCAGCCGGAGATTTTGGCT	41833	GTCCAACCAGAAATCCTCGCA
13188	VQPGPLV	27511	GTTCAGCCGGGGCCGCTTGTG	41834	GTCCAACCAGGACCACTCGTC
13189	VQPINQS	27512	GTGCAGCCTATTAATCAGTCG	41835	GTCCAACCAATCAACCAAAGC
13190	VQPLPAH	27513	GTGCAGCCTTTGCCTGCGCAT	41836	GTCCAACCACTCCCAGCACAC
13191	VQPMISN	27514	GTGCAGCCGATGATTTCGAAT	41837	GTCCAACCAATGATCAGCAAC
13192	VQPREYV	27515	GTTCAGCCTCGTGAGTATGTT	41838	GTCCAACCAAGAGAATACGTC
13193	VQPVQSD	27516	GTGCAGCCGGTGCAGTCTGAT	41839	GTCCAACCAGTCCAAAGCGAC
13194	VQQKGLA	27517	GTGCAGCAGAAGGGGCTGGCG	41840	GTCCAACAAAAAGGACTCGCA
13195	VQRMMGP	27518	GTGCAGCGGATGATGGGGCCT	41841	GTCCAAAGAATGATGGGACCA
13196	VQSDSTS	27519	GTTCAGTCTGATTCGACGTCG	41842	GTCCAAAGCGACAGCACAAGC
13197	VQSIPSA	27520	GTGCAGTCTATTCCGTCGGCG	41843	GTCCAAAGCATCCCAAGCGCA
13198	VQSLHTG	27521	GTGCAGTCGCTTCATACTGGT	41844	GTCCAAAGCCTCCACACAGGA
13199	VQSPTWV	27522	GTGCAGAGTCCGACTTGGGTT	41845	GTCCAAAGCCCAACATGGGTC
13200	VQSRPDS	27523	GTTCAGTCGCGGCCTGATTCG	41846	GTCCAAAGCAGACCAGACAGC
13201	VQSSVTL	27524	GTGCAGTCGAGTGTGACGTTG	41847	GTCCAAAGCAGCGTCACACTC
13202	VQSTLLE	27525	GTTCAGTCGACTCTTCTTGAG	41848	GTCCAAAGCACACTCCTCGAA
13203	VQSVMPH	27526	GTTCAGAGTGTTATGCCTCAT	41849	GTCCAAAGCGTCATGCCACAC
13204	VQSVRIS	27527	GTGCAGAGTGTTCGTATTTCG	41850	GTCCAAAGCGTCAGAATCAGC
13205	VQTAPAE	27528	GTGCAGACGGCGCCTGCGGAG	41851	GTCCAAACAGCACCAGCAGAA
13206	VQTHSAA	27529	GTGCAGACGCATTCTGCTGCT	41852	GTCCAAACACACAGCGCAGCA
13207	VQTQPYR	27530	GTTCAGACGCAGCCGTATAGG	41853	GTCCAAACACAACCATACAGA
13208	VQTSGYL	27531	GTTCAGACGAGTGGTTATTTG	41854	GTCCAAACAAGCGGATACCTC
13209	VQYMSKA	27532	GTGCAGTATATGTCGAAGGCT	41855	GTCCAATACATGAGCAAAGCA
13210	VQYPTES	27533	GTGCAGTATCCTACGGAGTCG	41856	GTCCAATACCCAACAGAAAGC
13211	VQYSGTP	27534	GTGCAGTATAGTGGTACTCCG	41857	GTCCAATACAGCGGAACACCA
13212	VRADAAG	27535	GTTCGGGCTGATGCTGCGGGG	41858	GTCAGAGCAGACGCAGCAGGA
13213	VRALPLS	27536	GTTAGGGCGTTGCCGCTGAGT	41859	GTCAGAGCACTCCCACTCAGC
13214	VRANPST	27537	GTGAGGGCGAATCCGTCGACG	41860	GTCAGAGCAAACCCAAGCACA
13215	VRAPPNA	27538	GTGCGTGCTCCTCCGAATGCT	41861	GTCAGAGCACCACCAAACGCA
13216	VRAPPSL	27539	GTGAGGGCGCCTCCTTCTCTT	41862	GTCAGAGCACCACCAAGCCTC
13217	VRAPREV	27540	GTTAGGGCGCCGCGGGAGGTT	41863	GTCAGAGCACCAAGAGAAGTC
13218	VRASNTL	27541	GTTCGTGCTAGTAATACGTTG	41864	GTCAGAGCAAGCAACACACTC
13219	VRATQTE	27542	GTGCGGGCTACGCAGACTGAG	41865	GTCAGAGCAACACAAACAGAA

13220	VRAVHPV	27543	GTGCGGGCTGTGCATCCGGTT	41866	GTCAGAGCAGTCCACCCAGTC
13221	VRAVQIN	27544	GTGAGGGCTGTTCAGATTAAT	41867	GTCAGAGCAGTCCAAATCAAC
13222	VRDAASC	27545	GTTAGGGATGCTGCTTCTTGT	41868	GTCAGAGACGCAGCAAGCTGC
13223	VRDDVGW	27546	GTTCGTGATGATGTTGGGTGG	41869	GTCAGAGACGACGTCGGATGG
13224	VRDPVTS	27547	GTTCGGGATCCTGTGACTTCG	41870	GTCAGAGACCCAGTCACAAGC
13225	VRDSMHS	27548	GTGCGGGATTCGATGCATTCG	41871	GTCAGAGACAGCATGCACAGC
13226	VRDTMGQ	27549	GTTCGTGATACGATGGGGCAG	41872	GTCAGAGACACAATGGGACAA
13227	VRDWQTQ	27550	GTGCGTGATTGGCAGACGCAG	41873	GTCAGAGACTGGCAAACACAA
13228	VREATSL	27551	GTGAGGGAGGCTACTTCTTTG	41874	GTCAGAGAAGCAACAAGCCTC
13229	VREVLGS	27552	GTTCGGGAGGTGCTGGGGTCG	41875	GTCAGAGAAGTCCTCGGAAGC
13230	VRFNEQA	27553	GTTAGGTTTAATGAGCAGGCG	41876	GTCAGATTCAACGAACAAGCA
13231	VRFNGQT	27554	GTGCGTTTTAATGGTCAGACT	41877	GTCAGATTCAACGGACAAACA
13232	VRGALTP	27555	GTTCGTGGTGCGCTTACGCCG	41878	GTCAGAGGAGCACTCACACCA
13233	VRGAVAA	27556	GTGAGGGGTGCGGTTGCGGCT	41879	GTCAGAGGAGCAGTCGCAGCA
13234	VRGIVAP	27557	GTGCGTGGGATTGTGGCTCCG	41880	GTCAGAGGAATCGTCGCACCA
13235	VRGPEMT	27558	GTTAGGGGTCCTGAGATGACG	41881	GTCAGAGGACCAGAAATGACA
13236	VRGPGED	27559	GTGCGTGGTCCTGGGGAGGAT	41882	GTCAGAGGACCAGGAGAAGAC
13237	VRGPHDT	27560	GTTAGGGGGCCTCATGATACG	41883	GTCAGAGGACCACACGACACA
13238	VRGSLSM	27561	GTTAGGGGGTCTCTTTCGATG	41884	GTCAGAGGAAGCCTCAGCATG
13239	VRGSLTS	27562	GTTCGTGGTAGTCTGACTAGT	41885	GTCAGAGGAAGCCTCACAAGC
13240	VRGSQYA	27563	GTGAGGGGGTCGCAGTATGCG	41886	GTCAGAGGAAGCCAATACGCA
13241	VRGSTQA	27564	GTTCGTGGGTCGACGCAGGCT	41887	GTCAGAGGAAGCACACAAGCA
13242	VRGVQLD	27565	GTTCGGGGTGTGCAGCTGGAT	41888	GTCAGAGGAGTCCAACTCGAC
13243	VRGVSDS	27566	GTTAGGGGTGTTTCGGATTCG	41889	GTCAGAGGAGTCAGCGACAGC
13244	VRHIKLE	27567	GTGCGTCATATTAAGCTGGAG	41890	GTCAGACACATCAAACTCGAA
13245	VRHPGPE	27568	GTGCGTCATCCGGGGCCGGAG	41891	GTCAGACACCCAGGACCAGAA
13246	VRKDYHL	27569	GTGCGGAAGGATTATCATCTT	41892	GTCAGAAAAGACTACCACCTC
13247	VRLDASI	27570	GTGCGTCTGGATGCTTCTATT	41893	GTCAGACTCGACGCAAGCATC
13248	VRLDMAA	27571	GTTCGTTTGGATATGGCTGCT	41894	GTCAGACTCGACATGGCAGCA
13249	VRLDREG	27572	GTTAGGCTGGATCGGGAGGGT	41895	GTCAGACTCGACAGAGAAGGA
13250	VRLPDTS	27573	GTTCGGCTGCCGGATACGTCG	41896	GTCAGACTCCCAGACACAAGC
13251	VRLQGGL	27574	GTGAGGTTGCAGGGTGGGCTT	41897	GTCAGACTCCAAGGAGGACTC
13252	VRLSEVP	27575	GTGAGGCTGTCGGAGGTTCCT	41898	GTCAGACTCAGCGAAGTCCCA
13253	VRMLPGD	27576	GTTCGGATGCTGCCTGGTGAT	41899	GTCAGAATGCTCCCAGGAGAC
13254	VRNAPGA	27577	GTGCGGAATGCTCCGGGGGCG	41900	GTCAGAAACGCACCAGGAGCA
13255	VRNASDL	27578	GTTCGGAATGCGTCTGATTTG	41901	GTCAGAAACGCAAGCGACCTC
13256	VRNIPSM	27579	GTTCGGAATATTCCGTCGATG	41902	GTCAGAAACATCCCAAGCATG
13257	VRNSAMN	27580	GTTAGGAATAGTGCGATGAAT	41903	GTCAGAAACAGCGCAATGAAC
13258	VRPADQF	27581	GTGAGGCCGGCTGATCAGTTT	41904	GTCAGACCAGCAGACCAATTC
13259	VRPEREN	27582	GTGAGGCCTGAGCGTGAGAAT	41905	GTCAGACCAGAAAGAGAAAAC
13260	VRPGKLI	27583	GTTCGGCCGGGTAAGTTGATT	41906	GTCAGACCAGGAAAACTCATC
13261	VRPHMTV	27584	GTGAGGCCGCATATGACTGTG	41907	GTCAGACCACACATGACAGTC
13262	VRPIPPN	27585	GTTCGGCCTATTCCGCCTAAT	41908	GTCAGACCAATCCCACCAAAC
13263	VRPLSIG	27586	GTTCGGCCGTTGTCGATTGGT	41909	GTCAGACCACTCAGCATCGGA
13264	VRPQTAY	27587	GTTCGTCCTCAGACGGCGTAT	41910	GTCAGACCACAAACAGCATAC

13265	VRPRDGM	27588	GTGCGTCCTCGTGATGGTATG	41911	GTCAGACCAAGAGACGGAATG
13266	VRPSILA	27589	GTTAGGCCGTCTATTTTGGCT	41912	GTCAGACCAAGCATCCTCGCA
13267	VRPSSLE	27590	GTTAGGCCTTCGTCTCTTGAG	41913	GTCAGACCAAGCAGCCTCGAA
13268	VRPTNSG	27591	GTTAGGCCTACGAATTCGGGT	41914	GTCAGACCAACAAACAGCGGA
13269	VRPTQNS	27592	GTTCGGCCTACTCAGAATTCT	41915	GTCAGACCAACACAAAACAGC
13270	VRPVKEV	27593	GTTCGGCCTGTTAAGGAGGTT	41916	GTCAGACCAGTCAAAGAAGTC
13271	VRPVNGV	27594	GTTAGGCCTGTTAATGGGGTG	41917	GTCAGACCAGTCAACGGAGTC
13272	VRQEIIS	27595	GTTCGGCAGGAGATTATTTCG	41918	GTCAGACAAGAAATCATCAGC
13273	VRQMTPG	27596	GTGAGGCAGATGACGCCGGGG	41919	GTCAGACAAATGACACCAGGA
13274	VRQPGVD	27597	GTGAGGCAGCCGGGGGTTGAT	41920	GTCAGACAACCAGGAGTCGAC
13275	VRQSSNT	27598	GTTCGTCAGTCTTCGAATACG	41921	GTCAGACAAAGCAGCAACACA
13276	VRRVASE	27599	GTTCGGAGGGTGGCTTCTGAG	41922	GTCAGAAGAGTCGCAAGCGAA
13277	VRSAISD	27600	GTTCGTTCGGCTATTTCTGAT	41923	GTCAGAAGCGCAATCAGCGAC
13278	VRSATFH	27601	GTTCGGAGTGCGACTTTTCAT	41924	GTCAGAAGCGCAACATTCCAC
13279	VRSLEQS	27602	GTGCGGTCTTTGGAGCAGTCG	41925	GTCAGAAGCCTCGAACAAAGC
13280	VRSPSHC	27603	GTTAGGTCTCCGTCGCATTGT	41926	GTCAGAAGCCCAAGCCACTGC
13281	VRSQLPP	27604	GTGAGGTCTCAGCTTCCGCCG	41927	GTCAGAAGCCAACTCCCACCA
13282	VRSSLDR	27605	GTGCGGAGTTCGTTGGATCGG	41928	GTCAGAAGCAGCCTCGACAGA
13283	VRSSTYT	27606	GTTCGGTCGTCTACGTATACG	41929	GTCAGAAGCAGCACATACACA
13284	VRSVAPE	27607	GTGAGGTCTGTGGCTCCTGAG	41930	GTCAGAAGCGTCGCACCAGAA
13285	VRTLPSP	27608	GTGAGGACTTTGCCTTCTCCG	41931	GTCAGAACACTCCCAAGCCCA
13286	VRTMPHS	27609	GTGAGGACGATGCCGCATTCG	41932	GTCAGAACAATGCCACACAGC
13287	VRTPFEA	27610	GTTCGGACTCCGTTTGAGGCT	41933	GTCAGAACACCATTCGAAGCA
13288	VRTQGLS	27611	GTGAGGACGCAGGGTCTTAGT	41934	GTCAGAACACAAGGACTCAGC
13289	VRTQGTN	27612	GTTCGGACGCAGGGTACTAAT	41935	GTCAGAACACAAGGAACAAAC
13290	VRTSIGT	27613	GTGCGTACTTCTATTGGTACT	41936	GTCAGAACAAGCATCGGAACA
13291	VRTSPMS	27614	GTTCGTACGTCGCCGATGTCG	41937	GTCAGAACAAGCCCAATGAGC
13292	VRVAVPM	27615	GTTCGGGTTGCTGTGCCTATG	41938	GTCAGAGTCGCAGTCCCAATG
13293	VRVGTIG	27616	GTTCGGGTGGGGACGATTGGT	41939	GTCAGAGTCGGAACAATCGGA
13294	VRVGTLN	27617	GTGCGGGTGGGTACTTTGAAT	41940	GTCAGAGTCGGAACACTCAAC
13295	VRVMGSS	27618	GTTCGTGTGATGGGTTCTAGT	41941	GTCAGAGTCATGGGAAGCAGC
13296	VSAASLT	27619	GTTTCTGCGGCTTCTTTGACT	41942	GTCAGCGCAGCAAGCCTCACA
13297	VSAATSF	27620	GTTAGTGCGGCTACGTCTTTT	41943	GTCAGCGCAGCAACAAGCTTC
13298	VSAHTNS	27621	GTGTCTGCGCATACTAATTCT	41944	GTCAGCGCACACACAAACAGC
13299	VSAIMDV	27622	GTGAGTGCGATTATGGATGTG	41945	GTCAGCGCAATCATGGACGTC
13300	VSAISAT	27623	GTGTCGGCTATTTCTGCTACT	41946	GTCAGCGCAATCAGCGCAACA
13301	VSAPEDH	27624	GTGAGTGCTCCTGAGGATCAT	41947	GTCAGCGCACCAGAAGACCAC
13302	VSAQISI	27625	GTGTCTGCTCAGATTAGTATT	41948	GTCAGCGCACAAATCAGCATC
13303	VSARESV	27626	GTTTCTGCGCGGGAGAGTGTT	41949	GTCAGCGCAAGAGAAAGCGTC
13304	VSARSFQ	27627	GTGTCGGCTAGGTCTTTTCAG	41950	GTCAGCGCAAGAAGCTTCCAA
13305	VSASAGR	27628	GTTTCTGCTAGTGCTGGGCGT	41951	GTCAGCGCAAGCGCAGGAAGA
13306	VSASLAL	27629	GTTTCTGCGAGTCTTGCTCTG	41952	GTCAGCGCAAGCCTCGCACTC
13307	VSASSSA	27630	GTTTCTGCTAGTTCTAGTGCT	41953	GTCAGCGCAAGCAGCAGCGCA
13308	VSATHVQ	27631	GTGTCTGCGACGCATGTTCAG	41954	GTCAGCGCAACACACGTCCAA
13309	VSATTSV	27632	GTGAGTGCGACTACGTCGGTG	41955	GTCAGCGCAACAACAAGCGTC

13310	VSDDKSS	27633	GTTTCGGATGATAAGAGTTCT	41956	GTCAGCGACGACAAAAGCAGC
13311	VSDGNKL	27634	GTTTCTGATGGTAATAAGTTG	41957	GTCAGCGACGGAAACAAACTC
13312	VSDNLWS	27635	GTGTCGGATAATCTTTGGTCT	41958	GTCAGCGACAACCTCTGGAGC
13313	VSDSYQW	27636	GTGTCGGATTCTTATCAGTGG	41959	GTCAGCGACAGCTACCAATGG
13314	VSDVAFY	27637	GTTTCTGATGTGGCTTTTTAT	41960	GTCAGCGACGTCGCATTCTAC
13315	VSDVTSD	27638	GTTTCTGATGTTACGTCGGAT	41961	GTCAGCGACGTCACAAGCGAC
13316	VSDYLTQ	27639	GTGAGTGATTATCTTACTCAG	41962	GTCAGCGACTACCTCACACAA
13317	VSFPYEE	27640	GTTTCGTTTCCGTATGAGGAG	41963	GTCAGCTTCCCATACGAAGAA
13318	VSFQPLG	27641	GTTTCGTTTCAGCCTCTTGGT	41964	GTCAGCTTCCAACCACTCGGA
13319	VSGFNQH	27642	GTGAGTGGTTTTAATCAGCAT	41965	GTCAGCGGATTCAACCAACAC
13320	VSGPNHY	27643	GTTTCTGGGCCTAATCATTAT	41966	GTCAGCGGACCAAACCACTAC
13321	VSGSLQY	27644	GTGAGTGGTTCGCTGCAGTAT	41967	GTCAGCGGAAGCCTCCAATAC
13322	VSGSTRT	27645	GTGAGTGGTAGTACGCGGACT	41968	GTCAGCGGAAGCACAAGAACA
13323	VSHATHQ	27646	GTTAGTCATGCTACGCATCAG	41969	GTCAGCCACGCAACACACCAA
13324	VSHGMNM	27647	GTGAGTCATGGTATGAATATG	41970	GTCAGCCACGGAATGAACATG
13325	VSHGMSS	27648	GTGAGTCATGGTATGTCGTCT	41971	GTCAGCCACGGAATGAGCAGC
13326	VSHPNAP	27649	GTTAGTCATCCGAATGCGCCG	41972	GTCAGCCACCCAAACGCACCA
13327	VSHTMQE	27650	GTTTCGCATACTATGCAGGAG	41973	GTCAGCCACACAATGCAAGAA
13328	VSIAGAS	27651	GTTTCGATTGCGGGGGCTTCT	41974	GTCAGCATCGCAGGAGCAAGC
13329	VSISIPS	27652	GTGTCTATTTCGATTCCGTCG	41975	GTCAGCATCAGCATCCCAAGC
13330	VSISMPP	27653	GTGTCGATTTCTATGCCTCCT	41976	GTCAGCATCAGCATGCCACCA
13331	VSKEMIL	27654	GTGAGTAAGGAGATGATTCTT	41977	GTCAGCAAAGAAATGATCCTC
13332	VSKPTNS	27655	GTTTCTAAGCCTACTAATTCT	41978	GTCAGCAAACCAACAAACAGC
13333	VSKSISS	27656	GTTAGTAAGTCTATTTCGAGT	41979	GTCAGCAAAAGCATCAGCAGC
13334	VSLGYPD	27657	GTTAGTCTTGGGTATCCGGAT	41980	GTCAGCCTCGGATACCCAGAC
13335	VSLLPTS	27658	GTGTCGCTGTTGCCTACGTCG	41981	GTCAGCCTCCTCCCAACAAGC
13336	VSLLTSK	27659	GTGAGTCTGTTGACTAGTAAG	41982	GTCAGCCTCCTCACAAGCAAA
13337	VSLPQER	27660	GTGTCGCTGCCTCAGGAGCGG	41983	GTCAGCCTCCCACAAGAAAGA
13338	VSLQGID	27661	GTTTCTCTGCAGGGGATTGAT	41984	GTCAGCCTCCAAGGAATCGAC
13339	VSLRAPT	27662	GTTTCTCTTCGGGCGCCTACT	41985	GTCAGCCTCAGAGCACCAACA
13340	VSLRHTA	27663	GTTTCTCTGCGGCATACGGCG	41986	GTCAGCCTCAGACACACAGCA
13341	VSLSPIS	27664	GTTTCTCTGTCGCCGATTTCT	41987	GTCAGCCTCAGCCCAATCAGC
13342	VSLSTTA	27665	GTGTCGCTTTCGACTACTGCT	41988	GTCAGCCTCAGCACAACAGCA
13343	VSLTLSS	27666	GTGTCGCTGACGCTGTCTAGT	41989	GTCAGCCTCACACTCAGCAGC
13344	VSMGRPL	27667	GTTTCGATGGGTCGGCCGTTG	41990	GTCAGCATGGGAAGACCACTC
13345	VSMHLEP	27668	GTTTCTATGCATTTGGAGCCG	41991	GTCAGCATGCACCTCGAACCA
13346	VSMKNLH	27669	GTGTCTATGAAGAATCTTCAT	41992	GTCAGCATGAAAAACCTCCAC
13347	VSMMEPE	27670	GTTTCGATGATGGAGCCGGAG	41993	GTCAGCATGATGGAACCAGAA
13348	VSMPSRS	27671	GTTAGTATGCCTTCTAGGAGT	41994	GTCAGCATGCCAAGCAGAAGC
13349	VSNAARM	27672	GTTTCGAATGCTGCTAGGATG	41995	GTCAGCAACGCAGCAAGAATG
13350	VSNFQNP	27673	GTGTCGAATTTTCAGAATCCT	41996	GTCAGCAACTTCCAAAACCCA
13351	VSNISSP	27674	GTGTCGAATATTTCTAGTCCG	41997	GTCAGCAACATCAGCAGCCCA
13352	VSNMQFA	27675	GTTTCTAATATGCAGTTTGCG	41998	GTCAGCAACATGCAATTCGCA
13353	VSNPDLM	27676	GTGTCGAATCCTGATTTGATG	41999	GTCAGCAACCCAGACCTCATG
13354	VSNPQVS	27677	GTGTCGAATCCTCAGGTGAGT	42000	GTCAGCAACCCACAAGTCAGC

13355	VSNQAGY	27678	GTTTCTAATCAGGCTGGGTAT	42001	GTCAGCAACCAAGCAGGATAC
13356	VSNQKQV	27679	GTGTCGAATCAGAAGCAGGTT	42002	GTCAGCAACCAAAAACAAGTC
13357	VSNRSTQ	27680	GTTTCTAATCGTTCTACTCAG	42003	GTCAGCAACAGAAGCACACAA
13358	VSNSMAH	27681	GTTAGTAATTCGATGGCGCAT	42004	GTCAGCAACAGCATGGCACAC
13359	VSNTLLV	27682	GTGTCTAATACGTTGCTGGTG	42005	GTCAGCAACACACTCCTCGTC
13360	VSPAFHK	27683	GTGTCTCCTGCTTTTCATAAG	42006	GTCAGCCCAGCATTCCACAAA
13361	VSPAWHG	27684	GTTTCTCCTGCGTGGCATGGG	42007	GTCAGCCCAGCATGGCACGGA
13362	VSPEEDR	27685	GTTAGTCCGGAGGAGGATCGG	42008	GTCAGCCCAGAAGAAGACAGA
13363	VSPEPLR	27686	GTGTCTCCTGAGCCTTTGCGG	42009	GTCAGCCCAGAACCACTCAGA
13364	VSPGNPA	27687	GTTTCGCCGGGGAATCCGGCG	42010	GTCAGCCCAGGAAACCCAGCA
13365	VSPHPVH	27688	GTGAGTCCGCATCCGGTGCAT	42011	GTCAGCCCACACCCAGTCCAC
13366	VSPLLPS	27689	GTGTCTCCGCTGCTGCCGAGT	42012	GTCAGCCCACTCCTCCCAAGC
13367	VSPLNTS	27690	GTTTCTCCTCTTAATACTTCT	42013	GTCAGCCCACTCAACACAAGC
13368	VSPMTEI	27691	GTTAGTCCGATGACGGAGATT	42014	GTCAGCCCAATGACAGAAATC
13369	VSPRPGQ	27692	GTGAGTCCGCGTCCGGGGCAG	42015	GTCAGCCCAAGACCAGGACAA
13370	VSPSNRG	27693	GTGAGTCCTTCGAATAGGGGG	42016	GTCAGCCCAAGCAACAGAGGA
13371	VSPSSAL	27694	GTTTCTCCTAGTTCTGCTCTT	42017	GTCAGCCCAAGCAGCGCACTC
13372	VSPTQHF	27695	GTGTCTCCGACGCAGCATTTT	42018	GTCAGCCCAACACAACACTTC
13373	VSPTYSL	27696	GTGTCGCCTACTTATTCTTTG	42019	GTCAGCCCAACATACAGCCTC
13374	VSPVYTS	27697	GTTAGTCCGGTTTATACGTCG	42020	GTCAGCCCAGTCTACACAAGC
13375	VSPYPRD	27698	GTTTCGCCTTATCCTCGGGAT	42021	GTCAGCCCATACCCAAGAGAC
13376	VSQLGSP	27699	GTGAGTCAGCTTGGGAGTCCG	42022	GTCAGCCAACTCGGAAGCCCA
13377	VSQLTQV	27700	GTGTCTCAGTTGACGCAGGTG	42023	GTCAGCCAACTCACACAAGTC
13378	VSQPSYG	27701	GTGTCGCAGCCTTCTTATGGT	42024	GTCAGCCAACCAAGCTACGGA
13379	VSQSYTN	27702	GTTTCTCAGTCTTATACGAAT	42025	GTCAGCCAAAGCTACACAAAC
13380	VSQVKQG	27703	GTGTCTCAGGTGAAGCAGGGT	42026	GTCAGCCAAGTCAAACAAGGA
13381	VSRATPN	27704	GTGTCGCGTGCTACTCCGAAT	42027	GTCAGCAGAGCAACACCAAAC
13382	VSREINS	27705	GTTTCGCGGGAGATTAATTCT	42028	GTCAGCAGAGAAATCAACAGC
13383	VSRQDSL	27706	GTGTCGAGGCAGGATTCTCTG	42029	GTCAGCAGACAAGACAGCCTC
13384	VSRSGNS	27707	GTTTCGCGGAGTGGTAATAGT	42030	GTCAGCAGAAGCGGAAACAGC
13385	VSRTMDT	27708	GTTTCTCGGACGATGGATACT	42031	GTCAGCAGAACAATGGACACA
13386	VSRVELA	27709	GTTTCTAGGGTGGAGTTGGCT	42032	GTCAGCAGAGTCGAACTCGCA
13387	VSSAHSI	27710	GTTTCGTCTGCTCATAGTATT	42033	GTCAGCAGCGCACACAGCATC
13388	VSSAHTS	27711	GTTTCGTCTGCTCATACGTCT	42034	GTCAGCAGCGCACACACAAGC
13389	VSSAISY	27712	GTTTCGTCGGCTATTAGTTAT	42035	GTCAGCAGCGCAATCAGCTAC
13390	VSSARGT	27713	GTTAGTTCGGCGCGGGGTACG	42036	GTCAGCAGCGCAAGAGGAACA
13391	VSSASPM	27714	GTTTCGTCTGCTTCGCCTATG	42037	GTCAGCAGCGCAAGCCCAATG
13392	VSSDRLL	27715	GTGTCTTCGGATAGGCTGTTG	42038	GTCAGCAGCGACAGACTCCTC
13393	VSSDYSN	27716	GTTTCGTCGGATTATTCGAAT	42039	GTCAGCAGCGACTACAGCAAC
13394	VSSFLED	27717	GTTAGTTCGTTTCTTGAGGAT	42040	GTCAGCAGCTTCCTCGAAGAC
13395	VSSLELA	27718	GTTAGTTCGCTGGAGCTTGCT	42041	GTCAGCAGCCTCGAACTCGCA
13396	VSSLKTY	27719	GTGAGTTCGCTTAAGACTTAT	42042	GTCAGCAGCCTCAAAACATAC
13397	VSSLRGP	27720	GTGTCGTCTCTGCGTGGTCCG	42043	GTCAGCAGCCTCAGAGGACCA
13398	VSSLSSL	27721	GTTTCTTCTCTGAGTAGTTTG	42044	GTCAGCAGCCTCAGCAGCCTC
13399	VSSMLDA	27722	GTTTCGTCTATGCTGGATGCG	42045	GTCAGCAGCATGCTCGACGCA

13400	VSSMNIV	27723	GTGTCGAGTATGAATATTGTT	42046	GTCAGCAGCATGAACATCGTC
13401	VSSMPVP	27724	GTTAGTTCTATGCCTGTGCCT	42047	GTCAGCAGCATGCCAGTCCCA
13402	VSSNSFA	27725	GTTTCGAGTAATTCGTTTGCG	42048	GTCAGCAGCAACAGCTTCGCA
13403	VSSPDSN	27726	GTGTCGTCTCCTGATAGTAAT	42049	GTCAGCAGCCCAGACAGCAAC
13404	VSSPLSG	27727	GTTTCTTCTCCTTTGAGTGGT	42050	GTCAGCAGCCCACTCAGCGGA
13405	VSSPPDL	27728	GTGTCTTCTCCTCCTGATCTT	42051	GTCAGCAGCCCACCAGACCTC
13406	VSSPREH	27729	GTTAGTTCGCCTCGGGAGCAT	42052	GTCAGCAGCCCAAGAGAACAC
13407	VSSQNVF	27730	GTTTCGTCGCAGAATGTTTTT	42053	GTCAGCAGCCAAAACGTCTTC
13408	VSSQRNG	27731	GTTAGTTCGCAGAGGAATGGG	42054	GTCAGCAGCCAAAGAAACGGA
13409	VSSRYHA	27732	GTGTCGTCGCGTTATCATGCT	42055	GTCAGCAGCAGATACCACGCA
13410	VSSSGMT	27733	GTGAGTAGTAGTGGTATGACG	42056	GTCAGCAGCAGCGGAATGACA
13411	VSSSLMS	27734	GTGTCTTCGTCGCTTATGTCG	42057	GTCAGCAGCAGCCTCATGAGC
13412	VSSSQMP	27735	GTTTCTTCTAGTCAGATGCCT	42058	GTCAGCAGCAGCCAAATGCCA
13413	VSSSVLR	27736	GTTTCTTCTTCGGTTCTTAGG	42059	GTCAGCAGCAGCGTCCTCAGA
13414	VSSTIVM	27737	GTGTCGAGTACTATTGTGATG	42060	GTCAGCAGCACAATCGTCATG
13415	VSSVVSG	27738	GTGTCGTCTGTGGTGTCGGGT	42061	GTCAGCAGCGTCGTCAGCGGA
13416	VSTAHQS	27739	GTGTCTACTGCTCATCAGTCG	42062	GTCAGCACAGCACACCAAAGC
13417	VSTFGPT	27740	GTTTCGACGTTTGGTCCTACG	42063	GTCAGCACATTCGGACCAACA
13418	VSTGLTK	27741	GTTAGTACGGGTTTGACGAAG	42064	GTCAGCACAGGACTCACAAAA
13419	VSTGYAV	27742	GTTTCGACTGGTTATGCTGTT	42065	GTCAGCACAGGATACGCAGTC
13420	VSTIAFE	27743	GTTTCTACGATTGCGTTTGAG	42066	GTCAGCACAATCGCATTCGAA
13421	VSTISSL	27744	GTGTCTACGATTTCGTCGTTG	42067	GTCAGCACAATCAGCAGCCTC
13422	VSTLQAG	27745	GTTTCTACGCTTCAGGCGGGG	42068	GTCAGCACACTCCAAGCAGGA
13423	VSTMRSP	27746	GTTTCGACTATGCGGAGTCCG	42069	GTCAGCACAATGAGAAGCCCA
13424	VSTPNNK	27747	GTTAGTACTCCTAATAATAAG	42070	GTCAGCACACCAAACAACAAA
13425	VSTQTYK	27748	GTGAGTACGCAGACTTATAAG	42071	GTCAGCACACAAACATACAAA
13426	VSTRQLL	27749	GTGTCGACGAGGCAGCTTCTT	42072	GTCAGCACAAGACAACTCCTC
13427	VSTSVLR	27750	GTGAGTACTAGTGTTCTGAGG	42073	GTCAGCACAAGCGTCCTCAGA
13428	VSTTFKV	27751	GTGAGTACGACGTTTAAGGTG	42074	GTCAGCACAACATTCAAAGTC
13429	VSVKVHD	27752	GTTTCGGTTAAGGTGCATGAT	42075	GTCAGCGTCAAAGTCCACGAC
13430	VSVQSSR	27753	GTTTCTGTGCAGTCGTCGCGG	42076	GTCAGCGTCCAAAGCAGCAGA
13431	VSVSTHH	27754	GTGTCGGTGTCGACGCATCAT	42077	GTCAGCGTCAGCACACACCAC
13432	VSVSVGE	27755	GTTTCGGTTAGTGTGGGTGAG	42078	GTCAGCGTCAGCGTCGGAGAA
13433	VSVTAGG	27756	GTTTCTGTTACTGCGGGTGGG	42079	GTCAGCGTCACAGCAGGAGGA
13434	VSVTSAG	27757	GTTTCTGTTACTTCTGCTGGT	42080	GTCAGCGTCACAAGCGCAGGA
13435	VSYAMEN	27758	GTGTCTTATGCTATGGAGAAT	42081	GTCAGCTACGCAATGGAAAAC
13436	VSYPAQA	27759	GTGTCGTATCCGGCTCAGGCT	42082	GTCAGCTACCCAGCACAAGCA
13437	VTAGPMR	27760	GTGACTGCTGGGCCTATGCGT	42083	GTCACAGCAGGACCAATGAGA
13438	VTALTIA	27761	GTGACTGCGCTTACTATTGCT	42084	GTCACAGCACTCACAATCGCA
13439	VTALVKD	27762	GTGACTGCTCTGGTTAAGGAT	42085	GTCACAGCACTCGTCAAAGAC
13440	VTANLPQ	27763	GTGACTGCTAATTTGCCTCAG	42086	GTCACAGCAAACCTCCCACAA
13441	VTANVLP	27764	GTTACTGCTAATGTTCTTCCT	42087	GTCACAGCAAACGTCCTCCCA
13442	VTAPVTG	27765	GTTACTGCTCCGGTGACTGGT	42088	GTCACAGCACCAGTCACAGGA
13443	VTAQSSV	27766	GTTACTGCGCAGTCGTCGGTG	42089	GTCACAGCACAAAGCAGCGTC
13444	VTARSLA	27767	GTGACTGCGCGTTCTCTGGCT	42090	GTCACAGCAAGAAGCCTCGCA

13445	VTASHRV	27768	GTGACTGCTAGTCATCGTGTT	42091	GTCACAGCAAGCCACAGAGTC
13446	VTDAVTT	27769	GTTACTGATGCTGTGACTACG	42092	GTCACAGACGCAGTCACAACA
13447	VTDNVRN	27770	GTTACTGATAATGTGCGGAAT	42093	GTCACAGACAACGTCAGAAAC
13448	VTDSTDD	27771	GTGACTGATTCGACTGATGAT	42094	GTCACAGACAGCACAGACGAC
13449	VTDTRER	27772	GTTACGGATACGCGTGAGAGG	42095	GTCACAGACACAAGAGAAAGA
13450	VTEARSA	27773	GTTACGGAGGCGCGTTCTGCG	42096	GTCACAGAAGCAAGAAGCGCA
13451	VTEESDM	27774	GTGACGGAGGAGAGTGATATG	42097	GTCACAGAAGAAAGCGACATG
13452	VTEESNT	27775	GTTACGGAGGAGTCTAATACT	42098	GTCACAGAAGAAAGCAACACA
13453	VTEHLKN	27776	GTTACGGAGCATCTGAAGAAT	42099	GTCACAGAACACCTCAAAAAC
13454	VTERMTL	27777	GTTACTGAGAGGATGACTCTT	42100	GTCACAGAAAGAATGACACTC
13455	VTFSSSG	27778	GTTACGTTTTCTTCTTCTGGT	42101	GTCACATTCAGCAGCAGCGGA
13456	VTGARLA	27779	GTTACTGGGGCGCGGTTGGCT	42102	GTCACAGGAGCAAGACTCGCA
13457	VTGHAIL	27780	GTTACTGGTCATGCGATTCTT	42103	GTCACAGGACACGCAATCCTC
13458	VTGKPSL	27781	GTTACTGGTAAGCCTTCTTTG	42104	GTCACAGGAAAACCAAGCCTC
13459	VTGPGLR	27782	GTTACTGGGCCGGGTTTGAGG	42105	GTCACAGGACCAGGACTCAGA
13460	VTGTRTV	27783	GTGACGGGGACGAGGACTGTG	42106	GTCACAGGAACAAGAACAGTC
13461	VTHLMQG	27784	GTTACGCATCTTATGCAGGGG	42107	GTCACACACCTCATGCAAGGA
13462	VTHPNLS	27785	GTTACGCATCCTAATTTGAGT	42108	GTCACACACCCAAACCTCAGC
13463	VTHTEFP	27786	GTGACTCATACGGAGTTTCCG	42109	GTCACACACACAGAATTCCCA
13464	VTHTGHK	27787	GTGACTCATACTGGTCATAAG	42110	GTCACACACACAGGACACAAA
13465	VTHYSSV	27788	GTGACGCATTATAGTTCGGTG	42111	GTCACACACTACAGCAGCGTC
13466	VTIDDYP	27789	GTGACTATTGATGATTATCCT	42112	GTCACAATCGACGACTACCCA
13467	VTKASAP	27790	GTTACGAAGGCTTCTGCTCCT	42113	GTCACAAAAGCAAGCGCACCA
13468	VTLKPLS	27791	GTTACTTTGAAGCCTTTGAGT	42114	GTCACACTCAAACCACTCAGC
13469	VTLLASR	27792	GTGACTCTTCTGGCGTCGAGG	42115	GTCACACTCCTCGCAAGCAGA
13470	VTLPLTR	27793	GTGACTTTGCCGCTTACTCGT	42116	GTCACACTCCCACTCACAAGA
13471	VTLQRPG	27794	GTTACTCTGCAGCGTCCTGGG	42117	GTCACACTCCAAAGACCAGGA
13472	VTLSAEG	27795	GTGACGCTGAGTGCTGAGGGG	42118	GTCACACTCAGCGCAGAAGGA
13473	VTLSDRL	27796	GTGACTCTGTCGGATAGGCTG	42119	GTCACACTCAGCGACAGACTC
13474	VTMSTIR	27797	GTTACTATGAGTACTATTCGT	42120	GTCACAATGAGCACAATCAGA
13475	VTNRVHP	27798	GTGACGAATAGGGTGCATCCT	42121	GTCACAAACAGAGTCCACCCA
13476	VTPDLRH	27799	GTTACTCCGGATCTGCGTCAT	42122	GTCACACCAGACCTCAGACAC
13477	VTPDSLK	27800	GTTACTCCGGATTCGCTGAAG	42123	GTCACACCAGACAGCCTCAAA
13478	VTPDYRN	27801	GTTACTCCTGATTATAGGAAT	42124	GTCACACCAGACTACAGAAAC
13479	VTPGLAY	27802	GTGACTCCGGGTCTTGCTTAT	42125	GTCACACCAGGACTCGCATAC
13480	VTPLLTA	27803	GTGACGCCTCTGCTTACGGCG	42126	GTCACACCACTCCTCACAGCA
13481	VTPQTNF	27804	GTGACGCCTCAGACGAATTTT	42127	GTCACACCACAAACAAACTTC
13482	VTPVGKT	27805	GTGACTCCGGTTGGGAAGACG	42128	GTCACACCAGTCGGAAAAACA
13483	VTQHTST	27806	GTTACGCAGCATACTTCTACG	42129	GTCACACAACACACAAGCACA
13484	VTQILRT	27807	GTGACTCAGATTCTGAGGACT	42130	GTCACACAAATCCTCAGAACA
13485	VTQPHAS	27808	GTGACGCAGCCGCATGCTTCT	42131	GTCACACAACCACACGCAAGC
13486	VTRALHD	27809	GTTACGCGTGCGTTGCATGAT	42132	GTCACAAGAGCACTCCACGAC
13487	VTRMESA	27810	GTTACTCGTATGGAGTCTGCT	42133	GTCACAAGAATGGAAAGCGCA
13488	VTSALVR	27811	GTTACGTCGGCTCTTGTGCGT	42134	GTCACAAGCGCACTCGTCAGA
13489	VTSAMQG	27812	GTGACTTCTGCTATGCAGGGT	42135	GTCACAAGCGCAATGCAAGGA

13490	VTSASTH	27813	GTGACGTCTGCGTCTACGCAT	42136	GTCACAAGCGCAAGCACACAC
13491	VTSFVAP	27814	GTGACTTCTTTTGTGGCTCCG	42137	GTCACAAGCTTCGTCGCACCA
13492	VTSHTGE	27815	GTGACTTCGCATACTGGGGAG	42138	GTCACAAGCCACACAGGAGAA
13493	VTSPTFE	27816	GTTACTTCGCCGACGTTTGAG	42139	GTCACAAGCCCAACATTCGAA
13494	VTSRSAV	27817	GTTACTAGTCGGTCGGCTGTT	42140	GTCACAAGCAGAAGCGCAGTC
13495	VTSSTQL	27818	GTGACGTCGTCGACGCAGTTG	42141	GTCACAAGCAGCACACAACTC
13496	VTSTSTN	27819	GTGACTTCGACTAGTACTAAT	42142	GTCACAAGCACAAGCACAAAC
13497	VTSVSPI	27820	GTGACTAGTGTTTCGCCGATT	42143	GTCACAAGCGTCAGCCCAATC
13498	VTTATGI	27821	GTTACTACTGCTACGGGGATT	42144	GTCACAACAGCAACAGGAATC
13499	VTTEPRF	27822	GTTACGACGGAGCCTCGGTTT	42145	GTCACAACAGAACCAAGATTC
13500	VTTIRAH	27823	GTGACTACGATTCGGGCTCAT	42146	GTCACAACAATCAGAGCACAC
13501	VTTKQTC	27824	GTGACTACTAAGCAGACGTGT	42147	GTCACAACAAAACAAACATGC
13502	VTTNGPI	27825	GTTACTACTAATGGTCCTATT	42148	GTCACAACAAACGGACCAATC
13503	VTTQFES	27826	GTGACGACTCAGTTTGAGTCT	42149	GTCACAACACAATTCGAAAGC
13504	VTTRPYP	27827	GTGACTACGAGGCCGTATCCG	42150	GTCACAACAAGACCATACCCA
13505	VTTSRYL	27828	GTGACGACGAGTCGTTATCTG	42151	GTCACAACAAGCAGATACCTC
13506	VTTSTSR	27829	GTGACTACGAGTACTTCGCGT	42152	GTCACAACAAGCACAAGCAGA
13507	VTTTQIT	27830	GTGACGACGACTCAGATTACT	42153	GTCACAACAACACAAATCACA
13508	VTTVILD	27831	GTGACGACGGTGATTCTTGAT	42154	GTCACAACAGTCATCCTCGAC
13509	VTVHSHF	27832	GTTACGGTTCATTCGCATTTT	42155	GTCACAGTCCACAGCCACTTC
13510	VTVPLPS	27833	GTTACGGTTCCTCTTCCGTCG	42156	GTCACAGTCCCACTCCCAAGC
13511	VTVQMNV	27834	GTTACTGTGCAGATGAATGTT	42157	GTCACAGTCCAAATGAACGTC
13512	VTVRGSI	27835	GTGACGGTGAGGGGGTCGATT	42158	GTCACAGTCAGAGGAAGCATC
13513	VTVTGTI	27836	GTTACGGTGACTGGGACGATT	42159	GTCACAGTCACAGGAACAATC
13514	VTYSPLG	27837	GTGACTTATTCGCCGCTTGGG	42160	GTCACATACAGCCCACTCGGA
13515	VVAGRSS	27838	GTGGTTGCTGGGCGTAGTAGT	42161	GTCGTCGCAGGAAGAAGCAGC
13516	VVAQPGH	27839	GTGGTGGCTCAGCCGGGTCAT	42162	GTCGTCGCACAACCAGGACAC
13517	VVATTLN	27840	GTGGTGGCTACGACGCTGAAT	42163	GTCGTCGCAACAACACTCAAC
13518	VVDSPRA	27841	GTGGTGGATTCTCCTCGGGCT	42164	GTCGTCGACAGCCCAAGAGCA
13519	VVDVPLR	27842	GTTGTTGATGTTCCTTTGCGG	42165	GTCGTCGACGTCCCACTCAGA
13520	VVETFEP	27843	GTTGTTGAGACTTTTGAGCCG	42166	GTCGTCGAAACATTCGAACCA
13521	VVGDGTI	27844	GTGGTTGGTGATGGGACGATT	42167	GTCGTCGGAGACGGAACAATC
13522	VVGDQAD	27845	GTGGTGGGTGATCAGGCTGAT	42168	GTCGTCGGAGACCAAGCAGAC
13523	VVGGQLL	27846	GTTGTGGGTGGGCAGTTGTTG	42169	GTCGTCGGAGGACAACTCCTC
13524	VVGIRGE	27847	GTTGTGGGGATTCGTGGGGAG	42170	GTCGTCGGAATCAGAGGAGAA
13525	VVGMGTG	27848	GTTGTTGGGATGGGTACGGGT	42171	GTCGTCGGAATGGGAACAGGA
13526	VVGPSLP	27849	GTTGTGGGTCCGTCGTTGCCG	42172	GTCGTCGGACCAAGCCTCCCA
13527	VVGRQER	27850	GTTGTGGGTCGTCAGGAGCGG	42173	GTCGTCGGAAGACAAGAAAGA
13528	VVGRSNP	27851	GTTGTTGGGAGGTCGAATCCT	42174	GTCGTCGGAAGAAGCAACCCA
13529	VVGSPTR	27852	GTTGTGGGTAGTCCTACTCGG	42175	GTCGTCGGAAGCCCAACAAGA
13530	VVGSSGP	27853	GTGGTGGGGTCTAGTGGTCCG	42176	GTCGTCGGAAGCAGCGGACCA
13531	VVHPPGQ	27854	GTTGTTCATCCGCCTGGTCAG	42177	GTCGTCCACCCACCAGGACAA
13532	VVHPSPG	27855	GTTGTGCATCCGAGTCCGGGT	42178	GTCGTCCACCCAAGCCCAGGA
13533	VVHSNEP	27856	GTTGTTCATTCTAATGAGCCG	42179	GTCGTCCACAGCAACGAACCA
13534	VVHTMSV	27857	GTGGTGCATACGATGTCTGTT	42180	GTCGTCCACACAATGAGCGTC

13535	VVHVSHP	27858	GTGGTGCATGTTTCTCATCCT	42181	GTCGTCCACGTCAGCCACCCA
13536	VVHVVNS	27859	GTTGTTCATGTGGTGAATTCG	42182	GTCGTCCACGTCGTCAACAGC
13537	VVIDQNG	27860	GTGGTGATTGATCAGAATGGG	42183	GTCGTCATCGACCAAAACGGA
13538	VVLKDNH	27861	GTTGTTTTGAAGGATAATCAT	42184	GTCGTCCTCAAAGACAACCAC
13539	VVMRDDP	27862	GTTGTGATGCGGGATGATCCG	42185	GTCGTCATGAGAGACGACCCA
13540	VVNASAN	27863	GTTGTGAATGCGTCTGCTAAT	42186	GTCGTCAACGCAAGCGCAAAC
13541	VVNNLRI	27864	GTTGTGAATAATTTGAGGATT	42187	GTCGTCAACAACCTCAGAATC
13542	VVNQAQL	27865	GTGGTTAATCAGGCTCAGTTG	42188	GTCGTCAACCAAGCACAACTC
13543	VVNTKAN	27866	GTGGTTAATACGAAGGCGAAT	42189	GTCGTCAACACAAAAGCAAAC
13544	VVNTKSG	27867	GTGGTGAATACTAAGTCTGGT	42190	GTCGTCAACACAAAAAGCGGA
13545	VVPALKM	27868	GTGGTGCCTGCGCTGAAGATG	42191	GTCGTCCCAGCACTCAAAATG
13546	VVPHSRQ	27869	GTTGTTCCGCATTCGAGGCAG	42192	GTCGTCCCACACAGCAGACAA
13547	VVPLGPV	27870	GTGGTGCCGTTGGGTCCTGTT	42193	GTCGTCCCACTCGGACCAGTC
13548	VVPRDPG	27871	GTTGTTCCGCGTGATCCGGGT	42194	GTCGTCCCAAGAGACCCAGGA
13549	VVPRMTG	27872	GTGGTGCCTAGGATGACTGGG	42195	GTCGTCCCAAGAATGACAGGA
13550	VVPRPGM	27873	GTTGTGCCGCGGCCGGGTATG	42196	GTCGTCCCAAGACCAGGAATG
13551	VVPRSGD	27874	GTTGTTCCGCGTAGTGGGGAT	42197	GTCGTCCCAAGAAGCGGAGAC
13552	VVPTDDG	27875	GTGGTTCCTACTGATGATGGT	42198	GTCGTCCCAACAGACGACGGA
13553	VVQPRAG	27876	GTGGTGCAGCCTAGGGCGGGT	42199	GTCGTCCAACCAAGAGCAGGA
13554	VVQQSSL	27877	GTGGTTCAGCAGTCGTCTCTT	42200	GTCGTCCAACAAAGCAGCCTC
13555	VVRASSV	27878	GTGGTTCGGGCTTCGTCTGTG	42201	GTCGTCAGAGCAAGCAGCGTC
13556	VVRGSSV	27879	GTGGTGCGTGGGTCGTCGGTT	42202	GTCGTCAGAGGAAGCAGCGTC
13557	VVRNAGG	27880	GTGGTGCGGAATGCGGGGGGG	42203	GTCGTCAGAAACGCAGGAGGA
13558	VVRNAIN	27881	GTTGTTCGTAATGCTATTAAT	42204	GTCGTCAGAAACGCAATCAAC
13559	VVRPSGL	27882	GTTGTTCGGCCTTCTGGTCTT	42205	GTCGTCAGACCAAGCGGACTC
13560	VVSAPLV	27883	GTGGTTTCTGCTCCGCTTGTT	42206	GTCGTCAGCGCACCACTCGTC
13561	VVSFDRA	27884	GTGGTTTCGTTTGATAGGGCT	42207	GTCGTCAGCTTCGACAGAGCA
13562	VVSGSRP	27885	GTGGTGTCTGGGTCTCGGCCG	42208	GTCGTCAGCGGAAGCAGACCA
13563	VVSHISV	27886	GTTGTTTCGCATATTTCGGTG	42209	GTCGTCAGCCACATCAGCGTC
13564	VVSIARV	27887	GTGGTTAGTATTGCGAGGGTT	42210	GTCGTCAGCATCGCAAGAGTC
13565	VVSQPSP	27888	GTGGTTTCGCAGCCGTCTCCG	42211	GTCGTCAGCCAACCAAGCCCA
13566	VVSRPIS	27889	GTTGTTAGTCGTCCGATTTCT	42212	GTCGTCAGCAGACCAATCAGC
13567	VVSRSYN	27890	GTGGTTTCTCGGTCGTATAAT	42213	GTCGTCAGCAGAAGCTACAAC
13568	VVSRVAS	27891	GTTGTTTCTCGTGTTGCGTCG	42214	GTCGTCAGCAGAGTCGCAAGC
13569	VVSSGSL	27892	GTTGTTTCTTCGGGTTCGTTG	42215	GTCGTCAGCAGCGGAAGCCTC
13570	VVSSSLM	27893	GTGGTGTCGTCGTCGTTGATG	42216	GTCGTCAGCAGCAGCCTCATG
13571	VVSTTLP	27894	GTGGTGAGTACGACTTTGCCT	42217	GTCGTCAGCACAACACTCCCA
13572	VVSVATS	27895	GTGGTTTCTGTTGCGACTTCG	42218	GTCGTCAGCGTCGCAACAAGC
13573	VVTDSGG	27896	GTTGTTACGGATTCGGGGGGT	42219	GTCGTCACAGACAGCGGAGGA
13574	VVTSASG	27897	GTTGTGACTAGTGCTTCGGGT	42220	GTCGTCACAAGCGCAAGCGGA
13575	VVTTRIT	27898	GTTGTTACGACTAGGATTACT	42221	GTCGTCACAACAAGAATCACA
13576	VVVAGSE	27899	GTGGTGGTGGCTGGTAGTGAG	42222	GTCGTCGTCGCAGGAAGCGAA
13577	VWADDNV	27900	GTTTGGGCTGATGATAATGTG	42223	GTCTGGGCAGACGACAACGTC
13578	VWARGSE	27901	GTGTGGGCTAGGGGTTCTGAG	42224	GTCTGGGCAAGAGGAAGCGAA
13579	VWPASGT	27902	GTGTGGCCTGCTTCGGGTACT	42225	GTCTGGCCAGCAAGCGGAACA

13580	VWQPSND	27903	GTGTGGCAGCCTTCGAATGAT	42226	GTCTGGCAACCAAGCAACGAC
13581	VWSGSSD	27904	GTTTGGTCTGGGTCTTCGGAT	42227	GTCTGGAGCGGAAGCAGCGAC
13582	VWTHETS	27905	GTTTGGACTCATGAGACGTCG	42228	GTCTGGACACACGAAACAAGC
13583	VYAPEKR	27906	GTGTATGCGCCTGAGAAGCGT	42229	GTCTACGCACCAGAAAAAAGA
13584	VYATLPE	27907	GTTTATGCGACGTTGCCTGAG	42230	GTCTACGCAACACTCCCAGAA
13585	VYEPSKY	27908	GTTTATGAGCCTAGTAAGTAT	42231	GTCTACGAACCAAGCAAATAC
13586	VYESNRF	27909	GTTTATGAGTCGAATCGTTTT	42232	GTCTACGAAAGCAACAGATTC
13587	VYGYSGS	27910	GTTTATGGGTATTCTGGTAGT	42233	GTCTACGGATACAGCGGAAGC
13588	VYHPNEF	27911	GTTTATCATCCGAATGAGTTT	42234	GTCTACCACCCAAACGAATTC
13589	VYIGRQE	27912	GTGTATATTGGTCGGCAGGAG	42235	GTCTACATCGGAAGACAAGAA
13590	VYKASNY	27913	GTTTATAAGGCTAGTAATTAT	42236	GTCTACAAAGCAAGCAACTAC
13591	VYLKSST	27914	GTTTATTTGAAGAGTAGTACT	42237	GTCTACCTCAAAAGCAGCACA
13592	VYNAGVD	27915	GTTTATAATGCTGGTGTTGAT	42238	GTCTACAACGCAGGAGTCGAC
13593	VYNTSTA	27916	GTTTATAATACTTCGACTGCT	42239	GTCTACAACACAAGCACAGCA
13594	VYPPSTT	27917	GTGTATCCGCCGAGTACGACT	42240	GTCTACCCACCAAGCACAACA
13595	VYPRDLT	27918	GTTTATCCGAGGGATTTGACT	42241	GTCTACCCAAGAGACCTCACA
13596	VYRDSTP	27919	GTTTATCGGGATAGTACTCCG	42242	GTCTACAGAGACAGCACACCA
13597	VYRSHET	27920	GTGTATCGTTCTCATGAGACG	42243	GTCTACAGAAGCCACGAAACA
13598	VYSLGGL	27921	GTGTATTCGCTTGGGGGGCTG	42244	GTCTACAGCCTCGGAGGACTC
13599	VYSNMTG	27922	GTGTATTCTAATATGACTGGG	42245	GTCTACAGCAACATGACAGGA
13600	VYSQGAR	27923	GTGTATTCGCAGGGGGCGCGG	42246	GTCTACAGCCAAGGAGCAAGA
13601	VYTAARA	27924	GTGTATACTGCGGCGAGGGCT	42247	GTCTACACAGCAGCAAGAGCA
13602	VYTQNSP	27925	GTTTATACTCAGAATTCGCCT	42248	GTCTACACACAAAACAGCCCA
13603	VYTSSMH	27926	GTTTATACTTCGTCGATGCAT	42249	GTCTACACAAGCAGCATGCAC
13604	VYYGKEP	27927	GTGTATTATGGTAAGGAGCCG	42250	GTCTACTACGGAAAAGAACCA
13605	WADKSHP	27928	TGGGCTGATAAGAGTCATCCT	42251	TGGGCAGACAAAAGCCACCCA
13606	WADNSVN	27929	TGGGCTGATAATAGTGTTAAT	42252	TGGGCAGACAACAGCGTCAAC
13607	WADTTTR	27930	TGGGCTGATACGACTACGCGT	42253	TGGGCAGACACAACAACAAGA
13608	WAGAMPM	27931	TGGGCTGGTGCTATGCCTATG	42254	TGGGCAGGAGCAATGCCAATG
13609	WAHKGLP	27932	TGGGCGCATAAGGGGTTGCCT	42255	TGGGCACACAAAGGACTCCCA
13610	WAKSQLA	27933	TGGGCGAAGTCGCAGCTTGCG	42256	TGGGCAAAAAGCCAACTCGCA
13611	WAPRSPG	27934	TGGGCGCCGCGGTCGCCGGGG	42257	TGGGCACCAAGAAGCCCAGGA
13612	WASAERQ	27935	TGGGCTTCTGCTGAGAGGCAG	42258	TGGGCAAGCGCAGAAAGACAA
13613	WASGHQA	27936	TGGGCTTCGGGGCATCAGGCT	42259	TGGGCAAGCGGACACCAAGCA
13614	WASPIRG	27937	TGGGCGAGTCCTATTAGGGGT	42260	TGGGCAAGCCCAATCAGAGGA
13615	WATELRG	27938	TGGGCGACTGAGTTGAGGGGG	42261	TGGGCAACAGAACTCAGAGGA
13616	WATGSSP	27939	TGGGCTACGGGTTCGTCGCCT	42262	TGGGCAACAGGAAGCAGCCCA
13617	WCQRPGA	27940	TGGTGTCAGAGGCCTGGTGCT	42263	TGGTGCCAAAGACCAGGAGCA
13618	WDAAVTL	27941	TGGGATGCTGCTGTTACGCTG	42264	TGGGACGCAGCAGTCACACTC
13619	WDAFSTD	27942	TGGGATGCGTTTTCGACGGAT	42265	TGGGACGCATTCAGCACAGAC
13620	WDALEPV	27943	TGGGATGCGCTTGAGCCTGTT	42266	TGGGACGCACTCGAACCAGTC
13621	WDAMTAP	27944	TGGGATGCTATGACGGCTCCT	42267	TGGGACGCAATGACAGCACCA
13622	WDATAPT	27945	TGGGATGCGACTGCGCCTACG	42268	TGGGACGCAACAGCACCAACA
13623	WDDGGTP	27946	TGGGATGATGGGGGTACTCCT	42269	TGGGACGACGGAGGAACACCA
13624	WDITKTF	27947	TGGGATATTACTAAGACTTTT	42270	TGGGACATCACAAAAACATTC

13625	WDKKPTI	27948	TGGGATAAGAAGCCTACGATT	42271	TGGGACAAAAAACCAACAATC
13626	WDPAYGS	27949	TGGGATCCTGCGTATGGTAGT	42272	TGGGACCCAGCATACGGAAGC
13627	WDPRNSQ	27950	TGGGATCCGCGGAATTCGCAG	42273	TGGGACCCAAGAAACAGCCAA
13628	WDPSRTT	27951	TGGGATCCGTCTCGTACTACT	42274	TGGGACCCAAGCAGAACAACA
13629	WDQLERA	27952	TGGGATCAGCTTGAGCGGGCT	42275	TGGGACCAACTCGAAAGAGCA
13630	WDQPHQA	27953	TGGGATCAGCCTCATCAGGCT	42276	TGGGACCAACCACACCAAGCA
13631	WDRDAAL	27954	TGGGATAGGGATGCGGCGCTG	42277	TGGGACAGAGACGCAGCACTC
13632	WDSGSLG	27955	TGGGATAGTGGGTCGCTGGGT	42278	TGGGACAGCGGAAGCCTCGGA
13633	WDSRHHV	27956	TGGGATTCTCGGCATCATGTG	42279	TGGGACAGCAGACACCACGTC
13634	WDTPGQS	27957	TGGGATACTCCTGGTCAGTCG	42280	TGGGACACACCAGGACAAAGC
13635	WDTQFSS	27958	TGGGATACTCAGTTTAGTTCT	42281	TGGGACACACAATTCAGCAGC
13636	WEAHWTP	27959	TGGGAGGCTCATTGGACGCCT	42282	TGGGAAGCACACTGGACACCA
13637	WEGANPV	27960	TGGGAGGGTGCGAATCCGGTG	42283	TGGGAAGGAGCAAACCCAGTC
13638	WEGSHPY	27961	TGGGAGGGGAGTCATCCTTAT	42284	TGGGAAGGAAGCCACCCATAC
13639	WEGSKDF	27962	TGGGAGGGGTCTAAGGATTTT	42285	TGGGAAGGAAGCAAAGACTTC
13640	WEMTRVD	27963	TGGGAGATGACTAGGGTTGAT	42286	TGGGAAATGACAAGAGTCGAC
13641	WERSRSA	27964	TGGGAGCGTTCTAGGTCTGCT	42287	TGGGAAAGAAGCAGAAGCGCA
13642	WESGGGF	27965	TGGGAGAGTGGTGGGGGTTTT	42288	TGGGAAAGCGGAGGAGGATTC
13643	WFEDRLD	27966	TGGTTTGAGGATCGGTTGGAT	42289	TGGTTCGAAGACAGACTCGAC
13644	WFEKCKD	27967	TGGTTTGAGAAGTGTAAGGAT	42290	TGGTTCGAAAAATGCAAAGAC
13645	WFPSGHA	27968	TGGTTTCCTTCGGGTCATGCG	42291	TGGTTCCCAAGCGGACACGCA
13646	WGAALTP	27969	TGGGGGGCTGCTCTGACTCCT	42292	TGGGGAGCAGCACTCACACCA
13647	WGARLDS	27970	TGGGGGGCGAGGTTGGATTCG	42293	TGGGGAGCAAGACTCGACAGC
13648	WGASQTS	27971	TGGGGTGCTAGTCAGACGAGT	42294	TGGGGAGCAAGCCAAACAAGC
13649	WGGTSPG	27972	TGGGGGGGTACGAGTCCGGGT	42295	TGGGGAGGAACAAGCCCAGGA
13650	WGHNNSP	27973	TGGGGGCATAATAATTCGCCG	42296	TGGGGACACAACAACAGCCCA
13651	WGHSSGV	27974	TGGGGTCATTCGTCTGGGGTG	42297	TGGGGACACAGCAGCGGAGTC
13652	WGLLHSA	27975	TGGGGTCTGTTGCATTCTGCT	42298	TGGGGACTCCTCCACAGCGCA
13653	WGLVTSP	27976	TGGGGGCTGGTTACTAGTCCT	42299	TGGGGACTCGTCACAAGCCCA
13654	WGNQQPR	27977	TGGGGGAATCAGCAGCCTAGG	42300	TGGGGAAACCAACAACCAAGA
13655	WGNSHNT	27978	TGGGGGAATTCTCATAATACT	42301	TGGGGAAACAGCCACAACACA
13656	WGPTTSH	27979	TGGGGTCCTACTACGTCTCAT	42302	TGGGGACCAACAACAAGCCAC
13657	WGSGAAG	27980	TGGGGGTCTGGGGCGGCGGGT	42303	TGGGGAAGCGGAGCAGCAGGA
13658	WGSGAET	27981	TGGGGGTCTGGGGCTGAGACT	42304	TGGGGAAGCGGAGCAGAAACA
13659	WGSSGQG	27982	TGGGGGTCTTCGGGGCAGGGT	42305	TGGGGAAGCAGCGGACAAGGA
13660	WGTQLAM	27983	TGGGGTACTCAGCTGGCGATG	42306	TGGGGAACACAACTCGCAATG
13661	WGTSDKS	27984	TGGGGTACGTCGGATAAGTCT	42307	TGGGGAACAAGCGACAAAAGC
13662	WGYLHVA	27985	TGGGGGTATTTGCATGTTGCG	42308	TGGGGATACCTCCACGTCGCA
13663	WHGTGLI	27986	TGGCATGGGACTGGTCTGATT	42309	TGGCACGGAACAGGACTCATC
13664	WHKSSSS	27987	TGGCATAAGTCGAGTAGTAGT	42310	TGGCACAAAAGCAGCAGCAGC
13665	WHPSGSR	27988	TGGCATCCTTCTGGTTCGCGT	42311	TGGCACCCAAGCGGAAGCAGA
13666	WHRTAQD	27989	TGGCATAGGACTGCGCAGGAT	42312	TGGCACAGAACAGCACAAGAC
13667	WHSAKLA	27990	TGGCATAGTGCTAAGCTTGCG	42313	TGGCACAGCGCAAAACTCGCA
13668	WHSLMEP	27991	TGGCATAGTTTGATGGAGCCG	42314	TGGCACAGCCTCATGGAACCA
13669	WHSRMYE	27992	TGGCATTCTCGGATGTATGAG	42315	TGGCACAGCAGAATGTACGAA

13670	WHSSATQ	27993	TGGCATAGTTCTGCTACTCAG	42316	TGGCACAGCAGCGCAACACAA
13671	WHSSDLV	27994	TGGCATTCGTCGGATCTTGTG	42317	TGGCACAGCAGCGACCTCGTC
13672	WIGNGGP	27995	TGGATTGGTAATGGGGGGCCG	42318	TGGATCGGAAACGGAGGACCA
13673	WIGQNTV	27996	TGGATTGGGCAGAATACTGTG	42319	TGGATCGGACAAAACACAGTC
13674	WIKEASS	27997	TGGATTAAGGAGGCTTCGTCT	42320	TGGATCAAAGAAGCAAGCAGC
13675	WIPGAPS	27998	TGGATTCCTGGGGCTCCGAGT	42321	TGGATCCCAGGAGCACCAAGC
13676	WIPQQDV	27999	TGGATTCCGCAGCAGGATGTT	42322	TGGATCCCACAACAAGACGTC
13677	WIPSGLS	28000	TGGATTCCGTCGGGTTTGAGT	42323	TGGATCCCAAGCGGACTCAGC
13678	WITTEPL	28001	TGGATTACTACGGAGCCGTTG	42324	TGGATCACAACAGAACCACTC
13679	WKANLPS	28002	TGGAAGGCTAATTTGCCTTCT	42325	TGGAAAGCAAACCTCCCAAGC
13680	WKDECQT	28003	TGGAAGGATGAGTGTCAGACG	42326	TGGAAAGACGAATGCCAAACA
13681	WKDSHYE	28004	TGGAAGGATTCGCATTATGAG	42327	TGGAAAGACAGCCACTACGAA
13682	WKEHGAA	28005	TGGAAGGAGCATGGTGCTGCG	42328	TGGAAAGAACACGGAGCAGCA
13683	WKHSTQS	28006	TGGAAGCATAGTACTCAGTCT	42329	TGGAAACACAGCACACAAAGC
13684	WKIMIAE	28007	TGGAAGATTATGATTGCGGAG	42330	TGGAAAATCATGATCGCAGAA
13685	WKKNMDF	28008	TGGAAGAAGAATATGGATTTT	42331	TGGAAAAAAAACATGGACTTC
13686	WKLNRDQ	28009	TGGAAGTTGAATAGGGATCAG	42332	TGGAAACTCAACAGAGACCAA
13687	WKNTSCG	28010	TGGAAGAATACTTCTTGTGGT	42333	TGGAAAAACACAAGCTGCGGA
13688	WKPAVPQ	28011	TGGAAGCCGGCTGTGCCTCAG	42334	TGGAAACCAGCAGTCCCACAA
13689	WKPEILP	28012	TGGAAGCCGGAGATTCTTCCG	42335	TGGAAACCAGAAATCCTCCCA
13690	WKPPLNP	28013	TGGAAGCCTCCTCTTAATCCT	42336	TGGAAACCACCACTCAACCCA
13691	WKQGSTG	28014	TGGAAGCAGGGGTCGACTGGT	42337	TGGAAACAAGGAAGCACAGGA
13692	WKSDSAS	28015	TGGAAGAGTGATTCTGCGTCG	42338	TGGAAAAGCGACAGCGCAAGC
13693	WKSNTLT	28016	TGGAAGTCTAATACGTTGACG	42339	TGGAAAAGCAACACACTCACA
13694	WKSQIPL	28017	TGGAAGTCTCAGATTCCGTTG	42340	TGGAAAAGCCAAATCCCACTC
13695	WKSQLPN	28018	TGGAAGAGTCAGTTGCCGAAT	42341	TGGAAAAGCCAACTCCCAAAC
13696	WKSQMNP	28019	TGGAAGTCTCAGATGAATCCT	42342	TGGAAAAGCCAAATGAACCCA
13697	WKSTDLT	28020	TGGAAGTCGACTGATCTGACT	42343	TGGAAAAGCACAGACCTCACA
13698	WKVSTDT	28021	TGGAAGGTTTCGACTGATACG	42344	TGGAAAGTCAGCACAGACACA
13699	WLADPSD	28022	TGGCTGGCTGATCCGTCTGAT	42345	TGGCTCGCAGACCCAAGCGAC
13700	WLENSQS	28023	TGGCTTGAGAATTCTCAGAGT	42346	TGGCTCGAAAACAGCCAAAGC
13701	WLESGTG	28024	TGGCTTGAGTCGGGGACTGGT	42347	TGGCTCGAAAGCGGAACAGGA
13702	WLGRADA	28025	TGGCTGGGTAGGGCGGATGCT	42348	TGGCTCGGAAGAGCAGACGCA
13703	WLHDTTS	28026	TGGCTTCATGATACTACTTCT	42349	TGGCTCCACGACACAACAAGC
13704	WLHEQPN	28027	TGGCTGCATGAGCAGCCTAAT	42350	TGGCTCCACGAACAACCAAAC
13705	WLHRSNA	28028	TGGCTTCATAGGTCGAATGCG	42351	TGGCTCCACAGAAGCAACGCA
13706	WLKQTDN	28029	TGGTTGAAGCAGACTGATAAT	42352	TGGCTCAAACAAACAGACAAC
13707	WLLNQEE	28030	TGGCTGCTTAATCAGGAGGAG	42353	TGGCTCCTCAACCAAGAAGAA
13708	WLNDSSR	28031	TGGCTGAATGATAGTAGTCGT	42354	TGGCTCAACGACAGCAGCAGA
13709	WLPKLPH	28032	TGGCTTCCGAAGTTGCCGCAT	42355	TGGCTCCCAAAACTCCCACAC
13710	WLPTQTE	28033	TGGCTTCCTACGCAGACTGAG	42356	TGGCTCCCAACACAAACAGAA
13711	WLRTPDA	28034	TGGCTTAGGACTCCTGATGCT	42357	TGGCTCAGAACACCAGACGCA
13712	WLTSLKM	28035	TGGCTGACGTCTTTGAAGATG	42358	TGGCTCACAAGCCTCAAAATG
13713	WLTSPNV	28036	TGGCTGACTTCGCCTAATGTG	42359	TGGCTCACAAGCCCAAACGTC
13714	WMAMRQD	28037	TGGATGGCTATGAGGCAGGAT	42360	TGGATGGCAATGAGACAAGAC

13715	WMLQETS	28038	TGGATGCTTCAGGAGACGTCG	42361	TGGATGCTCCAAGAAACAAGC
13716	WMMESRP	28039	TGGATGATGGAGTCGCGTCCT	42362	TGGATGATGGAAAGCAGACCA
13717	WMQSANR	28040	TGGATGCAGTCGGCTAATCGG	42363	TGGATGCAAAGCGCAAACAGA
13718	WMSRLPA	28041	TGGATGTCGCGGTTGCCGGCG	42364	TGGATGAGCAGACTCCCAGCA
13719	WNDVTAR	28042	TGGAATGATGTTACGGCTCGG	42365	TGGAACGACGTCACAGCAAGA
13720	WNKSLLS	28043	TGGAATAAGTCTTTGCTGAGT	42366	TGGAACAAAAGCCTCCTCAGC
13721	WNKTELD	28044	TGGAATAAGACGGAGCTGGAT	42367	TGGAACAAAACAGAACTCGAC
13722	WNLESTT	28045	TGGAATTTGGAGTCTACTACG	42368	TGGAACCTCGAAAGCACAACA
13723	WNNPDQL	28046	TGGAATAATCCGGATCAGCTT	42369	TGGAACAACCCAGACCAACTC
13724	WNPPLPA	28047	TGGAATCCTCCTCTGCCGGCT	42370	TGGAACCCACCACTCCCAGCA
13725	WNPRSSE	28048	TGGAATCCTCGTTCGAGTGAG	42371	TGGAACCCAAGAAGCAGCGAA
13726	WNTQQGV	28049	TGGAATACTCAGCAGGGTGTT	42372	TGGAACACACAACAAGGAGTC
13727	WNTTLPI	28050	TGGAATACGACGCTGCCTATT	42373	TGGAACACAACACTCCCAATC
13728	WNTVTIR	28051	TGGAATACGGTGACGATTCGG	42374	TGGAACACAGTCACAATCAGA
13729	WPAKTVE	28052	TGGCCGGCTAAGACTGTTGAG	42375	TGGCCAGCAAAAACAGTCGAA
13730	WPAQVSS	28053	TGGCCTGCGCAGGTTTCGAGT	42376	TGGCCAGCACAAGTCAGCAGC
13731	WPASVTD	28054	TGGCCGGCTTCGGTTACTGAT	42377	TGGCCAGCAAGCGTCACAGAC
13732	WPEKRLT	28055	TGGCCTGAGAAGAGGCTGACG	42378	TGGCCAGAAAAAAGACTCACA
13733	WPESYST	28056	TGGCCTGAGTCTTATAGTACT	42379	TGGCCAGAAAGCTACAGCACA
13734	WPGMSAG	28057	TGGCCTGGTATGAGTGCGGGT	42380	TGGCCAGGAATGAGCGCAGGA
13735	WPGSSHV	28058	TGGCCTGGTTCGAGTCATGTG	42381	TGGCCAGGAAGCAGCCACGTC
13736	WPNLVSG	28059	TGGCCGAATCTTGTGAGTGGT	42382	TGGCCAAACCTCGTCAGCGGA
13737	WPPASTL	28060	TGGCCGCCTGCTAGTACGCTG	42383	TGGCCACCAGCAAGCACACTC
13738	WPPAVSS	28061	TGGCCTCCTGCTGTTTCTAGT	42384	TGGCCACCAGCAGTCAGCAGC
13739	WPPSVNG	28062	TGGCCTCCTAGTGTGAATGGT	42385	TGGCCACCAAGCGTCAACGGA
13740	WPQSSSG	28063	TGGCCTCAGTCTAGTAGTGGG	42386	TGGCCACAAAGCAGCAGCGGA
13741	WPSMDGS	28064	TGGCCTAGTATGGATGGGAGT	42387	TGGCCAAGCATGGACGGAAGC
13742	WPSSIQI	28065	TGGCCGTCGTCGATTCAGATT	42388	TGGCCAAGCAGCATCCAAATC
13743	WPSSTLS	28066	TGGCCGTCGTCTACTTTGTCT	42389	TGGCCAAGCAGCACACTCAGC
13744	WPTIINR	28067	TGGCCGACGATTATTAATCGT	42390	TGGCCAACAATCATCAACAGA
13745	WPTKSTP	28068	TGGCCTACTAAGTCTACTCCT	42391	TGGCCAACAAAAAGCACACCA
13746	WPTNSRP	28069	TGGCCTACGAATTCGAGGCCG	42392	TGGCCAACAAACAGCAGACCA
13747	WPTNTIP	28070	TGGCCTACTAATACGATTCCT	42393	TGGCCAACAAACACAATCCCA
13748	WPVHHAA	28071	TGGCCTGTTCATCATGCTGCT	42394	TGGCCAGTCCACCACGCAGCA
13749	WPVTSYG	28072	TGGCCTGTTACTTCGTATGGT	42395	TGGCCAGTCACAAGCTACGGA
13750	WPYDPGR	28073	TGGCCTTATGATCCTGGGCGG	42396	TGGCCATACGACCCAGGAAGA
13751	WQGLTQG	28074	TGGCAGGGTCTTACGCAGGGT	42397	TGGCAAGGACTCACACAAGGA
13752	WQLATQP	28075	TGGCAGCTGGCTACTCAGCCT	42398	TGGCAACTCGCAACACAACCA
13753	WQMLLSE	28076	TGGCAGATGTTGCTTAGTGAG	42399	TGGCAAATGCTCCTCAGCGAA
13754	WQQLSAS	28077	TGGCAGCAGCTGTCGGCTAGT	42400	TGGCAACAACTCAGCGCAAGC
13755	WQRSGDV	28078	TGGCAGCGGTCGGGTGATGTG	42401	TGGCAAAGAAGCGGAGACGTC
13756	WQSQATM	28079	TGGCAGAGTCAGGCTACTATG	42402	TGGCAAAGCCAAGCAACAATG
13757	WQTQSRS	28080	TGGCAGACTCAGAGTAGGTCT	42403	TGGCAAACACAAAGCAGAAGC
13758	WQYSHEP	28081	TGGCAGTATTCGCATGAGCCT	42404	TGGCAATACAGCCACGAACCA
13759	WRAMLEE	28082	TGGCGGGCTATGTTGGAGGAG	42405	TGGAGAGCAATGCTCGAAGAA

13760	WRAPGSA	28083	TGGCGTGCGCCTGGGTCTGCT	42406	TGGAGAGCACCAGGAAGCGCA
13761	WRDATCC	28084	TGGCGGGATGCTACTTGTTGT	42407	TGGAGAGACGCAACATGCTGC
13762	WRERYAA	28085	TGGCGTGAGCGTTATGCGGCG	42408	TGGAGAGAAAGATACGCAGCA
13763	WRGLDIE	28086	TGGCGTGGTCTGGATATTGAG	42409	TGGAGAGGACTCGACATCGAA
13764	WRHDYNL	28087	TGGCGGCATGATTATAATTTG	42410	TGGAGACACGACTACAACCTC
13765	WRHTEAI	28088	TGGCGGCATACTGAGGCGATT	42411	TGGAGACACACAGAAGCAATC
13766	WRITAES	28089	TGGCGGATTACTGCGGAGTCT	42412	TGGAGAATCACAGCAGAAAGC
13767	WRPLVET	28090	TGGCGGCCTTTGGTGGAGACT	42413	TGGAGACCACTCGTCGAAACA
13768	WRPNMAA	28091	TGGCGTCCGAATATGGCGGCT	42414	TGGAGACCAAACATGGCAGCA
13769	WRPNMSV	28092	TGGCGTCCTAATATGTCTGTT	42415	TGGAGACCAAACATGAGCGTC
13770	WRPQRPV	28093	TGGCGGCCGCAGCGGCCTGTG	42416	TGGAGACCACAAAGACCAGTC
13771	WRQETSV	28094	TGGCGGCAGGAGACGTCTGTG	42417	TGGAGACAAGAAACAAGCGTC
13772	WRRDASP	28095	TGGAGGCGTGATGCTTCGCCT	42418	TGGAGAAGAGACGCAAGCCCA
13773	WRSASSA	28096	TGGCGGTCGGCGTCTTCGGCG	42419	TGGAGAAGCGCAAGCAGCGCA
13774	WRSREIA	28097	TGGCGTTCTCGGGAGATTGCT	42420	TGGAGAAGCAGAGAAATCGCA
13775	WRSSAEA	28098	TGGCGGTCGTCGGCTGAGGCT	42421	TGGAGAAGCAGCGCAGAAGCA
13776	WSADPDT	28099	TGGTCGGCGGATCCGGATACG	42422	TGGAGCGCAGACCCAGACACA
13777	WSASSHQ	28100	TGGTCGGCGTCTTCTCATCAG	42423	TGGAGCGCAAGCAGCCACCAA
13778	WSAVGEV	28101	TGGTCGGCTGTTGGGGAGGTG	42424	TGGAGCGCAGTCGGAGAAGTC
13779	WSDSTAV	28102	TGGAGTGATTCTACTGCTGTT	42425	TGGAGCGACAGCACAGCAGTC
13780	WSGHPVA	28103	TGGTCTGGTCATCCTGTGGCT	42426	TGGAGCGGACACCCAGTCGCA
13781	WSGKANA	28104	TGGTCGGGTAAGGCTAATGCG	42427	TGGAGCGGAAAAGCAAACGCA
13782	WSGPISL	28105	TGGTCTGGTCCGATTAGTCTT	42428	TGGAGCGGACCAATCAGCCTC
13783	WSHGPMP	28106	TGGTCTCATGGGCCTATGCCG	42429	TGGAGCCACGGACCAATGCCA
13784	WSHGSTT	28107	TGGTCTCATGGGTCGACTACG	42430	TGGAGCCACGGAAGCACAACA
13785	WSKVPDR	28108	TGGTCGAAGGTTCCTGATAGG	42431	TGGAGCAAAGTCCCAGACAGA
13786	WSLVHRE	28109	TGGTCTCTTGTTCATCGTGAG	42432	TGGAGCCTCGTCCACAGAGAA
13787	WSNHAHA	28110	TGGAGTAATCATGCGCATGCT	42433	TGGAGCAACCACGCACACGCA
13788	WSPARET	28111	TGGAGTCCTGCGAGGGAGACG	42434	TGGAGCCCAGCAAGAGAAACA
13789	WSPLYHA	28112	TGGTCTCCTTTGTATCATGCG	42435	TGGAGCCCACTCTACCACGCA
13790	WSPNSTP	28113	TGGAGTCCGAATTCGACTCCG	42436	TGGAGCCCAAACAGCACACCA
13791	WSPNVCP	28114	TGGTCGCCTAATGTGTGTCCT	42437	TGGAGCCCAAACGTCTGCCCA
13792	WSPRNTL	28115	TGGTCGCCTCGGAATACTCTT	42438	TGGAGCCCAAGAAACACACTC
13793	WSPSEGK	28116	TGGTCTCCGAGTGAGGGTAAG	42439	TGGAGCCCAAGCGAAGGAAAA
13794	WSPSQAY	28117	TGGTCTCCGAGTCAGGCTTAT	42440	TGGAGCCCAAGCCAAGCATAC
13795	WSPVVVR	28118	TGGTCGCCTGTTGTTGTGCGG	42441	TGGAGCCCAGTCGTCGTCAGA
13796	WSRAAVD	28119	TGGTCTCGTGCGGCGGTTGAT	42442	TGGAGCAGAGCAGCAGTCGAC
13797	WSRPAAD	28120	TGGAGTAGGCCGGCTGCTGAT	42443	TGGAGCAGACCAGCAGCAGAC
13798	WSRQDLP	28121	TGGAGTCGGCAGGATTTGCCG	42444	TGGAGCAGACAAGACCTCCCA
13799	WSSAYVS	28122	TGGTCTTCTGCTTATGTTTCT	42445	TGGAGCAGCGCATACGTCAGC
13800	WSSDAPE	28123	TGGTCTTCTGATGCTCCTGAG	42446	TGGAGCAGCGACGCACCAGAA
13801	WSSMSMH	28124	TGGTCTTCTATGAGTATGCAT	42447	TGGAGCAGCATGAGCATGCAC
13802	WSTKLEG	28125	TGGAGTACGAAGCTGGAGGGG	42448	TGGAGCACAAAACTCGAAGGA
13803	WSTNAYQ	28126	TGGTCTACTAATGCTTATCAG	42449	TGGAGCACAAACGCATACCAA
13804	WSTSTLH	28127	TGGTCTACTTCTACTTTGCAT	42450	TGGAGCACAAGCACACTCCAC

13805	WTAPSDV	28128	TGGACTGCTCCTTCTGATGTG	42451	TGGACAGCACCAAGCGACGTC
13806	WTAQNVQ	28129	TGGACTGCTCAGAATGTTCAG	42452	TGGACAGCACAAAACGTCCAA
13807	WTASRAS	28130	TGGACTGCTAGTAGGGCGTCT	42453	TGGACAGCAAGCAGAGCAAGC
13808	WTERVGT	28131	TGGACTGAGCGTGTGGGTACT	42454	TGGACAGAAAGAGTCGGAACA
13809	WTGSAHQ	28132	TGGACTGGTTCTGCTCATCAG	42455	TGGACAGGAAGCGCACACCAA
13810	WTGYSQQ	28133	TGGACGGGGTATAGTCAGCAG	42456	TGGACAGGATACAGCCAACAA
13811	WTNSTQP	28134	TGGACGAATTCGACTCAGCCT	42457	TGGACAAACAGCACACAACCA
13812	WTPHSPM	28135	TGGACGCCTCATAGTCCTATG	42458	TGGACACCACACAGCCCAATG
13813	WTPRVMH	28136	TGGACTCCGCGTGTTATGCAT	42459	TGGACACCAAGAGTCATGCAC
13814	WTPSMAP	28137	TGGACGCCTAGTATGGCTCCG	42460	TGGACACCAAGCATGGCACCA
13815	WTPSNKH	28138	TGGACTCCTTCTAATAAGCAT	42461	TGGACACCAAGCAACAAACAC
13816	WTRLESL	28139	TGGACTCGTTTGGAGTCTCTG	42462	TGGACAAGACTCGAAAGCCTC
13817	WTSDGNY	28140	TGGACGAGTGATGGTAATTAT	42463	TGGACAAGCGACGGAAACTAC
13818	WTSKIGP	28141	TGGACGTCGAAGATTGGGCCG	42464	TGGACAAGCAAAATCGGACCA
13819	WTSRDAS	28142	TGGACTTCGAGGGATGCTTCT	42465	TGGACAAGCAGAGACGCAAGC
13820	WTSSGGS	28143	TGGACTTCTAGTGGGGGGAGT	42466	TGGACAAGCAGCGGAGGAAGC
13821	WTTNTGG	28144	TGGACGACTAATACGGGTGGG	42467	TGGACAACAAACACAGGAGGA
13822	WTTSGSI	28145	TGGACTACGTCGGGTTCGATT	42468	TGGACAACAAGCGGAAGCATC
13823	WTVDLTH	28146	TGGACTGTTGATCTTACTCAT	42469	TGGACAGTCGACCTCACACAC
13824	WTVETSH	28147	TGGACTGTGGAGACTTCTCAT	42470	TGGACAGTCGAAACAAGCCAC
13825	WVHSSDS	28148	TGGGTGCATTCTTCGGATAGT	42471	TGGGTCCACAGCAGCGACAGC
13826	WVIQNCN	28149	TGGGTGATTCAGAATTGTAAT	42472	TGGGTCATCCAAAACTGCAAC
13827	WVQSGTP	28150	TGGGTTCAGTCTGGTACTCCT	42473	TGGGTCCAAAGCGGAACACCA
13828	WVTGLTD	28151	TGGGTGACGGGGCTGACGGAT	42474	TGGGTCACAGGACTCACAGAC
13829	WVTQHPS	28152	TGGGTGACTCAGCATCCTTCT	42475	TGGGTCACACAACACCCAAGC
13830	YAAAPSR	28153	TATGCTGCTGCGCCTTCTAGG	42476	TACGCAGCAGCACCAAGCAGA
13831	YAAAYAS	28154	TATGCTGCTGCGTATGCTTCT	42477	TACGCAGCAGCATACGCAAGC
13832	YAAHYKE	28155	TATGCTGCTCATTATAAGGAG	42478	TACGCAGCACACTACAAAGAA
13833	YAANRQP	28156	TATGCTGCTAATAGGCAGCCG	42479	TACGCAGCAAACAGACAACCA
13834	YAAPSSA	28157	TATGCTGCGCCTTCGTCTGCG	42480	TACGCAGCACCAAGCAGCGCA
13835	YAASHVS	28158	TATGCTGCGTCTCATGTTTCT	42481	TACGCAGCAAGCCACGTCAGC
13836	YAASNLT	28159	TATGCGGCTTCGAATCTGACG	42482	TACGCAGCAAGCAACCTCACA
13837	YAASSAT	28160	TATGCGGCTTCGTCGGCTACG	42483	TACGCAGCAAGCAGCGCAACA
13838	YAAVGLN	28161	TATGCTGCGGTGGGTCTTAAT	42484	TACGCAGCAGTCGGACTCAAC
13839	YAAVRSN	28162	TATGCGGCTGTTCGGTCGAAT	42485	TACGCAGCAGTCAGAAGCAAC
13840	YADLPSR	28163	TATGCGGATCTTCCGAGTCGT	42486	TACGCAGACCTCCCAAGCAGA
13841	YADSAPY	28164	TATGCGGATAGTGCTCCGTAT	42487	TACGCAGACAGCGCACCATAC
13842	YAERQGR	28165	TATGCGGAGCGGCAGGGGCGT	42488	TACGCAGAAAGACAAGGAAGA
13843	YAEYSRN	28166	TATGCTGAGTATTCGAGGAAT	42489	TACGCAGAATACAGCAGAAAC
13844	YAGAALG	28167	TATGCGGGTGCTGCGTTGGGT	42490	TACGCAGGAGCAGCACTCGGA
13845	YAGAQRS	28168	TATGCGGGGGCGCAGCGTAGT	42491	TACGCAGGAGCACAAAGAAGC
13846	YAGGKLI	28169	TATGCTGGTGGTAAGCTGATT	42492	TACGCAGGAGGAAAACTCATC
13847	YAGKEPE	28170	TATGCTGGTAAGGAGCCTGAG	42493	TACGCAGGAAAAGAACCAGAA
13848	YAGPNSP	28171	TATGCTGGGCCGAATTCTCCT	42494	TACGCAGGACCAAACAGCCCA
13849	YAGSEVM	28172	TATGCTGGGAGTGAGGTTATG	42495	TACGCAGGAAGCGAAGTCATG

13850	YAGSVTS	28173	TATGCTGGTAGTGTGACTTCT	42496	TACGCAGGAAGCGTCACAAGC
13851	YAHQKPM	28174	TATGCTCATCAGAAGCCTATG	42497	TACGCACACCAAAAACCAATG
13852	YAHTRVV	28175	TATGCTCATACGCGTGTTGTG	42498	TACGCACACACAAGAGTCGTC
13853	YAKPLTS	28176	TATGCTAAGCCTCTTACTTCG	42499	TACGCAAAACCACTCACAAGC
13854	YALDSAE	28177	TATGCGCTTGATTCGGCGGAG	42500	TACGCACTCGACAGCGCAGAA
13855	YALEHRN	28178	TATGCGCTTGAGCATCGTAAT	42501	TACGCACTCGAACACAGAAAC
13856	YALHQDK	28179	TATGCGTTGCATCAGGATAAG	42502	TACGCACTCCACCAAGACAAA
13857	YALQSKE	28180	TATGCGCTTCAGTCTAAGGAG	42503	TACGCACTCCAAAGCAAAGAA
13858	YALSGST	28181	TATGCTCTGTCTGGTAGTACT	42504	TACGCACTCAGCGGAAGCACA
13859	YANAMTL	28182	TATGCTAATGCTATGACTCTT	42505	TACGCAAACGCAATGACACTC
13860	YANDSGL	28183	TATGCTAATGATTCTGGGTTG	42506	TACGCAAACGACAGCGGACTC
13861	YANNLPH	28184	TATGCGAATAATTTGCCGCAT	42507	TACGCAAACAACCTCCCACAC
13862	YANTTSA	28185	TATGCGAATACTACGTCGGCG	42508	TACGCAAACACAACAAGCGCA
13863	YAPGLRS	28186	TATGCGCCGGGTCTTCGGAGT	42509	TACGCACCAGGACTCAGAAGC
13864	YAPQSVA	28187	TATGCGCCTCAGAGTGTTGCG	42510	TACGCACCACAAAGCGTCGCA
13865	YAQAFRN	28188	TATGCTCAGGCGTTTCGGAAT	42511	TACGCACAAGCATTCAGAAAC
13866	YAQYSAV	28189	TATGCGCAGTATTCTGCTGTG	42512	TACGCACAATACAGCGCAGTC
13867	YAREAHA	28190	TATGCTCGGGAGGCTCATGCG	42513	TACGCAAGAGAAGCACACGCA
13868	YARETLH	28191	TATGCTCGGGAGACTTTGCAT	42514	TACGCAAGAGAAACACTCCAC
13869	YARLTGP	28192	TATGCGAGGTTGACTGGGCCT	42515	TACGCAAGACTCACAGGACCA
13870	YARQITA	28193	TATGCGCGGCAGATTACTGCT	42516	TACGCAAGACAAATCACAGCA
13871	YARQPAV	28194	TATGCTCGGCAGCCTGCTGTG	42517	TACGCAAGACAACCAGCAGTC
13872	YASASHP	28195	TATGCGTCGGCTTCTCATCCT	42518	TACGCAAGCGCAAGCCACCCA
13873	YASLKGA	28196	TATGCTAGTCTTAAGGGTGCT	42519	TACGCAAGCCTCAAAGGAGCA
13874	YASPGRT	28197	TATGCGTCGCCTGGGCGGACT	42520	TACGCAAGCCCAGGAAGAACA
13875	YASSAAL	28198	TATGCTTCTTCTGCGGCGCTT	42521	TACGCAAGCAGCGCAGCACTC
13876	YASSSTR	28199	TATGCGTCGTCGAGTACTCGG	42522	TACGCAAGCAGCAGCACAAGA
13877	YATESGN	28200	TATGCTACTGAGTCTGGGAAT	42523	TACGCAACAGAAAGCGGAAAC
13878	YATFAPA	28201	TATGCTACTTTTGCGCCGGCT	42524	TACGCAACATTCGCACCAGCA
13879	YATHEPD	28202	TATGCTACGCATGAGCCGGAT	42525	TACGCAACACACGAACCAGAC
13880	YATPSHH	28203	TATGCTACTCCGAGTCATCAT	42526	TACGCAACACCAAGCCACCAC
13881	YATTVLT	28204	TATGCGACGACTGTGTTGACT	42527	TACGCAACAACAGTCCTCACA
13882	YATVIGL	28205	TATGCTACTGTGATTGGTCTG	42528	TACGCAACAGTCATCGGACTC
13883	YAVEASR	28206	TATGCTGTTGAGGCTTCGCGG	42529	TACGCAGTCGAAGCAAGCAGA
13884	YAVEGKN	28207	TATGCGGTGGAGGGTAAGAAT	42530	TACGCAGTCGAAGGAAAAAAC
13885	YAVSRPL	28208	TATGCTGTTTCTAGGCCTCTT	42531	TACGCAGTCAGCAGACCACTC
13886	YAYEGFA	28209	TATGCGTATGAGGGTTTTGCT	42532	TACGCATACGAAGGATTCGCA
13887	YAYERQI	28210	TATGCTTATGAGCGTCAGATT	42533	TACGCATACGAAAGACAAATC
13888	YCESFPD	28211	TATTGTGAGAGTTTTCCTGAT	42534	TACTGCGAAAGCTTCCCAGAC
13889	YCSHQSV	28212	TATTGTTCTCATCAGAGTGTG	42535	TACTGCAGCCACCAAAGCGTC
13890	YCTGNDA	28213	TATTGTACTGGGAATGATGCT	42536	TACTGCACAGGAAACGACGCA
13891	YDAISNP	28214	TATGATGCGATTAGTAATCCG	42537	TACGACGCAATCAGCAACCCA
13892	YDHVIAT	28215	TATGATCATGTTATTGCTACG	42538	TACGACCACGTCATCGCAACA
13893	YDKAMSP	28216	TATGATAAGGCGATGAGTCCG	42539	TACGACAAAGCAATGAGCCCA
13894	YDLGVTT	28217	TATGATCTTGGGGTTACGACT	42540	TACGACCTCGGAGTCACAACA

13895	YDMGPVP	28218	TATGATATGGGGCCGGTTCCT	42541	TACGACATGGGACCAGTCCCA
13896	YDNKTRL	28219	TATGATAATAAGACGCGGCTG	42542	TACGACAACAAAACAAGACTC
13897	YDNMHCK	28220	TATGATAATATGCATTGTAAG	42543	TACGACAACATGCACTGCAAA
13898	YDNQLNN	28221	TATGATAATCAGTTGAATAAT	42544	TACGACAACCAACTCAACAAC
13899	YDPYHSP	28222	TATGATCCGTATCATTCTCCT	42545	TACGACCCATACCACAGCCCA
13900	YDREPLD	28223	TATGATAGGGAGCCGCTTGAT	42546	TACGACAGAGAACCACTCGAC
13901	YDSNTET	28224	TATGATTCTAATACGGAGACG	42547	TACGACAGCAACACAGAAACA
13902	YDSRGPA	28225	TATGATTCTCGTGGGCCGGCT	42548	TACGACAGCAGAGGACCAGCA
13903	YDSSVPN	28226	TATGATTCGAGTGTGCCTAAT	42549	TACGACAGCAGCGTCCCAAAC
13904	YDSVATL	28227	TATGATTCGGTTGCTACTTTG	42550	TACGACAGCGTCGCAACACTC
13905	YDTHGSP	28228	TATGATACGCATGGTTCTCCG	42551	TACGACACACACGGAAGCCCA
13906	YDTKLQM	28229	TATGATACTAAGCTGCAGATG	42552	TACGACACAAAACTCCAAATG
13907	YEAPTRS	28230	TATGAGGCGCCGACGCGGTCT	42553	TACGAAGCACCAACAAGAAGC
13908	YEATSSN	28231	TATGAGGCGACGTCGAGTAAT	42554	TACGAAGCAACAAGCAGCAAC
13909	YEGSPRN	28232	TATGAGGGTTCGCCTCGTAAT	42555	TACGAAGGAAGCCCAAGAAAC
13910	YEGYKLP	28233	TATGAGGGGTATAAGCTTCCT	42556	TACGAAGGATACAAACTCCCA
13911	YEIQGTG	28234	TATGAGATTCAGGGGACTGGT	42557	TACGAAATCCAAGGAACAGGA
13912	YELAHHA	28235	TATGAGCTTGCTCATCATGCT	42558	TACGAACTCGCACACCACGCA
13913	YELQLFS	28236	TATGAGTTGCAGCTGTTTTCG	42559	TACGAACTCCAACTCTTCAGC
13914	YELRRIP	28237	TATGAGTTGCGGAGGATTCCG	42560	TACGAACTCAGAAGAATCCCA
13915	YEPGTDA	28238	TATGAGCCGGGGACTGATGCG	42561	TACGAACCAGGAACAGACGCA
13916	YEPKVRV	28239	TATGAGCCTAAGGTGCGTGTG	42562	TACGAACCAAAAGTCAGAGTC
13917	YESSNDP	28240	TATGAGTCGTCGAATGATCCT	42563	TACGAAAGCAGCAACGACCCA
13918	YESYIER	28241	TATGAGTCTTATATTGAGCGG	42564	TACGAAAGCTACATCGAAAGA
13919	YETAFRA	28242	TATGAGACTGCTTTTCGGGCG	42565	TACGAAACAGCATTCAGAGCA
13920	YETDISQ	28243	TATGAGACTGATATTAGTCAG	42566	TACGAAACAGACATCAGCCAA
13921	YETELRA	28244	TATGAGACTGAGCTTCGGGCT	42567	TACGAAACAGAACTCAGAGCA
13922	YFAGRTD	28245	TATTTTGCGGGTCGGACTGAT	42568	TACTTCGCAGGAAGAACAGAC
13923	YFASPTS	28246	TATTTTGCTAGTCCTACTTCG	42569	TACTTCGCAAGCCCAACAAGC
13924	YFEASSA	28247	TATTTTGAGGCTTCTTCGGCG	42570	TACTTCGAAGCAAGCAGCGCA
13925	YFGSSAT	28248	TATTTTGGTTCTTCGGCTACG	42571	TACTTCGGAAGCAGCGCAACA
13926	YFGSSDP	28249	TATTTTGGTTCGTCTGATCCG	42572	TACTTCGGAAGCAGCGACCCA
13927	YFHLATS	28250	TATTTTCATCTGGCGACTTCG	42573	TACTTCCACCTCGCAACAAGC
13928	YFPSMVD	28251	TATTTTCCGTCGATGGTGGAT	42574	TACTTCCCAAGCATGGTCGAC
13929	YFSHDET	28252	TATTTTTCGCATGATGAGACT	42575	TACTTCAGCCACGACGAAACA
13930	YFTNDSV	28253	TATTTTACTAATGATAGTGTG	42576	TACTTCACAAACGACAGCGTC
13931	YFTSRSE	28254	TATTTTACTAGTCGTAGTGAG	42577	TACTTCACAAGCAGAAGCGAA
13932	YFVANNP	28255	TATTTTGTGGCTAATAATCCT	42578	TACTTCGTCGCAAACAACCCA
13933	YFVKILI	28256	TATTTTGTTAAGATTCTTATT	42579	TACTTCGTCAAAATCCTCATC
13934	YGASPDT	28257	TATGGTGCGAGTCCGGATACG	42580	TACGGAGCAAGCCCAGACACA
13935	YGAVAKH	28258	TATGGTGCGGTGGCGAAGCAT	42581	TACGGAGCAGTCGCAAAACAC
13936	YGAVRHN	28259	TATGGTGCTGTGCGTCATAAT	42582	TACGGAGCAGTCAGACACAAC
13937	YGAVSPV	28260	TATGGTGCTGTGAGTCCGGTG	42583	TACGGAGCAGTCAGCCCAGTC
13938	YGDPGPP	28261	TATGGTGATCCTGGGCCGCCT	42584	TACGGAGACCCAGGACCACCA
13939	YGDVADS	28262	TATGGTGATGTTGCTGATAGT	42585	TACGGAGACGTCGCAGACAGC

13940	YGEPIRP	28263	TATGGGGAGCCGATTCGTCCG	42586	TACGGAGAACCAATCAGACCA
13941	YGGAGSL	28264	TATGGGGGTGCTGGGAGTTTG	42587	TACGGAGGAGCAGGAAGCCTC
13942	YGGHTVS	28265	TATGGGGGTCATACTGTTAGT	42588	TACGGAGGACACACAGTCAGC
13943	YGGPNMT	28266	TATGGTGGGCCTAATATGACT	42589	TACGGAGGACCAAACATGACA
13944	YGISPKT	28267	TATGGGATTTCGCCGAAGACG	42590	TACGGAATCAGCCCAAAAACA
13945	YGKMTSD	28268	TATGGTAAGATGACGAGTGAT	42591	TACGGAAAAATGACAAGCGAC
13946	YGLKSAI	28269	TATGGGCTGAAGTCGGCGATT	42592	TACGGACTCAAAAGCGCAATC
13947	YGLSAHS	28270	TATGGGCTGTCGGCGCATTCG	42593	TACGGACTCAGCGCACACAGC
13948	YGMKVAQ	28271	TATGGTATGAAGGTGGCTCAG	42594	TACGGAATGAAAGTCGCACAA
13949	YGMSFKE	28272	TATGGGATGTCGTTTAAGGAG	42595	TACGGAATGAGCTTCAAAGAA
13950	YGNARAV	28273	TATGGTAATGCTCGTGCGGTT	42596	TACGGAAACGCAAGAGCAGTC
13951	YGNGSLG	28274	TATGGGAATGGGAGTCTTGGT	42597	TACGGAAACGGAAGCCTCGGA
13952	YGNHLLS	28275	TATGGTAATCATCTTTTGTCT	42598	TACGGAAACCACCTCCTCAGC
13953	YGPALLS	28276	TATGGGCCTGCGTTGCTTAGT	42599	TACGGACCAGCACTCCTCAGC
13954	YGPDLRQ	28277	TATGGTCCTGATCTTCGTCAG	42600	TACGGACCAGACCTCAGACAA
13955	YGPHAKS	28278	TATGGTCCGCATGCGAAGAGT	42601	TACGGACCACACGCAAAAAGC
13956	YGQSGAS	28279	TATGGGCAGAGTGGGGCTTCT	42602	TACGGACAAAGCGGAGCAAGC
13957	YGQSKSS	28280	TATGGTCAGTCTAAGAGTAGT	42603	TACGGACAAAGCAAAAGCAGC
13958	YGRNMTQ	28281	TATGGTCGTAATATGACGCAG	42604	TACGGAAGAAACATGACACAA
13959	YGRSQSL	28282	TATGGGCGGTCTCAGTCGCTG	42605	TACGGAAGAAGCCAAAGCCTC
13960	YGSLNIA	28283	TATGGTTCGTTGAATATTGCT	42606	TACGGAAGCCTCAACATCGCA
13961	YGSPRVT	28284	TATGGTTCGCCTCGTGTGACG	42607	TACGGAAGCCCAAGAGTCACA
13962	YGSSCHT	28285	TATGGGTCTTCGTGTCATACG	42608	TACGGAAGCAGCTGCCACACA
13963	YGSSRTT	28286	TATGGTTCTTCGCGTACGACG	42609	TACGGAAGCAGCAGAACAACA
13964	YGTATQA	28287	TATGGTACTGCGACTCAGGCG	42610	TACGGAACAGCAACACAAGCA
13965	YGTETNY	28288	TATGGTACGGAGACTAATTAT	42611	TACGGAACAGAAACAAACTAC
13966	YGTGGHL	28289	TATGGGACGGGTGGGCATCTG	42612	TACGGAACAGGAGGACACCTC
13967	YGTLARH	28290	TATGGTACGCTTGCTCGGCAT	42613	TACGGAACACTCGCAAGACAC
13968	YGVRPST	28291	TATGGGGTTCGTCCGAGTACG	42614	TACGGAGTCAGACCAAGCACA
13969	YGYAALN	28292	TATGGTTATGCTGCTTTGAAT	42615	TACGGATACGCAGCACTCAAC
13970	YHAGPPD	28293	TATCATGCGGGGCCTCCGGAT	42616	TACCACGCAGGACCACCAGAC
13971	YHGRTVV	28294	TATCATGGGAGGACTGTGGTT	42617	TACCACGGAAGAACAGTCGTC
13972	YHKTGVH	28295	TATCATAAGACGGGGGTTCAT	42618	TACCACAAAACAGGAGTCCAC
13973	YHMTVKS	28296	TATCATATGACGGTTAAGTCT	42619	TACCACATGACAGTCAAAAGC
13974	YHNHGTS	28297	TATCATAATCATGGTACTAGT	42620	TACCACAACCACGGAACAAGC
13975	YHNLQGM	28298	TATCATAATCTGCAGGGTATG	42621	TACCACAACCTCCAAGGAATG
13976	YHNNSSP	28299	TATCATAATAATTCGTCGCCT	42622	TACCACAACAACAGCAGCCCA
13977	YHPPREN	28300	TATCATCCTCCTCGTGAGAAT	42623	TACCACCCACCAAGAGAAAAC
13978	YHPVIAP	28301	TATCATCCTGTGATTGCGCCT	42624	TACCACCCAGTCATCGCACCA
13979	YHSEVRA	28302	TATCATAGTGAGGTTCGTGCT	42625	TACCACAGCGAAGTCAGAGCA
13980	YHSNTTS	28303	TATCATAGTAATACGACTTCG	42626	TACCACAGCAACACAACAAGC
13981	YHSVSTS	28304	TATCATAGTGTTTCTACGAGT	42627	TACCACAGCGTCAGCACAAGC
13982	YHTASMN	28305	TATCATACTGCGTCGATGAAT	42628	TACCACACAGCAAGCATGAAC
13983	YHTLNKD	28306	TATCATACTTTGAATAAGGAT	42629	TACCACACACTCAACAAAGAC
13984	YHTVSSN	28307	TATCATACTGTTTCTAGTAAT	42630	TACCACACAGTCAGCAGCAAC

13985	YHVRAAS	28308	TATCATGTGAGGGCGGCGTCT	42631	TACCACGTCAGAGCAGCAAGC
13986	YIETRVT	28309	TATATTGAGACTCGTGTTACG	42632	TACATCGAAACAAGAGTCACA
13987	YIGERDP	28310	TATATTGGTGAGCGGGATCCT	42633	TACATCGGAGAAAGAGACCCA
13988	YIGPDLA	28311	TATATTGGTCCGGATCTGGCT	42634	TACATCGGACCAGACCTCGCA
13989	YIHPEQE	28312	TATATTCATCCGGAGCAGGAG	42635	TACATCCACCCAGAACAAGAA
13990	YIIAQEC	28313	TATATTATTGCTCAGGAGTGT	42636	TACATCATCGCACAAGAATGC
13991	YILTSET	28314	TATATTCTTACTTCTGAGACT	42637	TACATCCTCACAAGCGAAACA
13992	YINALIA	28315	TATATTAATGCTCTTATTGCG	42638	TACATCAACGCACTCATCGCA
13993	YIPSKFT	28316	TATATTCCGTCGAAGTTTACT	42639	TACATCCCAAGCAAATTCACA
13994	YIQVPKG	28317	TATATTCAGGTTCCTAAGGGG	42640	TACATCCAAGTCCCAAAAGGA
13995	YISAGTS	28318	TATATTTCTGCGGGGACTTCG	42641	TACATCAGCGCAGGAACAAGC
13996	YISPVSV	28319	TATATTTCGCCGGTTTCTGTG	42642	TACATCAGCCCAGTCAGCGTC
13997	YKAASVP	28320	TATAAGGCTGCTTCGGTTCCT	42643	TACAAAGCAGCAAGCGTCCCA
13998	YKGAPVT	28321	TATAAGGGTGCTCCTGTTACT	42644	TACAAAGGAGCACCAGTCACA
13999	YKGASLD	28322	TATAAGGGTGCTTCGCTGGAT	42645	TACAAAGGAGCAAGCCTCGAC
14000	YKGGNSF	28323	TATAAGGGTGGTAATTCGTTT	42646	TACAAAGGAGGAAACAGCTTC
14001	YKLNATY	28324	TATAAGTTGAATGCGACGTAT	42647	TACAAACTCAACGCAACATAC
14002	YKLQQVS	28325	TATAAGCTTCAGCAGGTGTCG	42648	TACAAACTCCAACAAGTCAGC
14003	YKPANVN	28326	TATAAGCCGGCGAATGTGAAT	42649	TACAAACCAGCAAACGTCAAC
14004	YKPSEGT	28327	TATAAGCCGAGTGAGGGGACG	42650	TACAAACCAAGCGAAGGAACA
14005	YKQHVIS	28328	TATAAGCAGCATGTGATTTCG	42651	TACAAACAACACGTCATCAGC
14006	YKSSAGS	28329	TATAAGTCGTCGGCTGGTAGT	42652	TACAAAAGCAGCGCAGGAAGC
14007	YKTGRLA	28330	TATAAGACGGGTCGTCTGGCT	42653	TACAAAACAGGAAGACTCGCA
14008	YKVLPSA	28331	TATAAGGTTTTGCCTTCTGCT	42654	TACAAAGTCCTCCCAAGCGCA
14009	YLAGERT	28332	TATCTTGCTGGTGAGAGGACT	42655	TACCTCGCAGGAGAAAGAACA
14010	YLAHGLQ	28333	TATCTTGCTCATGGGCTTCAG	42656	TACCTCGCACACGGACTCCAA
14011	YLALQYK	28334	TATTTGGCGCTTCAGTATAAG	42657	TACCTCGCACTCCAATACAAA
14012	YLDHIWE	28335	TATTTGGATCATATTTGGGAG	42658	TACCTCGACCACATCTGGGAA
14013	YLDTSPV	28336	TATCTGGATACTTCGCCTGTT	42659	TACCTCGACACAAGCCCAGTC
14014	YLERYGS	28337	TATTTGGAGCGGTATGGGTCT	42660	TACCTCGAAAGATACGGAAGC
14015	YLGDKMA	28338	TATCTTGGTGATAAGATGGCT	42661	TACCTCGGAGACAAAATGGCA
14016	YLGHSTK	28339	TATCTTGGGCATTCGACGAAG	42662	TACCTCGGACACAGCACAAAA
14017	YLGTQVN	28340	TATCTTGGTACGCAGGTTAAT	42663	TACCTCGGAACACAAGTCAAC
14018	YLKFTDS	28341	TATTTGAAGTTTACTGATTCT	42664	TACCTCAAATTCACAGACAGC
14019	YLKSNSP	28342	TATTTGAAGTCGAATTCGCCT	42665	TACCTCAAAAGCAACAGCCCA
14020	YLLSELS	28343	TATTTGCTTTCTGAGCTTTCT	42666	TACCTCCTCAGCGAACTCAGC
14021	YLLSHAG	28344	TATTTGCTGTCTCATGCTGGG	42667	TACCTCCTCAGCCACGCAGGA
14022	YLMHASA	28345	TATTTGATGCATGCGTCGGCG	42668	TACCTCATGCACGCAAGCGCA
14023	YLNVIPA	28346	TATTTGAATGTGACGCCTGCT	42669	TACCTCAACGTCACACCAGCA
14024	YLPKSNF	28347	TATCTTCCTAAGTCTAATTTT	42670	TACCTCCCAAAAAGCAACTTC
14025	YLPLTAV	28348	TATCTGCCGTTGACTGCTGTG	42671	TACCTCCCACTCACAGCAGTC
14026	YLPRGTF	28349	TATTTGCCGCGTGGTACGTTT	42672	TACCTCCCAAGAGGAACATTC
14027	YLPRGTS	28350	TATTTGCCGCGTGGTACGTCT	42673	TACCTCCCAAGAGGAACAAGC
14028	YLPTRHE	28351	TATCTTCCGACGAGGCATGAG	42674	TACCTCCCAACAAGACACGAA
14029	YLQAHYN	28352	TATCTTCAGGCGCATTATAAT	42675	TACCTCCAAGCACACTACAAC

14030	YLQHGHT	28353	TATCTTCAGCATGGGCATACG	42676	TACCTCCAACACGGACACACA
14031	YLQTEDP	28354	TATCTTCAGACGGAGGATCCT	42677	TACCTCCAAACAGAAGACCCA
14032	YLRLQTG	28355	TATTTGAGGCTTCAGACTGGT	42678	TACCTCAGACTCCAAACAGGA
14033	YLRPQSG	28356	TATTTGAGGCCGCAGTCTGGG	42679	TACCTCAGACCACAAAGCGGA
14034	YLSDPRM	28357	TATCTTTCGGATCCTCGGATG	42680	TACCTCAGCGACCCAAGAATG
14035	YLSGMIK	28358	TATTTGTCGGGTATGATTAAG	42681	TACCTCAGCGGAATGATCAAA
14036	YLSHRSE	28359	TATCTGTCTCATAGGTCTGAG	42682	TACCTCAGCCACAGAAGCGAA
14037	YLSNTEM	28360	TATTTGTCTAATACTGAGATG	42683	TACCTCAGCAACACAGAAATG
14038	YLSVDES	28361	TATTTGTCTGTTGATGAGTCT	42684	TACCTCAGCGTCGACGAAAGC
14039	YLSVQSN	28362	TATCTTAGTGTTCAGTCGAAT	42685	TACCTCAGCGTCCAAAGCAAC
14040	YLTKHTS	28363	TATCTTACTAAGCATACTTCG	42686	TACCTCACAAAACACACAAGC
14041	YLTQLST	28364	TATCTTACTCAGCTGTCGACG	42687	TACCTCACACAACTCAGCACA
14042	YLVETTK	28365	TATCTTGTTGAGACGACTAAG	42688	TACCTCGTCGAAACAACAAAA
14043	YLVGQRV	28366	TATCTGGTGGGTCAGCGTGTG	42689	TACCTCGTCGGACAAAGAGTC
14044	YMDTDDR	28367	TATATGGATACTGATGATCGT	42690	TACATGGACACAGACGACAGA
14045	YMGHALS	28368	TATATGGGGCATGCTCTTTCG	42691	TACATGGGACACGCACTCAGC
14046	YMHASNV	28369	TATATGCATGCGTCTAATGTG	42692	TACATGCACGCAAGCAACGTC
14047	YMHGSHA	28370	TATATGCATGGTTCGCATGCT	42693	TACATGCACGGAAGCCACGCA
14048	YMHSPTP	28371	TATATGCATTCGCCTACGCCG	42694	TACATGCACAGCCCAACACCA
14049	YMHSSRT	28372	TATATGCATTCGTCGAGGACG	42695	TACATGCACAGCAGCAGAACA
14050	YMHYTVT	28373	TATATGCATTATACGGTTACG	42696	TACATGCACTACACAGTCACA
14051	YMPAPVQ	28374	TATATGCCTGCTCCTGTTCAG	42697	TACATGCCAGCACCAGTCCAA
14052	YMQTRDT	28375	TATATGCAGACGCGGGATACT	42698	TACATGCAAACAAGAGACACA
14053	YMQVFSP	28376	TATATGCAGGTTTTTTCTCCG	42699	TACATGCAAGTCTTCAGCCCA
14054	YMSAIRM	28377	TATATGTCGGCGATTCGGATG	42700	TACATGAGCGCAATCAGAATG
14055	YMSATTR	28378	TATATGTCGGCGACTACGCGT	42701	TACATGAGCGCAACAACAAGA
14056	YMSRTAS	28379	TATATGTCTCGGACGGCTTCT	42702	TACATGAGCAGAACAGCAAGC
14057	YMSVTQQ	28380	TATATGTCGGTTACGCAGCAG	42703	TACATGAGCGTCACACAACAA
14058	YMTGRPH	28381	TATATGACTGGTCGTCCGCAT	42704	TACATGACAGGAAGACCACAC
14059	YMTKNFG	28382	TATATGACTAAGAATTTTGGG	42705	TACATGACAAAAAACTTCGGA
14060	YMTNLQP	28383	TATATGACGAATCTTCAGCCT	42706	TACATGACAAACCTCCAACCA
14061	YMTSQSR	28384	TATATGACTAGTCAGAGTCGT	42707	TACATGACAAGCCAAAGCAGA
14062	YMYDGSV	28385	TATATGTATGATGGTTCGGTT	42708	TACATGTACGACGGAAGCGTC
14063	YNAASGL	28386	TATAATGCGGCTTCTGGGCTG	42709	TACAACGCAGCAAGCGGACTC
14064	YNAGGPR	28387	TATAATGCTGGTGGTCCTAGG	42710	TACAACGCAGGAGGACCAAGA
14065	YNALLQP	28388	TATAATGCGCTTCTTCAGCCT	42711	TACAACGCACTCCTCCAACCA
14066	YNDVMSN	28389	TATAATGATGTTATGAGTAAT	42712	TACAACGACGTCATGAGCAAC
14067	YNGNLRL	28390	TATAATGGGAATCTGCGTTTG	42713	TACAACGGAAACCTCAGACTC
14068	YNGQHIA	28391	TATAATGGTCAGCATATTGCG	42714	TACAACGGACAACACATCGCA
14069	YNIGTSN	28392	TATAATATTGGTACGTCTAAT	42715	TACAACATCGGAACAAGCAAC
14070	YNINQLT	28393	TATAATATTAATCAGCTGACT	42716	TACAACATCAACCAACTCACA
14071	YNLRPLQ	28394	TATAATCTGCGTCCGCTGCAG	42717	TACAACCTCAGACCACTCCAA
14072	YNLSGPS	28395	TATAATTTGAGTGGTCCTTCG	42718	TACAACCTCAGCGGACCAAGC
14073	YNLSNPA	28396	TATAATCTTAGTAATCCTGCT	42719	TACAACCTCAGCAACCCAGCA
14074	YNLSVGF	28397	TATAATCTTAGTGTTGGGTTT	42720	TACAACCTCAGCGTCGGATTC

14075	YNNSNTT	28398	TATAATAATTCTAATACTACT	42721	TACAACAACAGCAACACAACA
14076	YNPLNQR	28399	TATAATCCTCTTAATCAGCGT	42722	TACAACCCACTCAACCAAAGA
14077	YNPPEPL	28400	TATAATCCGCCGGAGCCGCTG	42723	TACAACCCACCAGAACCACTC
14078	YNPPRSS	28401	TATAATCCGCCTCGGTCTTCT	42724	TACAACCCACCAAGAAGCAGC
14079	YNQHGPP	28402	TATAATCAGCATGGTCCTCCT	42725	TACAACCAACACGGACCACCA
14080	YNQLARP	28403	TATAATCAGCTTGCTCGTCCG	42726	TACAACCAACTCGCAAGACCA
14081	YNQRPIV	28404	TATAATCAGCGTCCTATTGTT	42727	TACAACCAAAGACCAATCGTC
14082	YNRANLS	28405	TATAATAGGGCTAATTTGTCT	42728	TACAACAGAGCAAACCTCAGC
14083	YNRGQMQ	28406	TATAATAGGGGTCAGATGCAG	42729	TACAACAGAGGACAAATGCAA
14084	YNRVATS	28407	TATAATCGTGTGGCTACGTCG	42730	TACAACAGAGTCGCAACAAGC
14085	YNSSGVP	28408	TATAATTCTTCTGGGGTGCCT	42731	TACAACAGCAGCGGAGTCCCA
14086	YNSSSLG	28409	TATAATAGTTCGTCGCTTGGT	42732	TACAACAGCAGCAGCCTCGGA
14087	YNSTGLR	28410	TATAATAGTACGGGTCTGCGG	42733	TACAACAGCACAGGACTCAGA
14088	YNTGRIT	28411	TATAATACTGGTCGGATTACT	42734	TACAACACAGGAAGAATCACA
14089	YNTIKAV	28412	TATAATACGATTAAGGCGGTT	42735	TACAACACAATCAAAGCAGTC
14090	YNTPRME	28413	TATAATACTCCTCGGATGGAG	42736	TACAACACACCAAGAATGGAA
14091	YNVETDN	28414	TATAATGTTGAGACGGATAAT	42737	TACAACGTCGAAACAGACAAC
14092	YNVYTVP	28415	TATAATGTGTATACGGTGCCG	42738	TACAACGTCTACACAGTCCCA
14093	YPALDVF	28416	TATCCTGCGCTGGATGTGTTT	42739	TACCCAGCACTCGACGTCTTC
14094	YPANRLL	28417	TATCCTGCTAATCGTCTGCTG	42740	TACCCAGCAAACAGACTCCTC
14095	YPDSDLL	28418	TATCCTGATAGTGATCTGCTG	42741	TACCCAGACAGCGACCTCCTC
14096	YPFGDMA	28419	TATCCGTTTGGGGATATGGCG	42742	TACCCATTCGGAGACATGGCA
14097	YPGATET	28420	TATCCTGGGGCTACTGAGACG	42743	TACCCAGGAGCAACAGAAACA
14098	YPGTKQM	28421	TATCCTGGGACTAAGCAGATG	42744	TACCCAGGAACAAAACAAATG
14099	YPGVTVK	28422	TATCCTGGTGTGACGGTGAAG	42745	TACCCAGGAGTCACAGTCAAA
14100	YPHAASW	28423	TATCCTCATGCTGCTTCTTGG	42746	TACCCACACGCAGCAAGCTGG
14101	YPHHSQH	28424	TATCCTCATCATTCGCAGCAT	42747	TACCCACACCACAGCCAACAC
14102	YPHTPAA	28425	TATCCTCATACTCCTGCGGCG	42748	TACCCACACACACCAGCAGCA
14103	YPIATVR	28426	TATCCTATTGCGACTGTTAGG	42749	TACCCAATCGCAACAGTCAGA
14104	YPIRPLG	28427	TATCCTATTAGGCCGTTGGGT	42750	TACCCAATCAGACCACTCGGA
14105	YPKVPTF	28428	TATCCTAAGGTGCCTACGTTT	42751	TACCCAAAAGTCCCAACATTC
14106	YPKVYSA	28429	TATCCTAAGGTGTATTCGGCG	42752	TACCCAAAAGTCTACAGCGCA
14107	YPLSTSA	28430	TATCCGCTGAGTACGTCGGCT	42753	TACCCACTCAGCACAAGCGCA
14108	YPMPSPP	28431	TATCCTATGCCGTCTCCGCCT	42754	TACCCAATGCCAAGCCCACCA
14109	YPNDSYA	28432	TATCCGAATGATTCTTATGCG	42755	TACCCAAACGACAGCTACGCA
14110	YPNHSRN	28433	TATCCGAATCATAGTCGTAAT	42756	TACCCAAACCACAGCAGAAAC
14111	YPNSLSL	28434	TATCCTAATAGTCTTTCGTTG	42757	TACCCAAACAGCCTCAGCCTC
14112	YPPDSHP	28435	TATCCTCCTGATTCTCATCCG	42758	TACCCACCAGACAGCCACCCA
14113	YPPIAQG	28436	TATCCTCCTATTGCGCAGGGT	42759	TACCCACCAATCGCACAAGGA
14114	YPPKLGS	28437	TATCCTCCTAAGCTTGGGTCT	42760	TACCCACCAAAACTCGGAAGC
14115	YPPKYAN	28438	TATCCTCCGAAGTATGCGAAT	42761	TACCCACCAAAATACGCAAAC
14116	YPPPKAS	28439	TATCCTCCTCCTAAGGCTTCG	42762	TACCCACCACCAAAAGCAAGC
14117	YPPSGYN	28440	TATCCTCCTTCTGGGTATAAT	42763	TACCCACCAAGCGGATACAAC
14118	YPPTARA	28441	TATCCGCCGACTGCGCGTGCG	42764	TACCCACCAACAGCAAGAGCA
14119	YPPTPLP	28442	TATCCGCCGACTCCGTTGCCG	42765	TACCCACCAACACCACTCCCA

14120	YPPWHNP	28443	TATCCTCCGTGGCATAATCCG	42766	TACCCACCATGGCACAACCCA
14121	YPRDASS	28444	TATCCGCGTGATGCGTCTTCT	42767	TACCCAAGAGACGCAAGCAGC
14122	YPREKSL	28445	TATCCGCGTGAGAAGTCTTTG	42768	TACCCAAGAGAAAAAAGCCTC
14123	YPRHPSF	28446	TATCCGCGGCATCCTTCTTTT	42769	TACCCAAGACACCCAAGCTTC
14124	YPRTLPE	28447	TATCCGCGGACGCTTCCGGAG	42770	TACCCAAGAACACTCCCAGAA
14125	YPSASSM	28448	TATCCGTCTGCGAGTAGTATG	42771	TACCCAAGCGCAAGCAGCATG
14126	YPSHLLN	28449	TATCCGAGTCATTTGCTGAAT	42772	TACCCAAGCCACCTCCTCAAC
14127	YPSPAGE	28450	TATCCTAGTCCGGCGGGGGAG	42773	TACCCAAGCCCAGCAGGAGAA
14128	YPSPSNL	28451	TATCCGTCGCCGAGTAATTTG	42774	TACCCAAGCCCAAGCAACCTC
14129	YPSSSMP	28452	TATCCTTCTTCTTCGATGCCG	42775	TACCCAAGCAGCAGCATGCCA
14130	YPTGETP	28453	TATCCTACGGGTGAGACGCCG	42776	TACCCAACAGGAGAAACACCA
14131	YPTHSHM	28454	TATCCTACTCATAGTCATATG	42777	TACCCAACACACAGCCACATG
14132	YPTKHLH	28455	TATCCTACTAAGCATCTTCAT	42778	TACCCAACAAAACACCTCCAC
14133	YPTTPLM	28456	TATCCTACTACGCCTCTGATG	42779	TACCCAACAACACCACTCATG
14134	YPVNAPT	28457	TATCCGGTTAATGCGCCTACT	42780	TACCCAGTCAACGCACCAACA
14135	YPVQDAL	28458	TATCCGGTGCAGGATGCTCTT	42781	TACCCAGTCCAAGACGCACTC
14136	YPVSTTQ	28459	TATCCTGTTAGTACTACTCAG	42782	TACCCAGTCAGCACAACACAA
14137	YQGIALG	28460	TATCAGGGTATTGCTCTGGGG	42783	TACCAAGGAATCGCACTCGGA
14138	YQGTLPS	28461	TATCAGGGTACGCTGCCTTCT	42784	TACCAAGGAACACTCCCAAGC
14139	YQLDNTP	28462	TATCAGTTGGATAATACGCCG	42785	TACCAACTCGACAACACACCA
14140	YQLQRSE	28463	TATCAGCTGCAGCGGTCGGAG	42786	TACCAACTCCAAAGAAGCGAA
14141	YQLRQSP	28464	TATCAGTTGAGGCAGAGTCCG	42787	TACCAACTCAGACAAAGCCCA
14142	YQLVTQP	28465	TATCAGCTGGTGACGCAGCCT	42788	TACCAACTCGTCACACAACCA
14143	YQPPDMG	28466	TATCAGCCTCCGGATATGGGT	42789	TACCAACCACCAGACATGGGA
14144	YQQDGRC	28467	TATCAGCAGGATGGTCGTTGT	42790	TACCAACAAGACGGAAGATGC
14145	YQRVSSS	28468	TATCAGAGGGTGAGTAGTTCG	42791	TACCAAAGAGTCAGCAGCAGC
14146	YQSDGNP	28469	TATCAGAGTGATGGTAATCCG	42792	TACCAAAGCGACGGAAACCCA
14147	YQTEITR	28470	TATCAGACTGAGATTACTCGG	42793	TACCAAACAGAAATCACAAGA
14148	YQTYTRE	28471	TATCAGACTTATACTCGTGAG	42794	TACCAAACATACACAAGAGAA
14149	YQVKTGP	28472	TATCAGGTGAAGACTGGGCCT	42795	TACCAAGTCAAAACAGGACCA
14150	YQVNAGM	28473	TATCAGGTGAATGCTGGGATG	42796	TACCAAGTCAACGCAGGAATG
14151	YRADGEA	28474	TATCGTGCTGATGGTGAGGCG	42797	TACAGAGCAGACGGAGAAGCA
14152	YRAMAPP	28475	TATCGTGCTATGGCTCCGCCT	42798	TACAGAGCAATGGCACCACCA
14153	YRANSPV	28476	TATCGTGCTAATTCGCCTGTG	42799	TACAGAGCAAACAGCCCAGTC
14154	YRASGEL	28477	TATCGGGCTTCTGGGGAGCTT	42800	TACAGAGCAAGCGGAGAACTC
14155	YRDHEVL	28478	TATAGGGATCATGAGGTTCTG	42801	TACAGAGACCACGAAGTCCTC
14156	YRDIQRG	28479	TATCGTGATATTCAGCGTGGG	42802	TACAGAGACATCCAAAGAGGA
14157	YRDNRPN	28480	TATAGGGATAATCGTCCTAAT	42803	TACAGAGACAACAGACCAAAC
14158	YRDSSNI	28481	TATCGTGATTCGTCGAATATT	42804	TACAGAGACAGCAGCAACATC
14159	YREMANR	28482	TATCGGGAGATGGCTAATCGG	42805	TACAGAGAAATGGCAAACAGA
14160	YRENARA	28483	TATCGTGAGAATGCTAGGGCG	42806	TACAGAGAAAACGCAAGAGCA
14161	YRGITLD	28484	TATAGGGGGATTACTCTTGAT	42807	TACAGAGGAATCACACTCGAC
14162	YRGNHAP	28485	TATCGTGGGAATCATGCTCCT	42808	TACAGAGGAAACCACGCACCA
14163	YRGYHVE	28486	TATCGTGGGTATCATGTGGAG	42809	TACAGAGGATACCACGTCGAA
14164	YRHGSIE	28487	TATAGGCATGGTTCTATTGAG	42810	TACAGACACGGAAGCATCGAA

14165	YRLYADD	28488	TATAGGCTGTATGCTGATGAT	42811	TACAGACTCTACGCAGACGAC
14166	YRMGTDQ	28489	TATCGGATGGGTACGGATCAG	42812	TACAGAATGGGAACAGACCAA
14167	YRPGASA	28490	TATCGTCCTGGTGCGTCGGCT	42813	TACAGACCAGGAGCAAGCGCA
14168	YRPLSTP	28491	TATCGTCCGCTTTCTACTCCT	42814	TACAGACCACTCAGCACACCA
14169	YRPQEND	28492	TATCGGCCTCAGGAGAATGAT	42815	TACAGACCACAAGAAAACGAC
14170	YRQALDH	28493	TATAGGCAGGCTTTGGATCAT	42816	TACAGACAAGCACTCGACCAC
14171	YRQLDFP	28494	TATCGTCAGCTGGATTTTCCG	42817	TACAGACAACTCGACTTCCCA
14172	YRQTRDP	28495	TATCGTCAGACGCGTGATCCG	42818	TACAGACAAACAAGAGACCCA
14173	YRQVTEV	28496	TATCGTCAGGTTACTGAGGTG	42819	TACAGACAAGTCACAGAAGTC
14174	YRSDTLR	28497	TATCGGTCTGATACGTTGCGT	42820	TACAGAAGCGACACACTCAGA
14175	YRSHTPP	28498	TATCGTTCTCATACTCCGCCT	42821	TACAGAAGCCACACACCACCA
14176	YRSIVPD	28499	TATCGGAGTATTGTTCCTGAT	42822	TACAGAAGCATCGTCCCAGAC
14177	YRSPDEM	28500	TATCGGTCTCCGGATGAGATG	42823	TACAGAAGCCCAGACGAAATG
14178	YRSSTPD	28501	TATCGGAGTTCGACGCCGGAT	42824	TACAGAAGCAGCACACCAGAC
14179	YRSVVQS	28502	TATCGTTCGGTTGTTCAGAGT	42825	TACAGAAGCGTCGTCCAAAGC
14180	YRTATPP	28503	TATCGTACGGCGACTCCTCCT	42826	TACAGAACAGCAACACCACCA
14181	YRTEQLG	28504	TATCGGACGGAGCAGCTGGGT	42827	TACAGAACAGAACAACTCGGA
14182	YRTIDSG	28505	TATCGTACGATTGATTCTGGG	42828	TACAGAACAATCGACAGCGGA
14183	YRTLDNP	28506	TATAGGACTTTGGATAATCCG	42829	TACAGAACACTCGACAACCCA
14184	YRTPASS	28507	TATCGGACGCCGGCGTCTTCG	42830	TACAGAACACCAGCAAGCAGC
14185	YRTQPTQ	28508	TATCGTACGCAGCCGACTCAG	42831	TACAGAACACAACCAACACAA
14186	YRVDSAN	28509	TATAGGGTTGATAGTGCTAAT	42832	TACAGAGTCGACAGCGCAAAC
14187	YRVSMLS	28510	TATCGTGTGTCGATGTTGTCT	42833	TACAGAGTCAGCATGCTCAGC
14188	YRVSMSS	28511	TATCGTGTGTCGATGTCGAGT	42834	TACAGAGTCAGCATGAGCAGC
14189	YRVVVGP	28512	TATCGGGTGGTTGTTGGGCCG	42835	TACAGAGTCGTCGTCGGACCA
14190	YSAHSAR	28513	TATTCTGCGCATTCTGCTCGT	42836	TACAGCGCACACAGCGCAAGA
14191	YSASSYL	28514	TATAGTGCTTCTTCGTATCTT	42837	TACAGCGCAAGCAGCTACCTC
14192	YSDPARP	28515	TATTCTGATCCGGCGCGGCCT	42838	TACAGCGACCCAGCAAGACCA
14193	YSDSPKQ	28516	TATAGTGATTCTCCGAAGCAG	42839	TACAGCGACAGCCCAAAACAA
14194	YSDTDSS	28517	TATTCGGATACGGATTCTTCT	42840	TACAGCGACACAGACAGCAGC
14195	YSDYGRP	28518	TATAGTGATTATGGTCGTCCG	42841	TACAGCGACTACGGAAGACCA
14196	YSEANIR	28519	TATAGTGAGGCGAATATTCGG	42842	TACAGCGAAGCAAACATCAGA
14197	YSEFTLN	28520	TATTCTGAGTTTACGCTGAAT	42843	TACAGCGAATTCACACTCAAC
14198	YSFPTSA	28521	TATTCTTTTCCTACTAGTGCT	42844	TACAGCTTCCCAACAAGCGCA
14199	YSGHDTS	28522	TATAGTGGGCATGATACTTCG	42845	TACAGCGGACACGACACAAGC
14200	YSGRIGP	28523	TATTCGGGGCGTATTGGTCCT	42846	TACAGCGGAAGAATCGGACCA
14201	YSGRPAS	28524	TATTCTGGGCGGCCTGCGAGT	42847	TACAGCGGAAGACCAGCAAGC
14202	YSGSSRN	28525	TATTCGGGTAGTAGTAGGAAT	42848	TACAGCGGAAGCAGCAGAAAC
14203	YSGTGFA	28526	TATTCTGGGACTGGTTTTGCG	42849	TACAGCGGAACAGGATTCGCA
14204	YSHANLP	28527	TATTCTCATGCGAATCTGCCT	42850	TACAGCCACGCAAACCTCCCA
14205	YSHEAVM	28528	TATTCTCATGAGGCTGTGATG	42851	TACAGCCACGAAGCAGTCATG
14206	YSHIEGS	28529	TATTCGCATATTGAGGGGTCT	42852	TACAGCCACATCGAAGGAAGC
14207	YSHTQMS	28530	TATAGTCATACTCAGATGTCT	42853	TACAGCCACACACAAATGAGC
14208	YSHVTTC	28531	TATTCTCATGTTACGACTTGT	42854	TACAGCCACGTCACAACATGC
14209	YSIAHQS	28532	TATTCGATTGCTCATCAGTCG	42855	TACAGCATCGCACACCAAAGC

14210	YSLAYSP	28533	TATAGTCTTGCGTATTCGCCT	42856	TACAGCCTCGCATACAGCCCA
14211	YSLEDAP	28534	TATAGTCTTGAGGATGCTCCG	42857	TACAGCCTCGAAGACGCACCA
14212	YSLGGPS	28535	TATTCGCTGGGGGGTCCGTCG	42858	TACAGCCTCGGAGGACCAAGC
14213	YSLPTDL	28536	TATAGTTTGCCGACTGATCTT	42859	TACAGCCTCCCAACAGACCTC
14214	YSLSHPS	28537	TATTCGCTGAGTCATCCTTCT	42860	TACAGCCTCAGCCACCCAAGC
14215	YSLTLHD	28538	TATTCTCTGACTTTGCATGAT	42861	TACAGCCTCACACTCCACGAC
14216	YSMHAAI	28539	TATTCGATGCATGCGGCTATT	42862	TACAGCATGCACGCAGCAATC
14217	YSMNKSP	28540	TATAGTATGAATAAGTCTCCT	42863	TACAGCATGAACAAAAGCCCA
14218	YSMVRTP	28541	TATAGTATGGTGCGTACTCCT	42864	TACAGCATGGTCAGAACACCA
14219	YSNEAPR	28542	TATTCTAATGAGGCGCCGCGT	42865	TACAGCAACGAAGCACCAAGA
14220	YSNEKWA	28543	TATTCTAATGAGAAGTGGGCG	42866	TACAGCAACGAAAAATGGGCA
14221	YSNQARG	28544	TATAGTAATCAGGCTCGTGGT	42867	TACAGCAACCAAGCAAGAGGA
14222	YSPHFRP	28545	TATTCTCCGCATTTTCGTCCT	42868	TACAGCCCACACTTCAGACCA
14223	YSPIKTH	28546	TATTCTCCGATTAAGACTCAT	42869	TACAGCCCAATCAAAACACAC
14224	YSPISGS	28547	TATTCTCCGATTTCGGGTTCT	42870	TACAGCCCAATCAGCGGAAGC
14225	YSPLPSR	28548	TATAGTCCGTTGCCTTCGCGG	42871	TACAGCCCACTCCCAAGCAGA
14226	YSPLSHH	28549	TATTCTCCGCTGAGTCATCAT	42872	TACAGCCCACTCAGCCACCAC
14227	YSPNLNG	28550	TATTCTCCGAATCTGAATGGT	42873	TACAGCCCAAACCTCAACGGA
14228	YSPPPSM	28551	TATTCGCCGCCGCCGTCTATG	42874	TACAGCCCACCACCAAGCATG
14229	YSPRTPT	28552	TATAGTCCGAGGACGCCTACT	42875	TACAGCCCAAGAACACCAACA
14230	YSPRTSL	28553	TATTCTCCGAGGACGTCTTTG	42876	TACAGCCCAAGAACAAGCCTC
14231	YSPTEAF	28554	TATTCGCCTACGGAGGCTTTT	42877	TACAGCCCAACAGAAGCATTC
14232	YSPTRSS	28555	TATAGTCCTACTAGGTCGTCG	42878	TACAGCCCAACAAGAAGCAGC
14233	YSQRGAD	28556	TATAGTCAGCGTGGTGCGGAT	42879	TACAGCCAAAGAGGAGCAGAC
14234	YSQRNDS	28557	TATTCGCAGCGGAATGATTCG	42880	TACAGCCAAAGAAACGACAGC
14235	YSRPSPL	28558	TATTCTAGGCCTTCTCCGCTT	42881	TACAGCAGACCAAGCCCACTC
14236	YSSGGLR	28559	TATTCGTCTGGTGGGCTGCGG	42882	TACAGCAGCGGAGGACTCAGA
14237	YSSHLRN	28560	TATTCGTCTCATTTGAGGAAT	42883	TACAGCAGCCACCTCAGAAAC
14238	YSSHSSS	28561	TATAGTTCTCATTCTAGTTCT	42884	TACAGCAGCCACAGCAGCAGC
14239	YSSLAAL	28562	TATTCGAGTCTTGCTGCGCTG	42885	TACAGCAGCCTCGCAGCACTC
14240	YSSNLAR	28563	TATTCTTCTAATTTGGCGCGG	42886	TACAGCAGCAACCTCGCAAGA
14241	YSSPDWS	28564	TATTCGAGTCCGGATTGGTCT	42887	TACAGCAGCCCAGACTGGAGC
14242	YSSPPIT	28565	TATAGTTCGCCGCCGATTACG	42888	TACAGCAGCCCACCAATCACA
14243	YSSQLSE	28566	TATTCGTCTCAGTTGTCGGAG	42889	TACAGCAGCCAACTCAGCGAA
14244	YSSRGEA	28567	TATTCGTCTCGTGGTGAGGCG	42890	TACAGCAGCAGAGGAGAAGCA
14245	YSSSVLA	28568	TATTCGTCTTCGGTGTTGGCG	42891	TACAGCAGCAGCGTCCTCGCA
14246	YSTDRYS	28569	TATAGTACGGATAGGTATTCG	42892	TACAGCACAGACAGATACAGC
14247	YSTFQPE	28570	TATAGTACGTTTCAGCCTGAG	42893	TACAGCACATTCCAACCAGAA
14248	YSTMRSM	28571	TATAGTACGATGCGTAGTATG	42894	TACAGCACAATGAGAAGCATG
14249	YSTQSLN	28572	TATTCTACTCAGTCTCTGAAT	42895	TACAGCACACAAAGCCTCAAC
14250	YSTRSLS	28573	TATAGTACTCGTTCGCTTAGT	42896	TACAGCACAAGAAGCCTCAGC
14251	YSTTGRL	28574	TATTCGACTACTGGTCGGCTG	42897	TACAGCACAACAGGAAGACTC
14252	YSTTVHA	28575	TATTCGACTACGGTTCATGCT	42898	TACAGCACAACAGTCCACGCA
14253	YSTVGSS	28576	TATTCGACGGTTGGTAGTAGT	42899	TACAGCACAGTCGGAAGCAGC
14254	YSVDAVW	28577	TATAGTGTTGATGCTGTTTGG	42900	TACAGCGTCGACGCAGTCTGG

14255	YSVRTMS	28578	TATTCTGTTCGTACGATGTCT	42901	TACAGCGTCAGAACAATGAGC
14256	YSVVTVD	28579	TATTCGGTTGTGACGGTTGAT	42902	TACAGCGTCGTCACAGTCGAC
14257	YSYNSDH	28580	TATTCTTATAATTCGGATCAT	42903	TACAGCTACAACAGCGACCAC
14258	YTAGVSA	28581	TATACTGCGGGGGTGTCGGCG	42904	TACACAGCAGGAGTCAGCGCA
14259	YTARAQS	28582	TATACGGCGCGTGCTCAGAGT	42905	TACACAGCAAGAGCACAAAGC
14260	YTASGDI	28583	TATACTGCTAGTGGGGATATT	42906	TACACAGCAAGCGGAGACATC
14261	YTEFAAN	28584	TATACGGAGTTTGCGGCTAAT	42907	TACACAGAATTCGCAGCAAAC
14262	YTGFTLD	28585	TATACTGGTTTTACGCTTGAT	42908	TACACAGGATTCACACTCGAC
14263	YTGGQLH	28586	TATACTGGTGGGCAGCTGCAT	42909	TACACAGGAGGACAACTCCAC
14264	YTGLEPS	28587	TATACGGGGTTGGAGCCGTCT	42910	TACACAGGACTCGAACCAAGC
14265	YTGSSVL	28588	TATACGGGGTCTTCTGTTCTG	42911	TACACAGGAAGCAGCGTCCTC
14266	YTHLTTA	28589	TATACGCATTTGACTACTGCT	42912	TACACACACCTCACAACAGCA
14267	YTHSIVT	28590	TATACTCATAGTATTGTTACT	42913	TACACACACAGCATCGTCACA
14268	YTHVLTP	28591	TATACTCATGTGCTGACTCCG	42914	TACACACACGTCCTCACACCA
14269	YTKMLGP	28592	TATACTAAGATGCTGGGGCCT	42915	TACACAAAAATGCTCGGACCA
14270	YTKNSTV	28593	TATACGAAGAATAGTACGGTT	42916	TACACAAAAAACAGCACAGTC
14271	YTLDQLS	28594	TATACGTTGGATCAGTTGTCG	42917	TACACACTCGACCAACTCAGC
14272	YTLSATT	28595	TATACTCTGTCTGCGACGACG	42918	TACACACTCAGCGCAACAACA
14273	YTMSPRP	28596	TATACGATGTCGCCTCGTCCG	42919	TACACAATGAGCCCAAGACCA
14274	YTNDRRS	28597	TATACTAATGATCGTAGGTCT	42920	TACACAAACGACAGAAGAAGC
14275	YTNNFVA	28598	TATACGAATAATTTTGTTGCG	42921	TACACAAACAACTTCGTCGCA
14276	YTPAGLS	28599	TATACTCCTGCTGGGCTTAGT	42922	TACACACCAGCAGGACTCAGC
14277	YTPHRMS	28600	TATACGCCTCATAGGATGTCT	42923	TACACACCACACAGAATGAGC
14278	YTPLMSS	28601	TATACGCCTCTGATGTCTTCG	42924	TACACACCACTCATGAGCAGC
14279	YTQSKTE	28602	TATACTCAGTCGAAGACTGAG	42925	TACACACAAAGCAAAACAGAA
14280	YTQTTWK	28603	TATACGCAGACGACGTGGAAG	42926	TACACACAAACAACATGGAAA
14281	YTRAPDG	28604	TATACTCGTGCGCCGGATGGT	42927	TACACAAGAGCACCAGACGGA
14282	YTSHPTC	28605	TATACGTCGCATCCGACTTGT	42928	TACACAAGCCACCCAACATGC
14283	YTSISNM	28606	TATACGTCGATTAGTAATATG	42929	TACACAAGCATCAGCAACATG
14284	YTSLSMA	28607	TATACGTCGCTTTCTATGGCG	42930	TACACAAGCCTCAGCATGGCA
14285	YTSMHVS	28608	TATACGTCTATGCATGTTTCT	42931	TACACAAGCATGCACGTCAGC
14286	YTSNIDM	28609	TATACGTCTAATATTGATATG	42932	TACACAAGCAACATCGACATG
14287	YTSPAHV	28610	TATACGTCGCCGGCTCATGTG	42933	TACACAAGCCCAGCACACGTC
14288	YTSRHIA	28611	TATACGTCGAGGCATATTGCT	42934	TACACAAGCAGACACATCGCA
14289	YTSRVLS	28612	TATACTTCTCGTGTGCTTTCT	42935	TACACAAGCAGAGTCCTCAGC
14290	YTSVYAH	28613	TATACTTCGGTTTATGCTCAT	42936	TACACAAGCGTCTACGCACAC
14291	YTSYTAP	28614	TATACTAGTTATACTGCTCCT	42937	TACACAAGCTACACAGCACCA
14292	YTTLPAR	28615	TATACTACGCTGCCTGCGCGT	42938	TACACAACACTCCCAGCAAGA
14293	YTTNRQS	28616	TATACGACGAATCGTCAGTCT	42939	TACACAACAAACAGACAAAGC
14294	YTTSPAL	28617	TATACTACTTCTCCGGCTCTT	42940	TACACAACAAGCCCAGCACTC
14295	YTTSPIK	28618	TATACTACTAGTCCTATTAAG	42941	TACACAACAAGCCCAATCAAA
14296	YTVRHVN	28619	TATACTGTTCGTCATGTTAAT	42942	TACACAGTCAGACACGTCAAC
14297	YVATEQK	28620	TATGTTGCTACTGAGCAGAAG	42943	TACGTCGCAACAGAACAAAAA
14298	YVDDPSG	28621	TATGTTGATGATCCTAGTGGG	42944	TACGTCGACGACCCAAGCGGA
14299	YVHLNTT	28622	TATGTTCATCTTAATACTACG	42945	TACGTCCACCTCAACACAACA

14300	YVKLYEK	28623	TATGTGAAGTTGTATGAGAAG	42946	TACGTCAAACTCTACGAAAAA
14301	YVKPNGA	28624	TATGTTAAGCCGAATGGTGCT	42947	TACGTCAAACCAAACGGAGCA
14302	YVKSQTA	28625	TATGTTAAGTCGCAGACGGCT	42948	TACGTCAAAAGCCAAACAGCA
14303	YVMSQSA	28626	TATGTGATGTCGCAGTCTGCG	42949	TACGTCATGAGCCAAAGCGCA
14304	YVPGRNE	28627	TATGTTCCGGGTCGGAATGAG	42950	TACGTCCCAGGAAGAAACGAA
14305	YVPMTSP	28628	TATGTGCCTATGACGTCTCCT	42951	TACGTCCCAATGACAAGCCCA
14306	YVPTSLG	28629	TATGTTCCTACTTCGCTTGGG	42952	TACGTCCCAACAAGCCTCGGA
14307	YVQQHVK	28630	TATGTGCAGCAGCATGTGAAG	42953	TACGTCCAACAACACGTCAAA
14308	YVRGMDA	28631	TATGTTCGGGGGATGGATGCT	42954	TACGTCAGAGGAATGGACGCA
14309	YVRVSNV	28632	TATGTGCGGGTGAGTAATGTT	42955	TACGTCAGAGTCAGCAACGTC
14310	YVSHVDL	28633	TATGTTTCGCATGTGGATTTG	42956	TACGTCAGCCACGTCGACCTC
14311	YVSMPNG	28634	TATGTTTCTATGCCGAATGGT	42957	TACGTCAGCATGCCAAACGGA
14312	YVTDRMP	28635	TATGTTACGGATCGGATGCCG	42958	TACGTCACAGACAGAATGCCA
14313	YVTGHHD	28636	TATGTGACTGGTCATCATGAT	42959	TACGTCACAGGACACCACGAC
14314	YVTKAPL	28637	TATGTTACTAAGGCGCCGCTT	42960	TACGTCACAAAAGCACCACTC
14315	YVTQIHG	28638	TATGTGACGCAGATTCATGGG	42961	TACGTCACACAAATCCACGGA
14316	YVVEPEP	28639	TATGTTGTGGAGCCGGAGCCG	42962	TACGTCGTCGAACCAGAACCA
14317	YVVNLPR	28640	TATGTTGTTAATCTGCCGCGT	42963	TACGTCGTCAACCTCCCAAGA
14318	YVVRADG	28641	TATGTTGTTCGGGCGGATGGG	42964	TACGTCGTCAGAGCAGACGGA
14319	YYDRSIG	28642	TATTATGATCGTAGTATTGGG	42965	TACTACGACAGAAGCATCGGA
14320	YYESSKQ	28643	TATTATGAGTCGTCGAAGCAG	42966	TACTACGAAAGCAGCAAACAA
14321	YYGSAPA	28644	TATTATGGGAGTGCGCCTGCT	42967	TACTACGGAAGCGCACCAGCA
14322	YYGVHPN	28645	TATTATGGGGTGCATCCTAAT	42968	TACTACGGAGTCCACCCAAAC
14323	YYNPSTS	28646	TATTATAATCCGAGTACTTCT	42969	TACTACAACCCAAGCACAAGC
14324	YYPRPGG	28647	TATTATCCGCGTCCTGGTGGG	42970	TACTACCCAAGACCAGGAGGA
14325	YYSAMAD	28648	TATTATAGTGCTATGGCTGAT	42971	TACTACAGCGCAATGGCAGAC
14326	YYSNTVT	28649	TATTATAGTAATACGGTTACT	42972	TACTACAGCAACACAGTCACA

Table 3. Targeting peptides (9-mers)

SEQ ID NO	Peptide Sequence	SEQ ID NO	Nucleotide sequence	SEQ ID NO	Alternate Nucleotide Sequence
42973	DGSPTVPFK	43000	GATGGGTCGCCTAC TGTGCCTTTTAAG	43027	GATGGGTCTCCTAC GGTGCCTTTTAAG
42974	DGTLEVPFK	43001	GATGGGACTCTGGA GGTGCCTTTTAAG	43028	GATGGGACGTTGG AGGTGCCTTTTAAG
42975	DGTPQVPFK	43002	GATGGGACGCCGC AGGTGCCTTTTAAG	43029	GATGGGACTCCTCA GGTGCCTTTTAAG
42976	DGTPTVPFK	43003	GATGGGACGCCGA CTGTGCCTTTTAAG	43030	GATGGGACTCCGAC GGTGCCTTTTAAG
42977	DGDLQVPFK	43004	GATGGGGATTTGCA GGTGCCTTTTAAG	43031	GACGGAGACCTCC AAGTCCCATTCAAA

42978	DGDLRVPFK	43005	GATGGGGATTTGAG GGTGCCTTTTAAG	43032	GACGGAGACCTCA GAGTCCCATTCAAA
42979	DGNLTVPFK	43006	GATGGGAATCTTAC GGTGCCTTTTAAG	43033	GACGGAAACCTCA CAGTCCCATTCAAA
42980	DGQPTVPFK	43007	GATGGGCAGCCTAC GGTGCCTTTTAAG	43034	GACGGACAACCAA CAGTCCCATTCAAA
42981	DGSIQVPFK	43008	GATGGGTCGATTCA GGTGCCTTTTAAG	43035	GACGGAAGCATCC AAGTCCCATTCAAA
42982	DGSLKVPFK	43009	GATGGGTCGTTGAA GGTGCCTTTTAAG	43036	GACGGAAGCCTCA AAGTCCCATTCAAA
42983	DGSPQVPFK	43010	GATGGGTCGCCGCA GGTGCCTTTTAAG	43037	GACGGAAGCCCAC AAGTCCCATTCAAA
42984	DGSRSVPFK	43011	GATGGGTCGCGGTC GGTGCCGTTTAAG	43038	GACGGAAGCAGAA GCGTCCCATTCAAA
42985	DGSTTVPFK	43012	GATGGGTCGACTAC TGTGCCTTTTAAG	43039	GACGGAAGCACAA CAGTCCCATTCAAA
42986	DGTARVPFK	43013	GATGGGACGGCGC GGGTGCCTTTTAAG	43040	GACGGAACAGCAA GAGTCCCATTCAAA
42987	DGTEKVPFK	43014	GATGGGACTGAGA AGGTGCCTTTTAAG	43041	GACGGAACAGAAA AAGTCCCATTCAAA
42988	DGTLHVPFK	43015	GATGGGACTCTGCA TGTGCCTTTTAAG	43042	GACGGAACACTCC ACGTCCCATTCAAA
42989	DGTLNVPFK	43016	GATGGGACTCTTAA TGTGCCTTTTAAG	43043	GACGGAACACTCA ACGTCCCATTCAAA
42990	DGTLQVPFK	43017	GATGGGACTCTGCA GGTGCCTTTTAAG	43044	GACGGAACACTCC AAGTCCCATTCAAA
42991	DGTLSVPFK	43018	GATGGGACGCTGA GTGTGCCTTTTAAG	43045	GACGGAACACTCA GCGTCCCATTCAAA
42992	DGTPLVPFK	43019	GATGGGACTCCTTT GGTGCCTTTTAAG	43046	GACGGAACACCAC TCGTCCCATTCAAA
42993	DGTPPVPFK	43020	GATGGGACTCCGCC TGTGCCTTTTAAG	43047	GACGGAACACCAC CAGTCCCATTCAAA
42994	DGTQAVPFK	43021	GATGGGACGCAGG CGGTGCCTTTTAAG	43048	GACGGAACACAAG CAGTCCCATTCAAA
42995	DGTREVPFK	43022	GATGGGACGCGTG AGGTGCCTTTTAAG	43049	GACGGAACAAGAG AAGTCCCATTCAAA
42996	DGTRQVPFK	43023	GATGGGACTAGGC AGGTGCCTTTTAAG	43050	GACGGAACAAGAC AAGTCCCATTCAAA
42997	DGTRTVPFK	43024	GATGGGACGCGTA CTGTGCCTTTTAAG	43051	GACGGAACAAGAA CAGTCCCATTCAAA

42998	DGTSKVPFK	43025	GATGGGACGAGTA AGGTGCCTTTTAAG	43052	GACGGAACAAGCA AAGTCCCATTCAAA
42999	DGTVNVPFK	43026	GATGGGACGGTTA ATGTGCCTTTTAAG	43053	GACGGAACAGTCA ACGTCCCATTCAAA

[0129] In any of the DNA and RNA sequences referenced and/or described herein, the single letter symbol has the following description: A for adenine; C for cytosine; G for guanine; T for thymine; U for Uracil; W for weak bases such as adenine or thymine; S for strong nucleotides such as cytosine and guanine; M for amino nucleotides such as adenine and cytosine; K for keto nucleotides such as guanine and thymine; R for purines adenine and guanine; Y for pyrimidine cytosine and thymine; B for any base that is not A (e.g., cytosine, guanine, and thymine); D for any base that is not C (e.g., adenine, guanine, and thymine); H for any base that is not G (e.g., adenine, cytosine, and thymine); V for any base that is not T (e.g., adenine, cytosine, and guanine); N for any nucleotide (which is not a gap); and Z is for zero.

[0130] In any of the amino acid sequences referenced and/or described herein, the single letter symbol has the following description: G (Gly) for Glycine; A (Ala) for Alanine; L (Leu) for Leucine; M (Met) for Methionine; F (Phe) for Phenylalanine; W (Trp) for Tryptophan; K (Lys) for Lysine; Q (Gln) for Glutamine; E (Glu) for Glutamic Acid; S (Ser) for Serine; P (Pro) for Proline; V (Val) for Valine; I (Ile) for Isoleucine; C (Cys) for Cysteine; Y (Tyr) for Tyrosine; H (His) for Histidine; R (Arg) for Arginine; N (Asn) for Asparagine; D (Asp) for Aspartic Acid; T (Thr) for Threonine; B (Asx) for Aspartic acid or Asparagine; J (Xle) for Leucine or Isoleucine; O (Pyl) for Pyrrolysine; U (Sec) for Selenocysteine; X (Xaa) for any amino acid; and Z (Glx) for Glutamine or Glutamic acid.

Use of targeting peptides in AAV particles

[0131] Targeting peptides may be stand-alone peptides or may be inserted into or conjugated to a parent sequence. In certain embodiments, the targeting peptides are inserted into the capsid protein of an AAV particle.

[0132] One or more targeting peptides may be inserted into a parent AAV capsid sequence to generate the AAV particles of the disclosure.

[0133] Targeting peptides may be inserted into a parent AAV capsid sequence in any location that results in fully functional AAV particles. The targeting peptide may be inserted in VP1, VP2 and/or VP3. Numbering of the amino acid residues differs across AAV serotypes, and so the exact amino acid position of the targeting peptide insertion may not be

critical. As used herein, amino acid positions of the parent AAV capsid sequence are described using AAV9 (SEQ ID NO: 2) as reference.

[0134] In certain embodiments, the targeting peptides are inserted in a hypervariable region of the AAV capsid sequence. Non-limiting examples of such hypervariable regions include Loop IV and Loop VIII of the parent AAV capsid. While not wishing to be bound by theory, these surface exposed loops are unstructured and poorly conserved, making them ideal regions for insertion of targeting peptides.

[0135] In certain embodiments, the targeting peptide is inserted into Loop IV. In another embodiment, the targeting peptide is used to replace a portion, or all of Loop IV. As a non-limiting example, addition of the targeting peptide to the parent AAV capsid sequence may result in the replacement or mutation of at least one amino acid of the parent AAV capsid.

[0136] In certain embodiments, the targeting peptide is inserted into Loop VIII. In another embodiment, the targeting peptide is used to replace a portion, or all of Loop VIII. As a non-limiting example, addition of the targeting peptide to the parent AAV capsid sequence may result in the replacement or mutation of at least one amino acid of the parent AAV capsid.

[0137] In certain embodiments, more than one targeting peptide is inserted into a parent AAV capsid sequence. As a non-limiting example, targeting peptides may be inserted at both Loop IV and Loop VIII in the same parent AAV capsid sequence.

[0138] Targeting peptides may be inserted at any amino acid position of the parent AAV capsid sequence, such as, but not limited to, between amino acids at positions 586-592, 588-589, 586-589, 452-458, 262-269, 464-473, 491-495, 546-557 and/or 659-668.

[0139] In a preferred embodiment, the targeting peptides are inserted into a parent AAV capsid sequence between amino acids at positions 588 and 589 (Loop VIII). In certain embodiments, the parent AAV capsid is AAV9 (SEQ ID NO: 2). In a second embodiment, the parent AAV capsid is K449R AAV9 (SEQ ID NO: 3).

[0140] The targeting peptides described herein may increase the transduction of the AAV particles of the disclosure to a target tissue as compared to the parent AAV particle lacking a targeting peptide insert. In certain embodiments, the targeting peptide increases the transduction of an AAV particle to a target tissue by at least about 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 100%, 125%, 150%, 200%, 300%, 400%, 500%, or more as compared to a parent AAV particle lacking a targeting peptide insert.

[0141] In certain embodiments, the targeting peptide increases the transduction of an AAV particle to a cell or tissue of the CNS by at least about 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 100%, 125%, 150%, 200%, 300%, 400%, 500%, or more as compared to a parent AAV particle lacking a targeting peptide insert.

[0142] In certain embodiments, the targeting peptide increases the transduction of an AAV particle to a cell or tissue of the PNS by at least about 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 100%, 125%, 150%, 200%, 300%, 400%, 500%, or more as compared to a parent AAV particle lacking a targeting peptide insert.

[0143] In certain embodiments, the targeting peptide increases the transduction of an AAV particle to a cell or tissue of the DRG by at least about 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 100%, 125%, 150%, 200%, 300%, 400%, 500%, or more as compared to a parent AAV particle lacking a targeting peptide insert.

Viral Genome of the AAV particle

[0144] AAV particles of the disclosure, comprising targeting peptides, may be used for the delivery of any viral genome to a target tissue (e.g., CNS and/or DRG). The viral genome may encode any payload, such as but not limited to a polypeptide, an antibody, an enzyme, an RNAi agent and/or components of a gene editing system. In certain embodiments, the AAV particles of the disclosure are used to deliver a payload to cells of the CNS, after intravenous delivery. In another embodiment, the AAV particles of the disclosure are used to deliver a payload to cells of the DRG, after intravenous delivery.

[0145] A viral genome of an AAV particle of the disclosure, comprises a nucleic acid sequence with at least one payload region encoding a payload, and at least one ITR. A viral genome typically comprises two ITR sequences, one at each of the 5' and 3' ends. Further, a viral genome of the AAV particles of the disclosure may comprise nucleic acid sequences for additional components, such as, but not limited to, a regulatory element (e.g., promoter), untranslated regions (UTR), a polyadenylation sequence (polyA), a filler or stuffer sequence, an intron, and/or a linker sequence for enhanced expression.

[0146] These viral genome components can be selected and/or engineered to further tailor the specificity and efficiency of expression of a given payload in a target tissue (e.g., CNS or DRG).

Viral Genome Component: Inverted Terminal Repeats (ITRs)

[0147] The AAV particles of the present disclosure comprise a viral genome with at least one ITR and a payload region. In certain embodiments, the viral genome has two ITRs. These two ITRs flank the payload region at the 5' and 3' ends. The ITRs function as origins of replication comprising recognition sites for replication. ITRs comprise sequence regions which can be complementary and symmetrically arranged. ITRs incorporated into viral genomes of the disclosure may be comprised of naturally occurring polynucleotide sequences or recombinantly derived polynucleotide sequences.

[0148] The ITRs may be derived from the same serotype as the capsid, selected from any of the known serotypes, or a derivative thereof. The ITR may be of a different serotype than the capsid. In certain embodiments, the AAV particle has more than one ITR. In a non-limiting example, the AAV particle has a viral genome comprising two ITRs. In certain embodiments, the ITRs are of the same serotype as one another. In another embodiment, the ITRs are of different serotypes. Non-limiting examples include zero, one or both of the ITRs having the same serotype as the capsid. In certain embodiments both ITRs of the viral genome of the AAV particle are AAV2 ITRs.

[0149] Independently, each ITR may be about 100 to about 150 nucleotides in length. An ITR may be about 100-105 nucleotides in length, 106-110 nucleotides in length, 111-115 nucleotides in length, 116-120 nucleotides in length, 121-125 nucleotides in length, 126-130 nucleotides in length, 131-135 nucleotides in length, 136-140 nucleotides in length, 141-145 nucleotides in length or 146-150 nucleotides in length. In certain embodiments, the ITRs are 140-142 nucleotides in length. Non-limiting examples of ITR length are 102, 105, 130, 140, 141, 142, 145 nucleotides in length. ITRs encompassed by the present disclosure include those with at least 90% identity, at least 95% identity, at least 98% identity, or at least 99% identity to a known AAV serotype ITR sequence.

Viral Genome Component: Promoters

[0150] In certain embodiments, the payload region of the viral genome comprises at least one element to enhance the payload target specificity and expression (See e.g., Powell et al. Viral Expression Cassette Elements to Enhance Transgene Target Specificity and Expression in Gene Therapy, 2015; the contents of which are herein incorporated by reference in their entirety). Non-limiting examples of elements to enhance payload target specificity and expression include promoters, endogenous miRNAs, post-transcriptional regulatory elements (PREs), polyadenylation (PolyA) signal sequences and upstream enhancers (USEs), CMV enhancers and introns.

[0151] A person skilled in the art may recognize that expression of a payload in a target cell may require a specific promoter, including but not limited to, a promoter that is species specific, inducible, tissue-specific, or cell cycle-specific (Parr et al., *Nat. Med.*3:1145-9 (1997); the contents of which are herein incorporated by reference in their entirety).

[0152] In certain embodiments, the promoter is deemed to be efficient when it drives expression of the payload encoded by the viral genome of the AAV particle.

[0153] In certain embodiments, the promoter is a promoter deemed to be efficient when it drives expression in a cell being targeted.

[0154] In certain embodiments, the promoter is a promoter having a tropism for a cell being targeted.

[0155] In certain embodiments, the promoter drives expression of the payload for a period of time in targeted tissues. Expression driven by a promoter may be for a period of 1 hour, 2, hours, 3 hours, 4 hours, 5 hours, 6 hours, 7 hours, 8 hours, 9 hours, 10 hours, 11 hours, 12 hours, 13 hours, 14 hours, 15 hours, 16 hours, 17 hours, 18 hours, 19 hours, 20 hours, 21 hours, 22 hours, 23 hours, 1 day, 2 days, 3 days, 4 days, 5 days, 6 days, 1 week, 8 days, 9 days, 10 days, 11 days, 12 days, 13 days, 2 weeks, 15 days, 16 days, 17 days, 18 days, 19 days, 20 days, 3 weeks, 22 days, 23 days, 24 days, 25 days, 26 days, 27 days, 28 days, 29 days, 30 days, 31 days, 1 month, 2 months, 3 months, 4 months, 5 months, 6 months, 7 months, 8 months, 9 months, 10 months, 11 months, 1 year, 13 months, 14 months, 15 months, 16 months, 17 months, 18 months, 19 months, 20 months, 21 months, 22 months, 23 months, 2 years, 3 years, 4 years, 5 years, 6 years, 7 years, 8 years, 9 years, 10 years or more than 10 years. Expression may be for 1-5 hours, 1-12 hours, 1-2 days, 1-5 days, 1-2 weeks, 1-3 weeks, 1-4 weeks, 1-2 months, 1-4 months, 1-6 months, 2-6 months, 3-6 months, 3-9 months, 4-8 months, 6-12 months, 1-2 years, 1-5 years, 2-5 years, 3-6 years, 3-8 years, 4-8 years or 5-10 years. As a non-limiting example, the promoter is a selected for sustained expression of a payload in tissues and/or cells of the central or peripheral nervous system.

[0156] Promoters may be naturally occurring or non-naturally occurring. Non-limiting examples of promoters include those derived from viruses, plants, mammals, or humans. In some embodiments, the promoters may be those derived from human cells or systems. In some embodiments, the promoter may be truncated or mutated.

[0157] Promoters which drive or promote expression in most tissues include, but are not limited to, the human elongation factor 1α-subunit (EF1α) promoter, the cytomegalovirus (CMV) immediate-early enhancer and/or promoter, the chicken β-actin (CBA) promoter and its derivative CAG, β glucuronidase (GUSB) promoter, or ubiquitin C

(UBC) promoter. Tissue-specific promoters can be used to restrict expression to certain cell types such as, but not limited to, cells of the central or peripheral nervous systems, targeted regions within (e.g., frontal cortex), and/or sub-sets of cells therein (e.g., excitatory neurons). As non-limiting examples, cell-type specific promoters may be used to restrict expression of a payload to excitatory neurons (e.g., glutamatergic), inhibitory neurons (e.g., GABA-ergic), neurons of the sympathetic or parasympathetic nervous system, sensory neurons, neurons of the dorsal root ganglia, motor neurons, or supportive cells of the nervous systems such as microglia, astrocytes, oligodendrocytes, and/or Schwann cells.

[0158] Cell-type specific promoters also exist for other tissues of the body, with non-limiting examples including, liver promoters (e.g., hAAT, TBG), skeletal muscle specific promoters (e.g., desmin, MCK, C512), B cell promoters, monocyte promoters, leukocyte promoters, macrophage promoters, pancreatic acinar cell promoters, endothelial cell promoters, lung tissue promoters, and/or cardiac or cardiovascular promoters (e.g., αMHC, cTnT, and CMV-MLC2k) .

[0159] Non-limiting examples of tissue-specific promoters for targeting payload expression to central nervous system tissues and cells include synapsin (Syn), glutamate vesicular transporter (VGLUT), vesicular GABA transporter (VGAT), parvalbumin (PV), sodium channel Na_V 1.8, tyrosine hydroxylase (TH), choline acetyltransferase (ChaT), methyl-CpG binding protein 2 (MeCP2), Ca^{2+}/calmodulin-dependent protein kinase II (CaMKII), metabotropic glutamate receptor 2 (mGluR2), neurofilament light (NFL) or heavy (NFH), neuron-specific enolase (NSE), β-globin minigene nβ2, preproenkephalin (PPE), enkephalin (Enk) and excitatory amino acid transporter 2 (EAAT2) promoters. Non-limiting examples of tissue-specific expression elements for astrocytes include glial fibrillary acidic protein (GFAP) and EAAT2 promoters. A non-limiting example of a tissue-specific expression element for oligodendrocytes includes the myelin basic protein (MBP) promoter.

[0160] In certain embodiments, the promoter may be less than 1 kb. The promoter may have a length of 200, 210, 220, 230, 240, 250, 260, 270, 280, 290, 300, 310, 320, 330, 340, 350, 360, 370, 380, 390, 400, 410, 420, 430, 440, 450, 460, 470, 480, 490, 500, 510, 520, 530, 540, 550, 560, 570, 580, 590, 600, 610, 620, 630, 640, 650, 660, 670, 680, 690, 700, 710, 720, 730, 740, 750, 760, 770, 780, 790, 800 or more than 800 nucleotides. The promoter may have a length between 200-300, 200-400, 200-500, 200-600, 200-700, 200-800, 300-400, 300-500, 300-600, 300-700, 300-800, 400-500, 400-600, 400-700, 400-800, 500-600, 500-700, 500-800, 600-700, 600-800 or 700-800 nucleotides.

[0161] In certain embodiments, the promoter may be a combination of two or more components of the same or different starting or parental promoters such as, but not limited to, CMV and CBA. Each component may have a length of 200, 210, 220, 230, 240, 250, 260, 270, 280, 290, 300, 310, 320, 330, 340, 350, 360, 370, 380, 381, 382, 383, 384, 385, 386, 387, 388, 389, 390, 400, 410, 420, 430, 440, 450, 460, 470, 480, 490, 500, 510, 520, 530, 540, 550, 560, 570, 580, 590, 600, 610, 620, 630, 640, 650, 660, 670, 680, 690, 700, 710, 720, 730, 740, 750, 760, 770, 780, 790, 800 or more than 800 nucleotides. Each component may have a length between 200-300, 200-400, 200-500, 200-600, 200-700, 200-800, 300-400, 300-500, 300-600, 300-700, 300-800, 400-500, 400-600, 400-700, 400-800, 500-600, 500-700, 500-800, 600-700, 600-800 or 700-800 nucleotides. In certain embodiments, the promoter is a combination of a 382 nucleotide CMV-enhancer sequence and a 260 nucleotide CBA-promoter sequence.

[0162] In certain embodiments, the viral genome comprises a ubiquitous promoter. Non-limiting examples of ubiquitous promoters include CMV, CBA (including derivatives CAG, CBh, etc.), EF-1α, PGK, UBC, GUSB (hGBp), and UCOE (promoter of HNRPA2B1-CBX3).

[0163] Yu et al. (Molecular Pain 2011, 7:63; the contents of which are herein incorporated by reference in their entirety) evaluated the expression of eGFP under the CAG, EFIα, PGK and UBC promoters in rat DRG cells and primary DRG cells using lentiviral vectors and found that UBC showed weaker expression than the other 3 promoters and only 10-12% glial expression was seen for all promoters. Soderblom et al. (E. Neuro 2015, 2(2): ENEURO.0001-15; the contents of which are herein incorporated by reference in their entirety) evaluated the expression of eGFP in AAV8 with CMV and UBC promoters and AAV2 with the CMV promoter after injection in the motor cortex. Intranasal administration of a plasmid containing a UBC or EFIα promoter showed a sustained airway expression greater than the expression with the CMV promoter (See e.g., Gill et al., Gene Therapy 2001, Vol. 8, 1539-1546; the contents of which are herein incorporated by reference in their entirety). Husain et al. (Gene Therapy 2009, 16(7): 927-932; the contents of which are herein incorporated by reference in their entirety) evaluated an HβH construct with a hGUSB promoter, a HSV-1LAT promoter and an NSE promoter and found that the HβH construct showed weaker expression than NSE in mouse brain. Passini and Wolfe (J. Virol. 2001, 12382-12392, the contents of which are herein incorporated by reference in their entirety) evaluated the long term effects of the HβH vector following an intraventricular injection in neonatal mice and found that there was sustained expression for at least 1 year. Low

expression in all brain regions was found by Xu et al. (Gene Therapy 2001, 8, 1323-1332; the contents of which are herein incorporated by reference in their entirety) when NFL and NFH promoters were used as compared to the CMV-lacZ, CMV-luc, EF, GFAP, hENK, nAChR, PPE, PPE + wpre, NSE (0.3 kb), NSE (1.8 kb) and NSE (1.8 kb + wpre). Xu et al. found that the promoter activity in descending order was NSE (1.8 kb), EF, NSE (0.3 kb), GFAP, CMV, hENK, PPE, NFL and NFH. NFL is a 650-nucleotide promoter and NFH is a 920 nucleotide promoter which are both absent in the liver but NFH is abundant in the sensory proprioceptive neurons, brain and spinal cord and NFH is present in the heart. SCN8A (Na_v 1.6) is a 470 nucleotide promoter which expresses throughout the DRG, spinal cord and brain with particularly high expression seen in the hippocampal neurons and cerebellar Purkinje cells, cortex, thalamus and hypothalamus (See e.g., Drews et al. *Identification of evolutionary conserved, functional noncoding elements in the promoter region of the sodium channel gene SCN8A,* Mamm Genome (2007) 18:723-731; and Raymond et al. *Expression of Alternatively Spliced Sodium Channel α-subunit genes,* Journal of Biological Chemistry (2004) 279(44) 46234-46241; the contents of each of which are herein incorporated by reference in their entireties).

[0164] Any of the promoters taught by the aforementioned Yu, Soderblom, Gill, Husain, Passini, Xu, Drews or Raymond may be used herein.

[0165] In certain embodiments, the promoter is not cell specific.

[0166] In certain embodiments, the promoter is a RNA pol III promoter. As a non-limiting example, the RNA pol III promoter is U6. As a non-limiting example, the RNA pol III promoter is H1.

[0167] In certain embodiments, the viral genome comprises an enhancer element.

[0168] In certain embodiments, the viral genome comprises an engineered promoter.

[0169] In another embodiment, the viral genome comprises a promoter from a naturally expressed protein.

Viral Genome Component: Untranslated Regions (UTRs)

[0170] By definition, wild type untranslated regions (UTRs) of a gene are transcribed but not translated. Generally, the 5' UTR starts at the transcription start site and ends at the start codon and the 3' UTR starts immediately following the stop codon and continues until the termination signal for transcription.

[0171] Features typically found in abundantly expressed genes of specific target organs (e.g., CNS tissue or DRG) may be engineered into UTRs to enhance stability and protein production. As a non-limiting example, a 5' UTR from mRNA normally expressed in the

brain (e.g., huntingtin) may be used in the viral genomes of the AAV particles of the disclosure to enhance expression in neuronal cells or other cells of the central nervous system.

[0172] While not wishing to be bound by theory, wild-type 5′ untranslated regions (UTRs) include features which play roles in translation initiation. Kozak sequences, which are commonly known to be involved in the process by which the ribosome initiates translation of many genes, are usually included in 5' UTRs. Kozak sequences have the consensus CCR(A/G)CCAUGG, where R is a purine (adenine or guanine) three bases upstream of the start codon (ATG), which is followed by another 'G'.

[0173] In certain embodiments, the 5'UTR in the viral genome includes a Kozak sequence.

[0174] In certain embodiments, the 5'UTR in the viral genome does not include a Kozak sequence.

[0175] While not wishing to be bound by theory, wild-type 3′ UTRs are known to have stretches of Adenosines and Uridines embedded therein. These AU rich signatures are particularly prevalent in genes with high rates of turnover. Based on their sequence features and functional properties, the AU rich elements (AREs) can be separated into three classes (Chen et al, 1995, the contents of which are herein incorporated by reference in its entirety): Class I AREs, such as, but not limited to, c-Myc and MyoD, contain several dispersed copies of an AUUUA motif within U-rich regions. Class II AREs, such as, but not limited to, GM-CSF and TNF-a, possess two or more overlapping UUAUUUA(U/A)(U/A) nonamers. Class III ARES, such as, but not limited to, c-Jun and Myogenin, are less well defined. These U rich regions do not contain an AUUUA motif. Most proteins binding to the AREs are known to destabilize the messenger, whereas members of the ELAV family, most notably HuR, have been documented to increase the stability of mRNA. HuR binds to AREs of all the three classes. Engineering the HuR specific binding sites into the 3′ UTR of nucleic acid molecules will lead to HuR binding and thus, stabilization of the message *in vivo*.

[0176] Introduction, removal or modification of 3′ UTR AU rich elements (AREs) can be used to modulate the stability of a polynucleotide. When engineering specific polynucleotides, e.g., payload regions of viral genomes, one or more copies of an ARE can be introduced to make polynucleotides less stable and thereby curtail translation and decrease production of the resultant protein. Likewise, AREs can be identified and removed or mutated to increase the intracellular stability and thus increase translation and production of the resultant protein.

[0177] In certain embodiments, the 3' UTR of the viral genome may include an oligo(dT) sequence for templated addition of a poly-A tail.

[0178] In certain embodiments, the viral genome may include at least one miRNA seed, binding site or full sequence. microRNAs (or miRNA or miR) are 19-25 nucleotide noncoding RNAs that bind to the sites of nucleic acid targets and down-regulate gene expression either by reducing nucleic acid molecule stability or by inhibiting translation. A microRNA sequence comprises a "seed" region, i.e., a sequence in the region of positions 2-8 of the mature microRNA, which has perfect Watson-Crick sequence complementarity to the miRNA target sequence of the nucleic acid.

[0179] In certain embodiments, the viral genome may be engineered to include, alter or remove at least one miRNA binding site, full sequence or seed region.

[0180] Any UTR from any gene known in the art may be incorporated into the viral genome of the AAV particle. These UTRs, or portions thereof, may be placed in the same orientation as in the gene from which they were selected or they may be altered in orientation or location. In certain embodiments, the UTR used in the viral genome of the AAV particle may be inverted, shortened, lengthened, made with one or more other 5′ UTRs or 3′ UTRs known in the art. As used herein, the term "altered" as it relates to a UTR, means that the UTR has been changed in some way in relation to a reference sequence. For example, a 3′ or 5′ UTR may be altered relative to a wild type or native UTR by the change in orientation or location as taught above or may be altered by the inclusion of additional nucleotides, deletion of nucleotides, swapping or transposition of nucleotides.

[0181] In certain embodiments, the viral genome of the AAV particle comprises at least one artificial UTR which is not a variant of a wild type UTR.

[0182] In certain embodiments, the viral genome of the AAV particle comprises UTRs which have been selected from a family of transcripts whose proteins share a common function, structure, feature or property.

Viral Genome Component: Polyadenylation Sequence

[0183] The viral genome of the AAV particles of the present disclosure may comprise at least one polyadenylation sequence. In certain embodiments, the viral genome of the AAV particle comprises a polyadenylation sequence between the 3' end of the payload encoding region and the 5' end of the 3'ITR.

[0184] In certain embodiments, the polyadenylation sequence or "polyA sequence" may range from absent to about 500 nucleotides in length. The polyadenylation sequence may be, but is not limited to, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22,

23, 24, 25, 26, 27, 28, 29, 30, 31, 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, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258, 259, 260, 261, 262, 263, 264, 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313, 314, 315, 316, 317, 318, 319, 320, 321, 322, 323, 324, 325, 326, 327, 328, 329, 330, 331, 332, 333, 334, 335, 336, 337, 338, 339, 340, 341, 342, 343, 344, 345, 346, 347, 348, 349, 350, 351, 352, 353, 354, 355, 356, 357, 358, 359, 360, 361, 362, 363, 364, 365, 366, 367, 368, 369, 370, 371, 372, 373, 374, 375, 376, 377, 378, 379, 380, 381, 382, 383, 384, 385, 386, 387, 388, 389, 390, 391, 392, 393, 394, 395, 396, 397, 398, 399, 400, 401, 402, 403, 404, 405, 406, 407, 408, 409, 410, 411, 412, 413, 414, 415, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427, 428, 429, 430, 431, 432, 433, 434, 435, 436, 437, 438, 439, 440, 441, 442, 443, 444, 445, 446, 447, 448, 449, 450, 451, 452, 453, 454, 455, 456, 457, 458, 459, 460, 461, 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, 479, 480, 481, 482, 483, 484, 485, 486, 487, 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, and 500 nucleotides in length.

[0185] In certain embodiments, the polyadenylation sequence is 50-100 nucleotides in length.

[0186] In certain embodiments, the polyadenylation sequence is 50-150 nucleotides in length.

[0187] In certain embodiments, the polyadenylation sequence is 50-160 nucleotides in length.

[0188] In certain embodiments, the polyadenylation sequence is 50-200 nucleotides in length.

[0189] In certain embodiments, the polyadenylation sequence is 60-100 nucleotides in length.

[0190] In certain embodiments, the polyadenylation sequence is 60-150 nucleotides in length.

[0191] In certain embodiments, the polyadenylation sequence is 60-160 nucleotides in length.

[0192] In certain embodiments, the polyadenylation sequence is 60-200 nucleotides in length.

[0193] In certain embodiments, the polyadenylation sequence is 70-100 nucleotides in length.

[0194] In certain embodiments, the polyadenylation sequence is 70-150 nucleotides in length.

[0195] In certain embodiments, the polyadenylation sequence is 70-160 nucleotides in length.

[0196] In certain embodiments, the polyadenylation sequence is 70-200 nucleotides in length.

[0197] In certain embodiments, the polyadenylation sequence is 80-100 nucleotides in length.

[0198] In certain embodiments, the polyadenylation sequence is 80-150 nucleotides in length.

[0199] In certain embodiments, the polyadenylation sequence is 80-160 nucleotides in length.

[0200] In certain embodiments, the polyadenylation sequence is 80-200 nucleotides in length.

[0201] In certain embodiments, the polyadenylation sequence is 90-100 nucleotides in length.

[0202] In certain embodiments, the polyadenylation sequence is 90-150 nucleotides in length.

[0203] In certain embodiments, the polyadenylation sequence is 90-160 nucleotides in length.

[0204] In certain embodiments, the polyadenylation sequence is 90-200 nucleotides in length.

Viral Genome Component: Introns

[0205] In certain embodiments, the viral genome of the AAV particles of the present disclosure comprises at least one element to enhance the payload target specificity and expression (See e.g., Powell et al. *Viral Expression Cassette Elements to Enhance Transgene Target Specificity and Expression in Gene Therapy*, Discov. Med, 2015, 19(102): 49-57; the contents of which are herein incorporated by reference in their entirety) such as an intron. Non-limiting examples of introns include, MVM (67-97 bps), F.IX truncated intron 1 (300 bps), β-globin SD/immunoglobulin heavy chain splice acceptor (250 bps), adenovirus splice donor/immunoglobin splice acceptor (500 bps), SV40 late splice donor/splice acceptor (19S/16S) (180 bps) and hybrid adenovirus splice donor/IgG splice acceptor (230 bps).

[0206] In certain embodiments, the intron or intron portion may be 100-500 nucleotides in length. The intron may have a length of 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 190, 200, 210, 220, 230, 240, 250, 260, 270, 280, 290, 300, 310, 320, 330, 340, 350, 360, 370, 380, 390, 400, 410, 420, 430, 440, 450, 460, 470, 480, 490 or 500 nucleotides. The intron may have a length between 80-100, 80-120, 80-140, 80-160, 80-180, 80-200, 80-250, 80-300, 80-350, 80-400, 80-450, 80-500, 200-300, 200-400, 200-500, 300-400, 300-500, or 400-500 nucleotides.

Viral Genome Component: Stuffer sequences

[0207] In certain embodiments, the viral genome of the AAV particles of the present disclosure comprises at least one element to improve packaging efficiency and expression, such as a stuffer or filler sequence. Non-limiting examples of stuffer sequences include albumin and/or alpha-1 antitrypsin. Any known viral, mammalian, or plant sequence may be manipulated for use as a stuffer sequence.

[0208] In certain embodiments, the stuffer or filler sequence may be from about 100-3500 nucleotides in length. The stuffer sequence may have a length of about 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1100, 1200, 1300, 1400, 1500, 1600, 1700, 1800, 1900, 2000, 2100, 2200, 2300, 2400, 2500, 2600, 2700, 2800, 2900 or 3000 nucleotides.

Viral Genome Component: miRNA

[0209] In certain embodiments, the viral genome comprises at least one sequence encoding a miRNA to reduce the expression of the payload in an "off-target" tissue. As used herein, "off-target" indicates a tissue or cell-type unintentionally targeted by the AAV particles of the disclosure. As an example, an "off-target" tissue or cell when targeting the DRG, may be neurons of other ganglia, such as those of the sympathetic or parasympathetic nervous system. miRNAs and their targeted tissues are well known in the art. As a non-

limiting example, a miR-122 miRNA may be encoded in the viral genome to reduce the expression of the viral genome in the liver.

Viral Genome Component: Selectable marker

[0210] In some embodiments, the viral genome of the AAV particles of the disclosure optionally encodes a selectable marker. The selectable marker may comprise a cell-surface marker, such as any protein expressed on the surface of the cell including, but not limited to receptors, CD markers, lectins, integrins, or truncated versions thereof.

[0211] In some embodiments, selectable marker reporter genes are described in International Publication Nos. WO 1996023810 and WO 1996030540; Heim et al., Current Biology 2:178-182 (1996); Heim et al., Proc. Natl. Acad. Sci. USA (1995); or Heim et al., Science 373:663-664 (1995), the contents of each of which are incorporated herein by reference in their entirety.

Genome Size

[0212] In certain embodiments, the AAV particles of the disclosure may comprise a single-stranded or double-stranded viral genome. The size of the viral genome may be small, medium, large or the maximum size. As described above, the viral genome may comprise a promoter and a polyA tail.

[0213] In certain embodiments, the viral genome may be a small single stranded viral genome. A small single stranded viral genome may be 2.1 to 3.5 kb in size such as, but not limited to, about 2.1, 2.2, 2.3, 2.4, 2.5, 2.6, 2.7, 2.8, 2.9, 3.0, 3.1, 3.2, 3.3, 3.4, and 3.5 kb in size.

[0214] In certain embodiments, the viral genome may be a small double stranded viral genome. A small double stranded viral genome may be 1.3 to 1.7 kb in size such as, but not limited to, about 1.3, 1.4, 1.5, 1.6, and 1.7 kb in size.

[0215] In certain embodiments, the viral genome may be a medium single stranded viral genome. A medium single stranded viral genome may be 3.6 to 4.3 kb in size such as, but not limited to, about 3.6, 3.7, 3.8, 3.9, 4.0, 4.1, 4.2 and 4.3 kb in size.

[0216] In certain embodiments, the viral genome may be a medium double stranded viral genome. A medium double stranded viral genome may be 1.8 to 2.1 kb in size such as, but not limited to, about 1.8, 1.9, 2.0, and 2.1 kb in size.

[0217] In certain embodiments, the viral genome may be a large single stranded viral genome. A large single stranded viral genome may be 4.4 to 6.0 kb in size such as, but not limited to, about 4.4, 4.5, 4.6, 4.7, 4.8, 4.9, 5.0, 5.1, 5.2, 5.3, 5.4, 5.5, 5.6, 5.7, 5.8, 5.9 and 6.0 kb in size.

[0218] In certain embodiments, the viral genome may be a large double stranded viral genome. A large double stranded viral genome may be 2.2 to 3.0 kb in size such as, but not limited to, about 2.2, 2.3, 2.4, 2.5, 2.6, 2.7, 2.8, 2.9 and 3.0 kb in size.

Payloads

[0219] The AAV particles of the present disclosure comprise a viral genome with at least one payload region. As used herein, a "payload region" is any nucleic acid sequence (e.g., within the viral genome) which encodes one or more "payloads" of the disclosure. As non-limiting examples, a payload region may be a nucleic acid sequence within the viral genome of an AAV particle, which encodes a payload, wherein the payload is an RNAi agent or a polypeptide. Payloads of the present disclosure may be, but are not limited to, peptides, polypeptides, proteins, antibodies, RNAi agents, etc.

[0220] The payload region may comprise a combination of coding and non-coding nucleic acid sequences.

[0221] In some embodiments, the payload region may encode a coding or non-coding RNA.

[0222] In certain embodiments, the AAV particle comprises a viral genome with a payload region encoding more than one payload of interest. In such an embodiment, a viral genome encoding more than one payload may be replicated and packaged into a viral particle. A target cell transduced with a viral particle comprising more than one payload may express each of the payloads in a single cell.

Polypeptides

[0223] Where the payload region encodes a polypeptide, the polypeptide may be a peptide or protein. As a non-limiting example, the payload region may encode at least one allele of apolipoprotein E (APOE) such as, but not limited to ApoE2, ApoE3 and/or ApoE4. In certain embodiments, the payload region encodes ApoE2 (cys112, cys158). In certain embodiments, the payload region encodes ApoE3 (cys112, arg158). In certain embodiments, the payload region of the encodes ApoE4 (arg112, arg158). As a second non-limiting example, the payload region may encode a human or a primate frataxin protein, or fragment or variant thereof. As another non-limiting example, the payload region may encode an antibody, or a fragment thereof. As another non-limiting example, the payload region may encode human aromatic L-amino acid decarboxylase (AADC), or a fragment or variant thereof. As another non-limiting example, the payload region may encode human survival of motor neuron (SMN) 1 or SMN2, or fragments or variants thereof. As another non-limiting example, the payload region may encode frataxin (FXN). As another non-limiting example, the payload

region may encode APOE (APOE2, APOE3, APOE4), or fragments or variants thereof. As another non-limiting example, the payload region may encode glucocerebrosidase (GBA1), or a fragment or variant thereof. As another non-limiting example, the payload region may encode granulin precursor or progranulin (GRN), or a fragment or variant thereof. As another non-limiting example, the payload region may encode aspartoacylase (ASPA), or a fragment or variant thereof. As another non-limiting example, the payload region may encode tripeptidyl peptidase I (CLN2), or a fragment or variant thereof. As another non-limiting example, the payload region may encode beta-galactosidase (GLB1), or a fragment or variant thereof. As another non-limiting example, the payload region may encode N-sulphoglucosamine sulphohydrolase (SGSH), or a fragment or variant thereof. As another non-limiting example, the payload region may encode N-acetyl-alpha-glucosaminidase (NAGLU), or a fragment or variant thereof. As another non-limiting example, the payload region may encode iduronate 2-sulfatase (IDS), or a fragment or variant thereof. As another non-limiting example, the payload region may encode Intracellular cholesterol transporter (NPC1), or a fragment or variant thereof. As another non-limiting example, the payload region may encode gigaxonin (GAN), or a fragment or variant thereof. The AAV viral genomes encoding polypeptides described herein may be useful in the fields of human disease, viruses, infections veterinary applications and a variety of *in vivo* and *in vitro* settings.

[0224] Amino acid sequences encoded by payload regions of the viral genomes of the disclosure may be translated as a whole polypeptide, a plurality of polypeptides or fragments of polypeptides, which independently may be encoded by one or more nucleic acids, fragments of nucleic acids or variants of any of the aforementioned. As used herein, "polypeptide" means a polymer of amino acid residues (natural or unnatural) linked together most often by peptide bonds. The term, as used herein, refers to proteins, polypeptides, and peptides of any size, structure, or function. In some instances, the polypeptide encoded is smaller than about 50 amino acids and the polypeptide is then termed a peptide. If the polypeptide is a peptide, it will be at least about 2, 3, 4, or at least 5 amino acid residues long. Thus, polypeptides include gene products, naturally occurring polypeptides, synthetic polypeptides, homologs, orthologs, paralogs, fragments and other equivalents, variants, and analogs of the foregoing. A polypeptide may be a single molecule or may be a multi-molecular complex such as a dimer, trimer or tetramer. They may also comprise single chain or multichain polypeptides and may be associated or linked. The term polypeptide may also

apply to amino acid polymers in which one or more amino acid residues are an artificial chemical analogue of a corresponding naturally occurring amino acid.

[0225] The term "polypeptide variant" refers to molecules which differ in their amino acid sequence from a native or reference sequence. The amino acid sequence variants may possess substitutions, deletions, and/or insertions at certain positions within the amino acid sequence, as compared to a native or reference sequence. Ordinarily, variants will possess at least about 50% identity (homology) to a native or reference sequence, and preferably, they will be at least about 80%, more preferably at least about 90% identical (homologous) to a native or reference sequence.

Antibodies

[0226] Where the payload region encodes an antibody, the "antibody" may be an antibody, a fragment, or any derivative thereof, which may contribute to the formation of a "functional antibody", exhibiting the desired biological activity. As non-limiting examples, an antibody may be a native antibody (e.g., with two heavy and two light chains), a heavy chain variable region, a light chain variable region, a heavy chain constant region, a light chain constant region, Fab, Fab', $F(ab')_2$, Fv, or scFv fragments, a diabody, a linear antibody, a single-chain antibody, a multi-specific antibody, an intrabody, one or more heavy chain complementarity determining regions (CDR), one or more light chain CDRs, a bi-specific antibody, a monoclonal antibody, a polyclonal antibody, a humanized antibody, an antibody mimetic, an antibody variant, a miniaturized antibody, a unibody, a maxibody, and/or a chimeric antigen receptor.

[0227] As used herein, "antibody-based" or "antibody-derived" compositions are monomeric or multi-meric polypeptides which comprise at least one amino-acid region derived from a known or parental antibody sequence and at least one amino acid region derived from a non-antibody sequence, e.g., mammalian protein.

[0228] Payload regions may encode polypeptides that form or function as any antibody, including antibodies that are known in the art and/or antibodies that are commercially available. The encoded antibodies may be therapeutic, diagnostic, or for research purposes. The encoded antibodies may be useful in the treatment of neurological disease or any disorders associated with the central and/or peripheral nervous systems.

[0229] In certain embodiments, the viral genome of the AAV particle may comprise nucleic acids which have been engineered to enable or enhance the expression of antibodies, antibody fragments, or components thereof.

[0230] Antibodies encoded in payload regions of the AAV particles of the present disclosure may be, but are not limited to, antibodies targeting β-amyloid, APOE, tau, SOD1, TDP43, huntingtin, and/or synuclein.

RNAi agents

[0231] RNAi (also known as post-transcriptional gene silencing (PTGS), quelling, or co-suppression) is a post-transcriptional gene silencing process in which RNA molecules, in a sequence specific manner, inhibit gene expression, typically by causing the destruction of specific mRNA molecules. RNAi mediated gene silencing can specifically inhibit targeted gene expression. Where the payload region of the viral genome of the AAV particles of the present disclosure encodes an RNAi agent, the RNAi agent may be, but is not limited to, dsRNA, siRNA, shRNA, pre-miRNA, pri-miRNA, miRNA, stRNA, lncRNA, piRNA, or snoRNA. Non-limiting examples of a target gene of an RNAi agent include, SOD1, MAPT, APOE, HTT, C9ORF72, TDP-43, APP, BACE, SNCA, ATXN1, ATXN2, ATXN3, ATXN7, SCN1A-SCN5A, or SCN8A-SCN11A.

[0232] The AAV particles of the present disclosure may comprise viral genomes encoding RNAi agents, wherein the RNAi agent targets the mRNA of a gene of interest to interfere with gene expression and/or protein production. Such AAV particles may be used as a therapeutic, a diagnostic, or for research purposes.

[0233] In certain embodiments, the RNAi agent may target the gene of interest along any segment of their respective nucleotide sequence.

[0234] In certain embodiments, the RNAi agent may target the gene of interest at the location of a single-nucleotide polymorphism (SNP) or variant within the nucleotide sequence.

[0235] In some embodiments, a nucleic acid sequence encoding an RNAi agent, or a single strand of an RNAi agent, is inserted into the viral genome of the AAV particle and introduced into cells, specifically cells in the central nervous system or cells of the DRG.

[0236] The RNAi agent may be an siRNA duplex, wherein the siRNA duplex contains an antisense strand (guide strand) and a sense strand (passenger strand) hybridized together forming a duplex structure, wherein the antisense strand is complementary to the nucleic acid sequence of the targeted gene, and wherein the sense strand is homologous to the nucleic acid sequence of the targeted gene. In some aspects, the 5'end of the antisense strand has a 5' phosphate group and the 3'end of the sense strand contains a 3'hydroxyl group. In other aspects, there are none, one or 2 nucleotide overhangs at the 3'end of each strand.

[0237] Each strand of an siRNA duplex targeting a gene of interest may be about 19 to 25, 19 to 24 or 19 to 21 nucleotides in length, preferably about 19 nucleotides, 20 nucleotides, 21 nucleotides, 22 nucleotides, 23 nucleotides, 24 nucleotides, or 25 nucleotides in length.

[0238] In certain embodiments, an siRNA or dsRNA includes at least two sequences that are complementary to each other. The dsRNA includes a sense strand having a first sequence and an antisense strand having a second sequence. The antisense strand includes a nucleotide sequence that is substantially complementary to at least part of an mRNA encoding the target gene, and the region of complementarity is 30 nucleotides or less, and at least 15 nucleotides in length. Generally, the dsRNA is 19 to 25, 19 to 24 or 19 to 21 nucleotides in length. In some embodiments, the dsRNA is from about 15 to about 25 nucleotides in length, and in other embodiments the dsRNA is from about 25 to about 30 nucleotides in length. In some embodiments, the dsRNA is about 15 nucleotides in length, 16 nucleotides in length,17 nucleotides in length, 18 nucleotides in length, 19 nucleotides, 20 nucleotides, 21 nucleotides, 22 nucleotides, 23 nucleotides, 24 nucleotides, 25 nucleotides in length, 26 nucleotides in length, 27 nucleotides in length, 28 nucleotides in length, 29 nucleotides in length, or 30 nucleotides in length.

[0239] The dsRNA, whether directly administered or encoded in a viral genome in an AAV particle, upon contacting with a cell expressing the target protein, inhibits the expression of the protein by at least 10%, at least 20%, at least 25%, at least 30%, at least 35% or at least 40% or more, such as when assayed by a method known in the art.

[0240] In certain embodiments, the RNAi agent may be used to reduce the expression of target protein by at least about 30%, 40%, 50%, 60%, 70%, 80%, 85%, 90%, 95% and 100%, or at least 20-30%, 20-40%, 20-50%, 20-60%, 20-70%, 20-80%, 20-90%, 20-95%, 20-100%, 30-40%, 30-50%, 30-60%, 30-70%, 30-80%, 30-90%, 30-95%, 30-100%, 40-50%, 40-60%, 40-70%, 40-80%, 40-90%, 40-95%, 40-100%, 50-60%, 50-70%, 50-80%, 50-90%, 50-95%, 50-100%, 60-70%, 60-80%, 60-90%, 60-95%, 60-100%, 70-80%, 70-90%, 70-95%, 70-100%, 80-90%, 80-95%, 80-100%, 90-95%, 90-100% or 95-100%. As a non-limiting example, the expression of target protein expression may be reduced 50-90%.

[0241] In certain embodiments, the RNAi agent may be used to reduce the expression of target mRNA by at least about 30%, 40%, 50%, 60%, 70%, 80%, 85%, 90%, 95% and 100%, or at least 20-30%, 20-40%, 20-50%, 20-60%, 20-70%, 20-80%, 20-90%, 20-95%, 20-100%, 30-40%, 30-50%, 30-60%, 30-70%, 30-80%, 30-90%, 30-95%, 30-100%, 40-50%, 40-60%, 40-70%, 40-80%, 40-90%, 40-95%, 40-100%, 50-60%, 50-70%, 50-80%, 50-90%, 50-95%, 50-100%, 60-70%, 60-80%, 60-90%, 60-95%, 60-100%, 70-80%, 70-90%, 70-95%, 70-

100%, 80-90%, 80-95%, 80-100%, 90-95%, 90-100% or 95-100%. As a non-limiting example, the expression of target mRNA expression may be reduced 50-90%.

[0242] In certain embodiments, RNAi agent may be used to reduce the expression of target protein and/or mRNA in at least one region of the CNS. The expression of target protein and/or mRNA is reduced by at least about 30%, 40%, 50%, 60%, 70%, 80%, 85%, 90%, 95% and 100%, or at least 20-30%, 20-40%, 20-50%, 20-60%, 20-70%, 20-80%, 20-90%, 20-95%, 20-100%, 30-40%, 30-50%, 30-60%, 30-70%, 30-80%, 30-90%, 30-95%, 30-100%, 40-50%, 40-60%, 40-70%, 40-80%, 40-90%, 40-95%, 40-100%, 50-60%, 50-70%, 50-80%, 50-90%, 50-95%, 50-100%, 60-70%, 60-80%, 60-90%, 60-95%, 60-100%, 70-80%, 70-90%, 70-95%, 70-100%, 80-90%, 80-95%, 80-100%, 90-95%, 90-100% or 95-100% in at least one region of the CNS. As a non-limiting example, the expression of target protein and mRNA in neurons (e.g., cortical neurons) is reduced by 50-90%. As a non-limiting example, the expression of target protein and mRNA in neurons (e.g., cortical neurons) is reduced by 40-50%.

[0243] In some embodiments, the AAV particle of the present disclosure comprising a viral genome encoding at least one RNAi agent targeting a gene of interest is administered to a subject in need for treating and/or ameliorating a disease, e.g., a neurological disorder of any disease associated with the central or peripheral nervous systems.

[0244] In certain embodiments, the RNAi agent is an siRNA.

Design of siRNA

[0245] AAV particles of the present disclosure may comprise a viral genome encoding one or more siRNA molecules (e.g., siRNA duplexes or encoded dsRNA) that are specifically designed to target a gene of interest and suppress target gene expression and protein production. In some aspects, the siRNA molecules are designed and used to selectively "knock out" target gene variants in cells, i.e., transcripts that are identified in neurological disease. In some aspects, the siRNA molecules are designed and used to selectively "knock down" target gene variants in cells.

[0246] In some embodiments, siRNA molecules targeting a gene of interest may be designed using any available design tools.

[0247] Some guidelines for designing siRNAs (for insertion into a viral genome of the AAV particles of the disclosure) have been proposed in the art. These guidelines generally recommend generating a 19-nucleotide duplexed region, symmetric 2-3 nucleotide 3'overhangs, 5-phosphate and 3-hydroxyl groups targeting a region in the gene to be silenced. Other rules that may govern siRNA sequence preference include, but are not limited

to, (i) A/U at the 5′ end of the antisense strand; (ii) G/C at the 5′ end of the sense strand; (iii) at least five A/U residues in the 5′ terminal one-third of the antisense strand; and (iv) the absence of any GC stretch of more than 9 nucleotides in length. In accordance with such considerations, together with the specific sequence of a target gene, highly effective siRNA molecules essential for suppressing mammalian target gene expression may be readily designed.

[0248] In certain embodiments, the sense and/or antisense strand is designed based on the method and rules outlined in European Patent Publication No. EP1752536, the contents of which are herein incorporated by reference in their entirety. As a non-limiting example, the 3'-terminal base of the sequence is adenine, thymine or uracil. As a non-limiting example, the 5'-terminal base of the sequence is guanine or cytosine. As a non-limiting example, the 3'-terminal sequence comprises seven bases rich in one or more bases of adenine, thymine and uracil.

[0249] In certain embodiments, an siRNA molecule comprises a sense strand and a complementary antisense strand in which both strands are hybridized together to form a duplex structure. The antisense strand has sufficient complementarity to the target mRNA sequence to direct target-specific RNAi, i.e., the siRNA molecule has a sequence sufficient to trigger the destruction of the target mRNA by the RNAi machinery or process.

[0250] In some embodiments, the antisense strand and target mRNA sequences have 100% complementarity. The antisense strand may be complementary to any part of the target mRNA sequence. Neither the identity of the sense sequence nor the homology of the antisense sequence need be 100% complementary to the target.

[0251] In other embodiments, the antisense strand and target mRNA sequences comprise at least one mismatch. As a non-limiting example, the antisense strand and the target mRNA sequence have at least 30%, 40%, 50%, 60%, 70%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% or at least 20-30%, 20-40%, 20-50%, 20-60%, 20-70%, 20-80%, 20-90%, 20-95%, 20-99%, 30-40%, 30-50%, 30-60%, 30-70%, 30-80%, 30-90%, 30-95%, 30-99%, 40-50%, 40-60%, 40-70%, 40-80%, 40-90%, 40-95%, 40-99%, 50-60%, 50-70%, 50-80%, 50-90%, 50-95%, 50-99%, 60-70%, 60-80%, 60-90%, 60-95%, 60-99%, 70-80%, 70-90%, 70-95%, 70-99%, 80-90%, 80-95%, 80-99%, 90-95%, 90-99% or 95-99% complementary.

[0252] The siRNA molecule may have a length from about 10-50 or more nucleotides, i.e., each strand comprising 10-50 nucleotides (or nucleotide analogs). Preferably, the siRNA molecule has a length from about 15-30, e.g., 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26,

27, 28, 29, or 30 nucleotides in each strand, wherein one of the strands is sufficiently complementary to a target region. In certain embodiments, the siRNA molecule has a length from about 19 to 25, 19 to 24 or 19 to 21 nucleotides.

[0253] In some embodiments, the siRNA molecule can be a synthetic RNA duplex comprising about 19 nucleotides to about 25 nucleotides, and two overhanging nucleotides at the 3'-end.

[0254] The siRNA molecule may comprise an antisense sequence and a sense sequence, or a fragment or variant thereof. As a non-limiting example, the antisense sequence and the sense sequence have at least 30%, 40%, 50%, 60%, 70%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% or at least 20-30%, 20-40%, 20-50%, 20-60%, 20-70%, 20-80%, 20-90%, 20-95%, 20-99%, 30-40%, 30-50%, 30-60%, 30-70%, 30-80%, 30-90%, 30-95%, 30-99%, 40-50%, 40-60%, 40-70%, 40-80%, 40-90%, 40-95%, 40-99%, 50-60%, 50-70%, 50-80%, 50-90%, 50-95%, 50-99%, 60-70%, 60-80%, 60-90%, 60-95%, 60-99%, 70-80%, 70-90%, 70-95%, 70-99%, 80-90%, 80-95%, 80-99%, 90-95%, 90-99% or 95-99% complementary.

[0255] The sense and antisense sequences may be completely complementary across a substantial portion of their length. In other embodiments, the sense sequence and antisense sequence may be at least 70, 80, 90, 95 or 99% complementary across independently at least 50, 60, 70, 80, 85, 90, 95, or 99% of the length of the strands.

[0256] In some embodiments, the sense and antisense strands of a siRNA duplex are linked by a short spacer sequence leading to the expression of a stem-loop structure termed short hairpin RNA (shRNA). The hairpin is recognized and cleaved by Dicer, thus generating mature siRNA molecules.

[0257] In some embodiments, the siRNA molecules, as well as associated spacer and/or flanking regions once designed, can be encoded by the viral genome of the AAV particles of the present disclosure, for delivery to a cell.

Molecular Scaffold

[0258] In certain embodiments, the siRNA molecules may be encoded in a modulatory polynucleotide which also comprises a molecular scaffold. As used herein a "molecular scaffold" is a framework or starting molecule that forms the sequence or structural basis against which to design or make a subsequent molecule.

[0259] In certain embodiments, the modulatory polynucleotide which comprises the payload (e.g., siRNA, miRNA or other RNAi agent described herein) includes a molecular scaffold which comprises at least one 5' flanking sequence which may be of any length and

may be derived in whole or in part from wild type microRNA sequence or be completely artificial. A 3' flanking sequence may mirror the 5' flanking sequence in size and origin. Either flanking sequence may be absent. In certain embodiments, both the 5' and 3' flanking sequences are absent. The 3' flanking sequence may optionally contain one or more CNNC motifs, where "N" represents any nucleotide.

[0260] In some embodiments the 5' and 3' flanking sequences are the same length.

[0261] In some embodiments the 5' flanking sequence is from 1-10 nucleotides in length, from 5-15 nucleotides in length, from 10-30 nucleotides in length, from 20-50 nucleotides in length, greater than 40 nucleotides in length, greater than 50 nucleotides in length, greater than 100 nucleotides in length or greater than 200 nucleotides in length.

[0262] In some embodiments, the 5' flanking sequence may be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 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, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258, 259, 260, 261, 262, 263, 264, 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313, 314, 315, 316, 317, 318, 319, 320, 321, 322, 323, 324, 325, 326, 327, 328, 329, 330, 331, 332, 333, 334, 335, 336, 337, 338, 339, 340, 341, 342, 343, 344, 345, 346, 347, 348, 349, 350, 351, 352, 353, 354, 355, 356, 357, 358, 359, 360, 361, 362, 363, 364, 365, 366, 367, 368, 369, 370, 371, 372, 373, 374, 375, 376, 377, 378, 379, 380, 381, 382, 383, 384, 385, 386, 387, 388, 389, 390, 391, 392, 393, 394, 395, 396, 397, 398, 399, 400, 401, 402, 403, 404, 405, 406, 407, 408, 409, 410, 411, 412, 413, 414, 415, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427, 428, 429, 430, 431, 432, 433, 434, 435, 436, 437, 438, 439, 440, 441, 442, 443, 444, 445, 446, 447, 448, 449,

450, 451, 452, 453, 454, 455, 456, 457, 458, 459, 460, 461, 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, 479, 480, 481, 482, 483, 484, 485, 486, 487, 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, or 500 nucleotides in length.

[0263] In certain embodiments, the molecular scaffold comprises at least one 3' flanking region. As a non-limiting example, the 3' flanking region may comprise a 3' flanking sequence which may be of any length and may be derived in whole or in part from wild type microRNA sequence or be a completely artificial sequence.

[0264] In some embodiments the 3' flanking sequence is from 1-10 nucleotides in length, from 5-15 nucleotides in length, from 10-30 nucleotides in length, from 20-50 nucleotides in length, greater than 40 nucleotides in length, greater than 50 nucleotides in length, greater than 100 nucleotides in length or greater than 200 nucleotides in length.

[0265] In some embodiments, the 3' flanking sequence may be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 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, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258, 259, 260, 261, 262, 263, 264, 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313, 314, 315, 316, 317, 318, 319, 320, 321, 322, 323, 324, 325, 326, 327, 328, 329, 330, 331, 332, 333, 334, 335, 336, 337, 338, 339, 340, 341, 342, 343, 344, 345, 346, 347, 348, 349, 350, 351, 352, 353, 354, 355, 356, 357, 358, 359, 360, 361, 362, 363, 364, 365, 366, 367, 368, 369, 370, 371, 372, 373, 374, 375, 376, 377, 378, 379, 380, 381, 382, 383, 384, 385, 386, 387, 388, 389, 390, 391, 392, 393, 394, 395, 396, 397, 398, 399, 400, 401, 402, 403, 404, 405, 406, 407, 408, 409, 410, 411, 412, 413,

414, 415, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427, 428, 429, 430, 431, 432, 433, 434, 435, 436, 437, 438, 439, 440, 441, 442, 443, 444, 445, 446, 447, 448, 449, 450, 451, 452, 453, 454, 455, 456, 457, 458, 459, 460, 461, 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, 479, 480, 481, 482, 483, 484, 485, 486, 487, 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, or 500 nucleotides in length.

[0266] In some embodiments the 5' and 3' flanking sequences are the same sequence. In some embodiments they differ by 2%, 3%, 4%, 5%, 10%, 20% or more than 30% when aligned to each other.

[0267] Forming the stem of a stem loop structure is a minimum of at least one payload sequence. In some embodiments, the payload sequence comprises at least one nucleic acid sequence which is in part complementary or will hybridize to the target sequence. In some embodiments, the payload is an siRNA molecule or fragment of an siRNA molecule.

[0268] In some embodiments, the 5' arm of the stem loop comprises a sense sequence.

[0269] In some embodiments, the 3' arm of the stem loop comprises an antisense sequence. The antisense sequence, in some instances, comprises a "G" nucleotide at the 5' most end.

[0270] In other embodiments, the sense sequence may reside on the 3' arm while the antisense sequence resides on the 5' arm of the stem of the stem loop structure.

[0271] Separating the sense and antisense sequence of the stem loop structure is a loop (also known as a loop motif). The loop may be of any length, between 4-30 nucleotides, between 4-20 nucleotides, between 4-15 nucleotides, between 5-15 nucleotides, between 6-12 nucleotides, 6 nucleotides, 7, nucleotides, 8 nucleotides, 9 nucleotides, 10 nucleotides, 11 nucleotides, and/or 12 nucleotides.

[0272] In some embodiments, the loop comprises at least one UGUG motif. In some embodiments, the UGUG motif is located at the 5' terminus of the loop.

[0273] Spacer regions may be present in the modulatory polynucleotide to separate one or more modules from one another. There may be one or more such spacer regions present.

[0274] In certain embodiments, a spacer region of between 8-20, i.e., 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 nucleotides may be present between the sense sequence and a flanking sequence.

[0275] In certain embodiments, the spacer is 13 nucleotides and is located between the 5' terminus of the sense sequence and a flanking sequence. In certain embodiments, a spacer is of sufficient length to form approximately one helical turn of the sequence.

[0276] In certain embodiments, a spacer region of between 8-20, i.e., 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 nucleotides may be present between the antisense sequence and a flanking sequence.

[0277] In certain embodiments, the spacer sequence is between 10-13, i.e., 10, 11, 12 or 13 nucleotides and is located between the 3' terminus of the antisense sequence and a flanking sequence. In certain embodiments, a spacer is of sufficient length to form approximately one helical turn of the sequence.

[0278] In certain embodiments, the modulatory polynucleotide comprises in the 5' to 3' direction, a 5' flanking sequence, a 5' arm, a loop motif, a 3' arm and a 3' flanking sequence. As a non-limiting example, the 5' arm may comprise a sense sequence and the 3' arm comprises the antisense sequence. In another non-limiting example, the 5' arm comprises the antisense sequence and the 3' arm comprises the sense sequence.

[0279] In certain embodiments, the 5' arm, payload (e.g., sense and/or antisense sequence), loop motif and/or 3' arm sequence may be altered (e.g., substituting 1 or more nucleotides, adding nucleotides and/or deleting nucleotides). The alteration may cause a beneficial change in the function of the construct (e.g., increase knock-down of the target sequence, reduce degradation of the construct, reduce off target effect, increase efficiency of the payload, and reduce degradation of the payload).

[0280] In certain embodiments, the molecular scaffold of the modulatory polynucleotides is aligned in order to have the rate of excision of the guide or antisense strand be greater than the rate of excision of the passenger or sense strand. The rate of excision of the guide or passenger strand may be, independently, 1%, 2%, 3%, 4%, 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 99% or more than 99%. As a non-limiting example, the rate of excision of the guide strand is at least 80%. As another non-limiting example, the rate of excision of the guide strand is at least 90%.

[0281] In certain embodiments, the rate of excision of the guide strand is greater than the rate of excision of the passenger strand. In one aspect, the rate of excision of the guide strand may be at least 1%, 2%, 3%, 4%, 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 99% or more than 99% greater than the passenger strand.

[0282] In certain embodiments, the efficiency of excision of the guide strand is at least 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 99% or more than 99%. As a non-limiting example, the efficiency of the excision of the guide strand is greater than 80%.

[0283] In certain embodiments, the efficiency of the excision of the guide strand is greater than the excision of the passenger strand from the molecular scaffold. The excision of the guide strand may be 2, 3, 4, 5, 6, 7, 8, 9, 10 or more than 10 times more efficient than the excision of the passenger strand from the molecular scaffold.

[0284] In certain embodiments, the molecular scaffold comprises a dual-function targeting modulatory polynucleotide. As used herein, a "dual-function targeting" modulatory polynucleotide is a polynucleotide where both the guide and passenger strands knock down the same target or the guide and passenger strands knock down different targets.

[0285] In certain embodiments, the molecular scaffold may comprise one or more linkers known in the art. The linkers may separate regions or one molecular scaffold from another. As a non-limiting example, the molecular scaffold may be polycistronic.

[0286] In certain embodiments, the modulatory polynucleotide is designed using at least one of the following properties: loop variant, seed mismatch/bulge/wobble variant, stem mismatch, loop variant and basal stem mismatch variant, seed mismatch and basal stem mismatch variant, stem mismatch and basal stem mismatch variant, seed wobble and basal stem wobble variant, or a stem sequence variant.

AAV Production

[0287] Viral production disclosed herein describes processes and methods for producing AAV particles (with enhanced, improved and/or increased tropism for a target tissue) that may be used to contact a target cell to deliver a payload.

[0288] The present disclosure provides methods for the generation of AAV particles comprising targeting peptides. In certain embodiments, the AAV particles are prepared by viral genome replication in a viral replication cell. Any method known in the art may be used for the preparation of AAV particles. In certain embodiments, AAV particles are produced in mammalian cells (e.g., HEK293). In another embodiment, AAV particles are produced in insect cells (e.g., Sf9)

[0289] Methods of making AAV particles are well known in the art and are described in e.g., U.S. Patent Nos. US6204059, US5756283, US6258595, US6261551, US6270996, US6281010, US6365394, US6475769, US6482634, US6485966, US6943019, US6953690, US7022519, US7238526, US7291498 and US7491508, US5064764, US6194191, US6566118, US8137948; or International Publication Nos. WO1996039530, WO1998010088, WO1999014354, WO1999015685, WO1999047691, WO2000055342, WO2000075353 and WO2001023597; Methods In Molecular Biology, ed. Richard, Humana Press, NJ (1995); O'Reilly et al., Baculovirus Expression Vectors, A Laboratory Manual,

Oxford Univ. Press (1994); Samulski et al.,*J. Vir.*63:3822-8 (1989); Kajigaya et al., *Proc. Nat'l. Acad. Sci. USA* 88: 4646-50 (1991); Ruffing et al., *J. Vir.* 66:6922-30 (1992); Kimbauer et al., *Vir.,* 219:37-44 (1996); Zhao et al., *Vir.*272:382-93 (2000); the contents of each of which are herein incorporated by reference in their entirety. In certain embodiments, the AAV particles are made using the methods described in International Patent Publication WO2015191508, the contents of which are herein incorporated by reference in their entirety.

[0290] The viral replication cell may be selected from any biological organism, including prokaryotic (*e.g.*, bacterial) cells, and eukaryotic cells, including, insect cells, yeast cells and mammalian cells. Viral replication cells commonly used for production of recombinant AAV viral particles include, but are not limited to, HEK293 cells, COS cells, HeLa cells, KB cells, and other mammalian cell lines as described in U.S. Patent. Nos. US6156303, US5387484, US5741683, US5691176, and US5688676; U.S. Patent Application Publication No. 2002/0081721, and International Patent Publication Nos. WO 2000047757, WO 2000024916, and WO 1996017947, the contents of each of which are herein incorporated by reference in their entirety. Viral replication cells may comprise other mammalian cells such as A549, WEH1, 3T3, 10T1/2, BHK, MDCK, COS 1, COS 7, BSC 1, BSC 40, BMT 10, VERO, W138, Saos, C2C12, L cells, HT1080, HepG2 and primary fibroblast, hepatocyte and myoblast cells derived from mammals. Viral replication cells may comprise cells derived from mammalian species including, but not limited to, human, monkey, mouse, rat, rabbit, and hamster. Viral replication cells may comprise cells derived from a cell type, including but not limited to fibroblast, hepatocyte, tumor cell, cell line transformed cell, etc.

[0291] In some embodiments, the present disclosure provides a method for producing an AAV particle in mammalian cells, comprising the steps of 1) simultaneously co-transfecting mammalian cells, such as, but not limited to HEK293 cells, with a viral genome comprising a payload region (payload construct), a viral genome comprising polynucleotide sequences for rep and cap genes (rep/cap construct) and a viral genome comprising polynucleotide sequences encoding helper components (helper construct), 2) harvesting and purifying the AAV particles comprising a viral genome. This triple transfection method of AAV particle production may be utilized to produce small lots of virus.

[0292] In certain embodiments, the AAV particles may be produced in a viral replication cell that comprises an insect cell.

[0293] Growing conditions for insect cells in culture, and production of heterologous products in insect cells in culture are well-known in the art, *see* U.S. Pat. No. 6,204,059, the contents of which are herein incorporated by reference in their entirety.

[0294] Any insect cell which allows for replication of parvovirus and which can be maintained in culture can be used in accordance with the present disclosure. Cell lines may be used from *Spodoptera frugiperda,* including, but not limited to the Sf9 or Sf21 cell lines, *Drosophila* cell lines, or mosquito cell lines, such as *Aedes albopictus* derived cell lines. Use of insect cells for expression of heterologous proteins is well documented, as are methods of introducing nucleic acids, such as vectors, *e.g.*, insect-cell compatible vectors, into such cells and methods of maintaining such cells in culture. *See*, for example, Methods in Molecular Biology, ed. Richard, Humana Press, NJ (1995); O'Reilly *et al.*, Baculovirus Expression Vectors, A Laboratory Manual, Oxford Univ. Press (1994); Samulski *et al.*, *J. Vir.*63:3822-8 (1989); Kajigaya *et al.*, *Proc. Nat'l. Acad. Sci. USA* 88: 4646-50 (1991); Ruffing *et al.*, J. *Vir.* 66:6922-30 (1992); Kimbauer *et al.*, *Vir.*219:37-44 (1996); Zhao *et al.*, Vir.272:382-93 (2000); and Samulski *et al.*, U.S. Pat. No. 6,204,059, the contents of each of which is herein incorporated by reference in its entirety.

[0295] In some embodiments, the present disclosure provides a method for producing an AAV particle in a baculovirus/Sf9 system, comprising the steps of: 1) co-transfecting competent bacterial cells with a bacmid vector and either a viral construct vector and/or AAV payload construct vector, 2) isolating the resultant viral construct expression vector and AAV payload construct expression vector and separately transfecting viral replication cells, 3) isolating and purifying resultant payload and viral construct particles comprising viral construct expression vector or AAV payload construct expression vector, 4) co-infecting a viral replication cell with both the AAV payload and viral construct particles comprising viral construct expression vector or AAV payload construct expression vector, and 5) harvesting and purifying AAV particles comprising a viral genome.

[0296] Briefly, the viral construct vector and the AAV payload construct vector are each incorporated by a transposon donor/acceptor system into a bacmid, also known as a baculovirus plasmid, by standard molecular biology techniques known and performed by a person skilled in the art. Transfection of separate viral replication cell populations produces two baculoviruses, one that comprises the viral construct expression vector, and another that comprises the AAV payload construct expression vector. The two baculoviruses may be used to infect a single viral replication cell population for production of AAV particles.

[0297] Baculovirus expression vectors for producing viral particles in insect cells, including but not limited to *Spodoptera frugiperda* (Sf9) cells, provide high titers of viral particle product. Recombinant baculovirus encoding the viral construct expression vector and AAV payload construct expression vector initiates a productive infection of viral replicating

cells. Infectious baculovirus particles released from the primary infection secondarily infect additional cells in the culture, exponentially infecting the entire cell culture population in a number of infection cycles that is a function of the initial multiplicity of infection, *see* Urabe, M. *et al.*, J Virol. 2006 Feb; 80 (4):1874-85, the contents of which are herein incorporated by reference in their entirety.

[0298] Production of AAV particles with baculovirus in an insect cell system may address known baculovirus genetic and physical instability. In certain embodiments, the production system addresses baculovirus instability over multiple passages by utilizing a titerless infected-cells preservation and scale-up system. Small scale seed cultures of viral producing cells are transfected with viral expression constructs encoding the structural, non-structural, components of the viral particle. Baculovirus-infected viral producing cells are harvested into aliquots that may be cryopreserved in liquid nitrogen; the aliquots retain viability and infectivity for infection of large scale viral producing cell culture Wasilko DJ *et al.*, Protein Expr Purif. 2009 Jun; 65(2):122-32, the contents of which are herein incorporated by reference in their entirety.

[0299] A genetically stable baculovirus may be used as the source of one or more of the components for producing AAV particles in invertebrate cells. In certain embodiments, defective baculovirus expression vectors may be maintained episomally in insect cells. In such an embodiment the bacmid vector is engineered with replication control elements, including but not limited to promoters, enhancers, and/or cell-cycle regulated replication elements.

[0300] In certain embodiments, stable viral replication cells permissive for baculovirus infection are engineered with at least one stable integrated copy of any of the elements necessary for AAV replication and viral particle production including, but not limited to, the entire AAV genome, Rep and Cap genes, Rep genes, Cap genes, each Rep protein as a separate transcription cassette, each VP protein as a separate transcription cassette, the AAP (assembly activation protein), or at least one of the baculovirus helper genes with native or non-native promoters.

[0301] AAV particles described herein may be produced by triple transfection or baculovirus mediated virus production, or any other method known in the art. Any suitable permissive or packaging cell known in the art may be employed to produce the particles. Mammalian cells are often preferred. Also preferred are trans-complementing packaging cell lines that provide functions deleted from a replication-defective helper virus, e.g., 293 cells or other E1a trans-complementing cells. A packaging cell line may be used that is stably

transformed to express cap and/or rep genes. Alternatively, a packaging cell line may be used that is stably transformed to express helper constructs necessary for AAV particle assembly.

[0302] Recombinant AAV virus particles are, in some cases, produced and purified from culture supernatants according to the procedure as described in US20160032254, the contents of which are incorporated by reference.

[0303] In certain embodiments, AAV particles are produced wherein all three VP proteins are expressed at a stoichiometry around 1:1:10 (VP1:VP2:VP3). While not wishing to be bound by theory, the regulatory mechanisms that allow this controlled level of expression include the production of two mRNAs, one for VP1, and the other for VP2 and VP3, produced by differential splicing.

[0304] In certain embodiments, the viral construct vector(s) used for AAV production may contain a nucleotide sequence encoding the AAV capsid proteins where the initiation codon of the AAV VP1 capsid protein is a non-ATG, i.e., a suboptimal initiation codon, allowing the expression of a modified ratio of the viral capsid proteins in the production system, to provide improved infectivity of the host cell. In a non-limiting example, a viral construct vector may contain a nucleic acid construct comprising a nucleotide sequence encoding AAV VP1, VP2, and VP3 capsid proteins, wherein the initiation codon for translation of the AAV VP1 capsid protein is CTG, TTG, or GTG, as described in US Patent No. US8163543, the contents of which are herein incorporated by reference in its entirety.

[0305] In certain embodiments, the viral construct vector(s) used for AAV production may contain a nucleotide sequence encoding the AAV rep proteins where the initiation codon of the AAV rep protein or proteins is a non-ATG. In certain embodiments, a single coding sequence is used for the Rep78 and Rep52 proteins, wherein initiation codon for translation of the Rep78 protein is a suboptimal initiation codon, selected from the group consisting of ACG, TTG, CTG and GTG, that effects partial exon skipping upon expression in insect cells, as described in US Patent No. 8,512,981, the contents of which is herein incorporated by reference in its entirety, for example to promote less abundant expression of Rep78 as compared to Rep52, which may be advantageous in that it promotes high vector yields.

Small-scale production

[0306] In some cases, 293T cells (adhesion/suspension) are transfected with polyethyleneimine (PEI) with plasmids required for production of AAV, i.e., AAV2 rep, an adenoviral helper construct and a ITR flanked payload cassette. The AAV2 rep plasmid also contains the cap sequence of the particular virus being studied. Twenty-four hours after

transfection (no medium changes for suspension), which occurs in DMEM/F17 with/without serum, the medium is replaced with fresh medium with or without serum. Three (3) days after transfection, a sample is taken from the culture medium of the 293 adherent cells. Subsequently cells are scraped, or suspension cells are pelleted, and transferred into a receptacle. For adhesion cells, after centrifugation to remove cellular pellet, a second sample is taken from the supernatant after scraping. Next, cell lysis is achieved by three consecutive freeze-thaw cycles (-80C to 37C) or adding detergent triton. Cellular debris is removed by centrifugation or depth filtration and sample 3 is taken from the medium. The samples are quantified for AAV particles by DNase resistant genome titration by DNA qPCR. The total production yield from such a transfection is equal to the particle concentration from sample 3.

[0307] AAV particle titers are measured according to genome copy number (genome particles per milliliter). Genome particle concentrations are based on DNA qPCR of the vector DNA as previously reported (Clark et al. (1999) Hum. Gene Ther., 10:1031-1039; Veldwijk et al. (2002) Mol. Ther., 6:272-278).

Large-scale production

[0308] In some embodiments, AAV particle production may be modified to increase the scale of production. Large scale viral production methods according to the present disclosure may include any of those taught in US Patent Nos. 5,756,283, 6,258,595, 6,261,551, 6,270,996, 6,281,010, 6,365,394, 6,475,769, 6,482,634, 6,485,966, 6,943,019, 6,953,690, 7,022,519, 7,238,526, 7,291,498 and 7,491,508 or International Publication Nos. WO1996039530, WO1998010088, WO1999014354, WO1999015685, WO1999047691, WO2000055342, WO2000075353 and WO2001023597, the contents of each of which are herein incorporated by reference in their entirety. Methods of increasing viral particle production scale typically comprise increasing the number of viral replication cells. In some embodiments, viral replication cells comprise adherent cells. To increase the scale of viral particle production by adherent viral replication cells, larger cell culture surfaces are required. In some cases, large-scale production methods comprise the use of roller bottles to increase cell culture surfaces. Other cell culture substrates with increased surface areas are known in the art. Examples of additional adherent cell culture products with increased surface areas include, but are not limited to CELLSTACK®, CELLCUBE® (Corning Corp., Corning, NY) and NUNC™ CELL FACTORY™ (Thermo Scientific, Waltham, MA). In some cases, large-scale adherent cell surfaces may comprise from about 1,000 cm^2 to about 100,000 cm^2. In some cases, large-scale adherent cell cultures may comprise from about 10^7 to about 10^9 cells, from about 10^8 to about 10^{10} cells, from about 10^9 to about 10^{12} cells or at least 10^{12}

cells. In some cases, large-scale adherent cultures may produce from about 10^9 to about 10^{12}, from about 10^{10} to about 10^{13}, from about 10^{11} to about 10^{14}, from about 10^{12} to about 10^{15} or at least 10^{15} viral particles.

[0309] In some embodiments, large-scale viral production methods of the present disclosure may comprise the use of suspension cell cultures. Suspension cell culture allows for significantly increased numbers of cells. Typically, the number of adherent cells that can be grown on about 10-50 cm^2 of surface area can be grown in about 1 cm^3 volume in suspension.

[0310] Transfection of replication cells in large-scale culture formats may be carried out according to any methods known in the art. For large-scale adherent cell cultures, transfection methods may include, but are not limited to the use of inorganic compounds (*e.g.* calcium phosphate), organic compounds [*e.g.* polyethyleneimine (PEI)] or the use of non-chemical methods (*e.g.* electroporation.) With cells grown in suspension, transfection methods may include, but are not limited to the use of calcium phosphate and the use of PEI. In some cases, transfection of large scale suspension cultures may be carried out according to the section entitled "Transfection Procedure" described in Feng, L. *et al.*, 2008. Biotechnol Appl. Biochem. 50:121-32, the contents of which are herein incorporated by reference in their entirety. According to such embodiments, PEI-DNA complexes may be formed for introduction of plasmids to be transfected. In some cases, cells being transfected with PEI-DNA complexes may be 'shocked' prior to transfection. This comprises lowering cell culture temperatures to 4°C for a period of about 1 hour. In some cases, cell cultures may be shocked for a period of from about 10 minutes to about 5 hours. In some cases, cell cultures may be shocked at a temperature of from about 0°C to about 20°C.

[0311] In some cases, transfections may include one or more vectors for expression of an RNA effector molecule to reduce expression of nucleic acids from one or more AAV payload constructs. Such methods may enhance the production of viral particles by reducing cellular resources wasted on expressing payload constructs. In some cases, such methods may be carried out according to those methods taught in US Publication No. US2014/0099666, the contents of which are herein incorporated by reference in their entirety.

III. METHODS AND USES OF THE COMPOSITIONS OF THE DISCLOSURE

[0312] The AAV particles of the present disclosure, having enhanced tropism for a desired target tissue, may be used for the delivery of a payload to the target tissue. In certain embodiments the payload is a polypeptide. In a second embodiment, the payload is an antibody. In a third embodiment, the payload is an RNAi agent and/or modulatory

polynucleotide. The AAV particles of the present disclosure may be delivered by intravenous injection or infusion for the targeting of CNS and/or PNS tissues (e.g., neurons, DRG).

[0313] The AAV particles of the present disclosure may be used for regulating expression of a gene of interest (or its protein product) in a cell, tissue, organ or subject.

[0314] In accordance with the present disclosure, methods for increasing expression of a target protein in a cell, tissue, organ or subject are provided; the method comprising administering to the cell, tissue, organ or subject an effective amount of the AAV particles of the disclosure comprising a viral genome with a payload region encoding the target protein.

[0315] Accordingly, the target protein may be increased by at least about 10%, preferably by at least about 10%, 30%, 40%, 50%, 60%, 70%, 80%, 85%, 90%, 95% and 100%, or at least 20-30%, 20-40%, 20-50%, 20-60%, 20-70%, 20-80%, 20-90%, 20-95%, 20-100%, 30-40%, 30-50%, 30-60%, 30-70%, 30-80%, 30-90%, 30-95%, 30-100%, 40-50%, 40-60%, 40-70%, 40-80%, 40-90%, 40-95%, 40-100%, 50-60%, 50-70%, 50-80%, 50-90%, 50-95%, 50-100%, 60-70%, 60-80%, 60-90%, 60-95%, 60-100%, 70-80%, 70-90%, 70-95%, 70-100%, 80-90%, 80-95%, 80-100%, 90-95%, 90-100% or 95-100%.

[0316] In certain embodiments, the AAV particles of the present disclosure may be used to increase the expression of a target protein in a cell of the CNS, such as a neuron, astrocyte, microglial cell, and/or oligodendrocyte. In some embodiments, the gene may encode a protein including, but not limited to, an antibody, aromatic L-amino acid decarboxylase (AADC), survival motor neuron 1 (SMN1), frataxin (FXN), APOE (APOE2, APOE3, or APOE4), GBA1, GRN, ASPA, CLN2, GLB1, SGSH, NAGLU, IDS, NPC1, or GAN.

[0317] In accordance with the present disclosure, methods for decreasing, inhibiting or suppressing the expression of a target gene or protein in a cell, tissue, organ or subject are also provided; the method comprising administering to the cell, tissue, organ or subject an effective amount of the AAV particles of the disclosure comprising a viral genome with a payload region encoding an RNAi agent and/or modulatory polynucleotide.

[0318] Accordingly, the RNAi agent may be, but is not limited to, dsRNA, siRNA, shRNA, pre-miRNA, pri-miRNA, miRNA, stRNA, lncRNA, piRNA, or snoRNA specific for a target gene of interest. Non-limiting examples of a target gene of interest include, SOD1, MAPT, APOE, HTT, C9ORF72, TDP-43, APP, BACE, SNCA, ATXN1, ATXN2, ATXN3, ATXN7, SCN1A-SCN5A, or SCN8A-SCN11A.

[0319] In some embodiments, the present disclosure provides methods for inhibiting/silencing target gene expression in a cell. Accordingly, the RNAi agent can be used to substantially inhibit target gene expression in a cell, such as but not limited to, in

astrocytes, microglia, or cortical, hippocampal, entorhinal, thalamic, motor or sensory neurons. In some aspects, the inhibition of target gene expression refers to an inhibition by at least about 20%, such as by at least about 30%, 40%, 50%, 60%, 70%, 80%, 85%, 90%, 95% and 100%, or at least 20-30%, 20-40%, 20-50%, 20-60%, 20-70%, 20-80%, 20-90%, 20-95%, 20-100%, 30-40%, 30-50%, 30-60%, 30-70%, 30-80%, 30-90%, 30-95%, 30-100%, 40-50%, 40-60%, 40-70%, 40-80%, 40-90%, 40-95%, 40-100%, 50-60%, 50-70%, 50-80%, 50-90%, 50-95%, 50-100%, 60-70%, 60-80%, 60-90%, 60-95%, 60-100%, 70-80%, 70-90%, 70-95%, 70-100%, 80-90%, 80-95%, 80-100%, 90-95%, 90-100% or 95-100%. Accordingly, the protein product of the targeted gene may be inhibited by at least about 20%, preferably by at least about 30%, 40%, 50%, 60%, 70%, 80%, 85%, 90%, 95% and 100%, or at least 20-30%, 20-40%, 20-50%, 20-60%, 20-70%, 20-80%, 20-90%, 20-95%, 20-100%, 30-40%, 30-50%, 30-60%, 30-70%, 30-80%, 30-90%, 30-95%, 30-100%, 40-50%, 40-60%, 40-70%, 40-80%, 40-90%, 40-95%, 40-100%, 50-60%, 50-70%, 50-80%, 50-90%, 50-95%, 50-100%, 60-70%, 60-80%, 60-90%, 60-95%, 60-100%, 70-80%, 70-90%, 70-95%, 70-100%, 80-90%, 80-95%, 80-100%, 90-95%, 90-100% or 95-100%.

[0320] In some embodiments, the gene to be inhibited may include but is not limited to SOD1, MAPT, APOE, HTT, C9ORF72, TDP-43, APP, BACE, SNCA, ATXN1, ATXN2, ATXN3, ATXN7, SCN1A-SCN5A, or SCN8A-SCN11A.

Therapeutic Applications

[0321] The present disclosure provides a method for treating a disease, disorder and/or condition in a mammalian subject, including a human subject, comprising administering to the subject any of the AAV particles described herein or administering to the subject any of the described compositions, including pharmaceutical compositions, described herein.

[0322] In certain embodiments, the AAV particles of the present disclosure are administered to a subject prophylactically, to prevent on-set of disease. In another embodiment, the AAV particles of the present disclosure are administered to treat (lessen the effects of) a disease or symptoms thereof. In yet another embodiment, the AAV particles of the present disclosure are administered to cure (eliminate) a disease. In another embodiment, the AAV particles of the present disclosure are administered to prevent or slow progression of disease. In yet another embodiment, the AAV particles of the present disclosure are used to reverse the deleterious effects of a disease. Disease status and/or progression may be determined or monitored by standard methods known in the art.

[0323] In some embodiments, the AAV particles of the disclosure are useful in the field of medicine for the treatment, prophylaxis, palliation or amelioration of neurological diseases and/or disorders.

[0324] In some embodiments, the AAV particles of the disclosure are useful in the field of medicine for the treatment, prophylaxis, palliation or amelioration of tauopathy.

[0325] In some embodiments, the AAV particles of the disclosure are useful in the field of medicine for the treatment, prophylaxis, palliation or amelioration of Alzheimer's Disease.

[0326] In some embodiments, the AAV particles of the disclosure are useful in the field of medicine for the treatment, prophylaxis, palliation or amelioration of Friedreich's ataxia, or any disease stemming from a loss or partial loss of frataxin protein.

[0327] In some embodiments, the AAV particles of the disclosure are useful in the field of medicine for the treatment, prophylaxis, palliation or amelioration of Parkinson's Disease.

[0328] In some embodiments, the AAV particles of the disclosure are useful in the field of medicine for the treatment, prophylaxis, palliation or amelioration of Amyotrophic lateral sclerosis.

[0329] In some embodiments, the AAV particles of the disclosure are useful in the field of medicine for the treatment, prophylaxis, palliation or amelioration of Huntington's Disease.

[0330] In some embodiments, the AAV particles of the disclosure are useful in the field of medicine for the treatment, prophylaxis, palliation or amelioration of chronic or neuropathic pain.

[0331] In some embodiments, the AAV particles of the disclosure are useful in the field of medicine for treatment, prophylaxis, palliation or amelioration of a disease associated with the central nervous system.

[0332] In some embodiments, the AAV particles of the disclosure are useful in the field of medicine for treatment, prophylaxis, palliation or amelioration of a disease associated with the peripheral nervous system.

[0333] In certain embodiments, the AAV particles of the present disclosure are administered to a subject having at least one of the diseases or symptoms described herein.

[0334] As used herein, any disease associated with the central or peripheral nervous system and components thereof (e.g., neurons) may be considered a "neurological disease".

[0335] Any neurological disease may be treated with the AAV particles of the disclosure, or pharmaceutical compositions thereof, including but not limited to, Absence of the Septum Pellucidum, Acid Lipase Disease, Acid Maltase Deficiency, Acquired Epileptiform Aphasia, Acute Disseminated Encephalomyelitis, Attention Deficit-Hyperactivity Disorder (ADHD),

Adie's Pupil, Adie's Syndrome, Adrenoleukodystrophy, Agenesis of the Corpus Callosum, Agnosia, Aicardi Syndrome, Aicardi-Goutieres Syndrome Disorder, AIDS - Neurological Complications, Alexander Disease, Alpers' Disease, Alternating Hemiplegia, Alzheimer's Disease, Amyotrophic Lateral Sclerosis (ALS), Anencephaly, Aneurysm, Angelman Syndrome, Angiomatosis, Anoxia, Antiphospholipid Syndrome, Aphasia, Apraxia, Arachnoid Cysts, Arachnoiditis, Arnold-Chiari Malformation, Arteriovenous Malformation, Asperger Syndrome, Ataxia, Ataxia Telangiectasia, Ataxias and Cerebellar or Spinocerebellar Degeneration, Atrial Fibrillation and Stroke, Attention Deficit-Hyperactivity Disorder, Autism Spectrum Disorder, Autonomic Dysfunction, Back Pain, Barth Syndrome, Batten Disease, Becker's Myotonia, Bechet's Disease, Bell's Palsy, Benign Essential Blepharospasm, Benign Focal Amyotrophy, Benign Intracranial Hypertension, Bernhardt-Roth Syndrome, Binswanger's Disease, Blepharospasm, Bloch-Sulzberger Syndrome, Brachial Plexus Birth Injuries, Brachial Plexus Injuries, Bradbury-Eggleston Syndrome, Brain and Spinal Tumors, Brain Aneurysm, Brain Injury, Brown-Sequard Syndrome, Bulbar palsy, Bulbospinal Muscular Atrophy, Cerebral Autosomal Dominant Arteriopathy with Sub-cortical Infarcts and Leukoencephalopathy (CADASIL), Canavan Disease, Carpal Tunnel Syndrome, Causalgia, Cavernomas, Cavernous Angioma, Cavernous Malformation, Central Cervical Cord Syndrome, Central Cord Syndrome, Central Pain Syndrome, Central Pontine Myelinolysis, Cephalic Disorders, Ceramidase Deficiency, Cerebellar Degeneration, Cerebellar Hypoplasia, Cerebral Aneurysms, Cerebral Arteriosclerosis, Cerebral Atrophy, Cerebral Beriberi, Cerebral Cavernous Malformation, Cerebral Gigantism, Cerebral Hypoxia, Cerebral Palsy, Cerebro-Oculo-Facio-Skeletal Syndrome (COFS), Charcot-Marie-Tooth Disease, Chiari Malformation, Cholesterol Ester Storage Disease, Chorea, Choreoacanthocytosis, Chronic Inflammatory Demyelinating Polyneuropathy (CIDP), Chronic Orthostatic Intolerance, Chronic Pain, Cockayne Syndrome Type II, Coffin Lowry Syndrome, Colpocephaly, Coma, Complex Regional Pain Syndrome, Concentric sclerosis (Baló's sclerosis), Congenital Facial Diplegia, Congenital Myasthenia, Congenital Myopathy, Congenital Vascular Cavernous Malformations, Corticobasal Degeneration, Cranial Arteritis, Craniosynostosis, Cree encephalitis, Creutzfeldt-Jakob Disease, Chronic progressive external ophthalmoplegia, Cumulative Trauma Disorders, Cushing's Syndrome, Cytomegalic Inclusion Body Disease, Cytomegalovirus Infection, Dancing Eyes-Dancing Feet Syndrome, Dandy-Walker Syndrome, Dawson Disease, De Morsier's Syndrome, Dejerine-Klumpke Palsy, Dementia, Dementia -Multi-Infarct, Dementia - Semantic, Dementia -Subcortical, Dementia With Lewy Bodies, Demyelination diseases, Dentate Cerebellar Ataxia,

Dentatorubral Atrophy, Dermatomyositis, Developmental Dyspraxia, Devic's Syndrome, Diabetic Neuropathy, Diffuse Sclerosis, Distal hereditary motor neuronopathies, Dravet Syndrome, Dysautonomia, Dysgraphia, Dyslexia, Dysphagia, Dyspraxia, Dyssynergia Cerebellaris Myoclonica, Dyssynergia Cerebellaris Progressiva, Dystonias, Early Infantile Epileptic Encephalopathy, Empty Sella Syndrome, Encephalitis, Encephalitis Lethargica, Encephaloceles, Encephalomyelitis, Encephalopathy, Encephalopathy (familial infantile), Encephalotrigeminal Angiomatosis, Epilepsy, Epileptic Hemiplegia, Episodic ataxia, Erb's Palsy, Erb-Duchenne and Dejerine-Klumpke Palsies, Essential Tremor, Extrapontine Myelinolysis, Faber's disease, Fabry Disease, Fahr's Syndrome, Fainting, Familial Dysautonomia, Familial Hemangioma, Familial Idiopathic Basal Ganglia Calcification, Familial Periodic Paralyses, Familial Spastic Paralysis, Farber's Disease, Febrile Seizures, Fibromuscular Dysplasia, Fisher Syndrome, Floppy Infant Syndrome, Foot Drop, Friedreich's Ataxia, Frontotemporal Dementia, Gaucher Disease, Generalized Gangliosidoses (GM1, GM2), Gerstmann's Syndrome, Gerstmann-Straussler-Scheinker Disease, Giant Axonal Neuropathy, Giant Cell Arteritis, Giant Cell Inclusion Disease, Globoid Cell Leukodystrophy, Glossopharyngeal Neuralgia, Glycogen Storage Disease, Guillain-Barré Syndrome, Hallervorden-Spatz Disease, Head Injury, Headache, Hemicrania Continua, Hemifacial Spasm, Hemiplegia Alterans, Hereditary Neuropathies, Hereditary Spastic Paraplegia, Heredopathia Atactica Polyneuritiformis, Herpes Zoster, Herpes Zoster Oticus, Hirayama Syndrome, Holmes-Adie syndrome, Holoprosencephaly, HTLV-1 Associated Myelopathy, Hughes Syndrome, Huntington's Disease, Hurler syndrome, Hydranencephaly, Hydrocephalus, Hydrocephalus - Normal Pressure, Hydromyelia, Hypercortisolism, Hypersomnia, Hypertonia, Hypotonia, Hypoxia, Immune-Mediated Encephalomyelitis, Inclusion Body Myositis, Incontinentia Pigmenti, Infantile Hypotonia, Infantile Neuroaxonal Dystrophy, Infantile Phytanic Acid Storage Disease, Infantile Refsum Disease, Infantile Spasms, Inflammatory Myopathies, Iniencephaly, Intestinal Lipodystrophy, Intracranial Cysts, Intracranial Hypertension, Isaacs' Syndrome, Joubert Syndrome, Kearns-Sayre Syndrome, Kennedy's Disease, Kinsbourne syndrome, Kleine-Levin Syndrome, Klippel-Feil Syndrome, Klippel-Trenaunay Syndrome (KTS), Klüver-Bucy Syndrome, Korsakoff's Amnesic Syndrome, Krabbe Disease, Kugelberg-Welander Disease, Kuru, Lambert-Eaton Myasthenic Syndrome, Landau-Kleffner Syndrome, Lateral Femoral Cutaneous Nerve Entrapment, Lateral Medullary Syndrome, Learning Disabilities, Leigh's Disease, Lennox-Gastaut Syndrome, Lesch-Nyhan Syndrome, Leukodystrophy, Levine-Critchley Syndrome, Lewy Body Dementia, Lichtheim's disease, Lipid Storage Diseases, Lipoid Proteinosis,

Lissencephaly, Locked-In Syndrome, Lou Gehrig's Disease, Lupus - Neurological Sequelae, Lyme Disease - Neurological Complications, Lysosomal storage disorders, Machado-Joseph Disease, Macrencephaly, Megalencephaly, Melkersson-Rosenthal Syndrome, Meningitis, Meningitis and Encephalitis, Menkes Disease, Meralgia Paresthetica, Metachromatic Leukodystrophy, Microcephaly, Migraine, Miller Fisher Syndrome, Mini Stroke, Mitochondrial Myopathy, Mitochondrial DNA depletion syndromes, Moebius Syndrome, Monomelic Amyotrophy, Morvan Syndrome, Motor Neuron Diseases, Moyamoya Disease, Mucolipidoses, Mucopolysaccharidoses, Multi-Infarct Dementia, Multifocal Motor Neuropathy, Multiple Sclerosis, Multiple System Atrophy, Multiple System Atrophy with Orthostatic Hypotension, Muscular Dystrophy, Myasthenia - Congenital, Myasthenia Gravis, Myelinoclastic Diffuse Sclerosis, Myelitis, Myoclonic Encephalopathy of Infants, Myoclonus, Myoclonus epilepsy, Myopathy, Myopathy- Congenital, Myopathy -Thyrotoxic, Myotonia, Myotonia Congenita, Narcolepsy, NARP (neuropathy, ataxia and retinitis pigmentosa), Neuroacanthocytosis, Neurodegeneration with Brain Iron Accumulation, Neurodegenerative disease, Neurofibromatosis, Neuroleptic Malignant Syndrome, Neurological Complications of AIDS, Neurological Complications of Lyme Disease, Neurological Consequences of Cytomegalovirus Infection, Neurological Manifestations of Pompe Disease, Neurological Sequelae Of Lupus, Neuromyelitis Optica, Neuromyotonia, Neuronal Ceroid Lipofuscinosis, Neuronal Migration Disorders, Neuropathic pain, Neuropathy- Hereditary, Neuropathy, Neurosarcoidosis, Neurosyphilis, Neurotoxicity, Nevus Cavernosus, Niemann-Pick Disease, O'Sullivan-McLeod Syndrome, Occipital Neuralgia, Ohtahara Syndrome, Olivopontocerebellar Atrophy, Opsoclonus Myoclonus, Orthostatic Hypotension, Overuse Syndrome, Pain -Chronic, Pantothenate Kinase-Associated Neurodegeneration, Paraneoplastic Syndromes, Paresthesia, Parkinson's Disease, Paroxysmal Choreoathetosis, Paroxysmal Hemicrania, Parry-Romberg, Pelizaeus-Merzbacher Disease, Pena Shokeir II Syndrome, Perineural Cysts, Peroneal muscular atrophy, Periodic Paralyses, Peripheral Neuropathy, Periventricular Leukomalacia, Persistent Vegetative State, Pervasive Developmental Disorders, Phytanic Acid Storage Disease, Pick's Disease, Pinched Nerve, Piriformis Syndrome, Pituitary Tumors, Polymyositis, Pompe Disease, Porencephaly, Post-Polio Syndrome, Postherpetic Neuralgia, Postinfectious Encephalomyelitis, Postural Hypotension, Postural Orthostatic Tachycardia Syndrome, Postural Tachycardia Syndrome, Primary Dentatum Atrophy, Primary Lateral Sclerosis, Primary Progressive Aphasia, Prion Diseases, Progressive bulbar palsy, Progressive Hemifacial Atrophy, Progressive Locomotor Ataxia, Progressive Multifocal Leukoencephalopathy, Progressive Muscular Atrophy,

Progressive Sclerosing Poliodystrophy, Progressive Supranuclear Palsy, Prosopagnosia, Pseudobulbar palsy, Pseudo-Torch syndrome, Pseudotoxoplasmosis syndrome, Pseudotumor Cerebri, Psychogenic Movement, Ramsay Hunt Syndrome I, Ramsay Hunt Syndrome II, Rasmussen's Encephalitis, Reflex Sympathetic Dystrophy Syndrome, Refsum Disease, Refsum Disease - Infantile, Repetitive Motion Disorders, Repetitive Stress Injuries, Restless Legs Syndrome, Retrovirus-Associated Myelopathy, Rett Syndrome, Reye's Syndrome, Rheumatic Encephalitis, Riley-Day Syndrome, Sacral Nerve Root Cysts, Saint Vitus Dance, Salivary Gland Disease, Sandhoff Disease, Schilder's Disease, Schizencephaly, Seitelberger Disease, Seizure Disorder, Semantic Dementia, Septo-Optic Dysplasia, Severe Myoclonic Epilepsy of Infancy (SMEI), Shaken Baby Syndrome, Shingles, Shy-Drager Syndrome, Sjögren's Syndrome, Sleep Apnea, Sleeping Sickness, Sotos Syndrome, Spasticity, Spina Bifida, Spinal Cord Infarction, Spinal Cord Injury, Spinal Cord Tumors, Spinal Muscular Atrophy, Spinocerebellar Ataxia, Spinocerebellar Atrophy, Spinocerebellar Degeneration, Sporadic ataxia, Steele-Richardson-Olszewski Syndrome, Stiff-Person Syndrome, Striatonigral Degeneration, Stroke, Sturge-Weber Syndrome, Subacute Sclerosing Panencephalitis, Subcortical Arteriosclerotic Encephalopathy, Short-lasting, Unilateral, Neuralgiform (SUNCT) Headache, Swallowing Disorders, Sydenham Chorea, Syncope, Syphilitic Spinal Sclerosis, Syringohydromyelia, Syringomyelia, Systemic Lupus Erythematosus, Tabes Dorsalis, Tardive Dyskinesia, Tarlov Cysts, Tay-Sachs Disease, Temporal Arteritis, Tethered Spinal Cord Syndrome, Thomsen's Myotonia, Thoracic Outlet Syndrome, Thyrotoxic Myopathy, Tic Douloureux, Todd's Paralysis, Tourette Syndrome, Transient Ischemic Attack, Transmissible Spongiform Encephalopathies, Transverse Myelitis, Traumatic Brain Injury, Tremor, Trigeminal Neuralgia, Tropical Spastic Paraparesis, Troyer Syndrome, Tuberous Sclerosis, Vascular Erectile Tumor, Vasculitis Syndromes of the Central and Peripheral Nervous Systems, Vitamin B12 deficiency, Von Economo's Disease, Von Hippel-Lindau Disease (VHL), Von Recklinghausen's Disease, Wallenberg's Syndrome, Werdnig-Hoffman Disease, Wernicke-Korsakoff Syndrome, West Syndrome, Whiplash, Whipple's Disease, Williams Syndrome, Wilson Disease, Wolman's Disease, X-Linked Spinal and Bulbar Muscular Atrophy.

Methods of Treatment of Neurological Disease

AAV Particles Encoding protein payloads

[0336] Provided in the present disclosure are methods for introducing the AAV particles of the present disclosure into cells, the method comprising introducing into said cells any of the vectors in an amount sufficient for an increase in the production of target mRNA and

protein to occur. In some aspects, the cells may be neurons such as but not limited to, motor, hippocampal, entorhinal, thalamic, cortical, sensory, sympathetic, or parasympathetic neurons, and glial cells such as astrocytes, microglia, and/or oligodendrocytes.

[0337] Disclosed herein are methods for treating neurological disease associated with insufficient function/presence of a target protein (e.g., ApoE, FXN) in a subject in need of treatment. The method optionally comprises administering to the subject a therapeutically effective amount of a composition comprising AAV particles of the present disclosure. As a non-limiting example, the AAV particles can increase target gene expression, increase target protein production, and thus reduce one or more symptoms of neurological disease in the subject such that the subject is therapeutically treated.

[0338] In certain embodiments, the composition comprising the AAV particles of the present disclosure is administered to the central nervous system of the subject via systemic administration. In certain embodiments, the systemic administration is intravenous injection.

[0339] In some embodiments, the composition comprising the AAV particles of the present disclosure is administered to the central nervous system of the subject. In other embodiments, the composition comprising the AAV particles of the present disclosure is administered to a CNS tissue of a subject (e.g., putamen, thalamus or cortex of the subject).

[0340] In certain embodiments, the composition comprising the AAV particles of the present disclosure is administered to the central nervous system of the subject via intraparenchymal injection. Non-limiting examples of intraparenchymal injections include intraputamenal, intracortical, intrathalamic, intrastriatal, intrahippocampal or into the entorhinal cortex.

[0341] In certain embodiments, the composition comprising the AAV particles of the present disclosure is administered to the central nervous system of the subject via intraparenchymal injection and intravenous injection.

[0342] In certain embodiments, the AAV particles of the present disclosure may be delivered into specific types of targeted cells, including, but not limited to, thalamic, hippocampal, entorhinal, cortical, motor, sensory, excitatory, inhibitory, sympathetic, or parasympathetic neurons; glial cells including oligodendrocytes, astrocytes and microglia; and/or other cells surrounding neurons such as T cells.

[0343] In certain embodiments, the AAV particles of the present disclosure may be delivered to neurons in the putamen, thalamus and/or cortex.

[0344] In some embodiments, the AAV particles of the present disclosure may be used as a therapy for neurological disease.

[0345] In some embodiments, the AAV particles of the present disclosure may be used as a therapy for tauopathies.

[0346] In some embodiments, the AAV particles of the present disclosure may be used as a therapy for Alzheimer's Disease.

[0347] In some embodiments, the AAV particles of the present disclosure may be used as a therapy for Amyotrophic Lateral Sclerosis.

[0348] In some embodiments, the AAV particles of the present disclosure may be used as a therapy for Huntington's Disease.

[0349] In some embodiments, the AAV particles of the present disclosure may be used as a therapy for Parkinson's Disease.

[0350] In some embodiments, the AAV particles of the present disclosure may be used as a therapy for Friedreich's Ataxia.

[0351] In some embodiments, the AAV particles of the present disclosure may be used as a therapy for chronic or neuropathic pain.

[0352] In certain embodiments, administration of the AAV particles described herein to a subject may increase target protein levels in a subject. The target protein levels may be increased by about 30%, 40%, 50%, 60%, 70%, 80%, 85%, 90%, 95% and 100%, or at least 20-30%, 20-40%, 20-50%, 20-60%, 20-70%, 20-80%, 20-90%, 20-95%, 20-100%, 30-40%, 30-50%, 30-60%, 30-70%, 30-80%, 30-90%, 30-95%, 30-100%, 40-50%, 40-60%, 40-70%, 40-80%, 40-90%, 40-95%, 40-100%, 50-60%, 50-70%, 50-80%, 50-90%, 50-95%, 50-100%, 60-70%, 60-80%, 60-90%, 60-95%, 60-100%, 70-80%, 70-90%, 70-95%, 70-100%, 80-90%, 80-95%, 80-100%, 90-95%, 90-100% or 95-100% in a subject such as, but not limited to, the CNS, a region of the CNS, or a specific cell of the CNS of a subject. As a non-limiting example, the AAV particles may increase the protein levels of a target protein by at least 50%. As a non-limiting example, the AAV particles may increase the proteins levels of a target protein by at least 40%. As a non-limiting example, a subject may have an increase of 10% of target protein. As a non-limiting example, the AAV particles may increase the protein levels of a target protein by fold increases over baseline. In certain embodiments, AAV particles lead to 5-6 times higher levels of a target protein.

[0353] In certain embodiments, administration of the AAV particles described herein to a subject may increase the expression of a target protein in a subject. The expression of the target protein may be increased by about 30%, 40%, 50%, 60%, 70%, 80%, 85%, 90%, 95% and 100%, or at least 20-30%, 20-40%, 20-50%, 20-60%, 20-70%, 20-80%, 20-90%, 20-95%, 20-100%, 30-40%, 30-50%, 30-60%, 30-70%, 30-80%, 30-90%, 30-95%, 30-100%,

40-50%, 40-60%, 40-70%, 40-80%, 40-90%, 40-95%, 40-100%, 50-60%, 50-70%, 50-80%, 50-90%, 50-95%, 50-100%, 60-70%, 60-80%, 60-90%, 60-95%, 60-100%, 70-80%, 70-90%, 70-95%, 70-100%, 80-90%, 80-95%, 80-100%, 90-95%, 90-100% or 95-100% in a subject such as, but not limited to, the CNS, a region of the CNS, or a specific cell of the CNS of a subject. As a non-limiting example, the AAV particles may increase the expression of a target protein by at least 50%. As a non-limiting example, the AAV particles may increase the expression of a target protein by at least 40%.

[0354] In certain embodiments, intravenous administration of the AAV particles described herein to a subject may increase the CNS expression of a target protein in a subject. The expression of the target protein may be increased by about 30%, 40%, 50%, 60%, 70%, 80%, 85%, 90%, 95% and 100%, or at least 20-30%, 20-40%, 20-50%, 20-60%, 20-70%, 20-80%, 20-90%, 20-95%, 20-100%, 30-40%, 30-50%, 30-60%, 30-70%, 30-80%, 30-90%, 30-95%, 30-100%, 40-50%, 40-60%, 40-70%, 40-80%, 40-90%, 40-95%, 40-100%, 50-60%, 50-70%, 50-80%, 50-90%, 50-95%, 50-100%, 60-70%, 60-80%, 60-90%, 60-95%, 60-100%, 70-80%, 70-90%, 70-95%, 70-100%, 80-90%, 80-95%, 80-100%, 90-95%, 90-100% or 95-100% in a subject such as, but not limited to, the CNS, a region of the CNS, or a specific cell of the CNS of a subject. As a non-limiting example, the AAV particles may increase the expression of a target protein in the CNS by at least 50%. As a non-limiting example, the AAV particles may increase the expression of a target protein in the CNS by at least 40%.

[0355] In some embodiments, the AAV particles of the present disclosure may be used to increase target protein expression in astrocytes in order to treat a neurological disease. Target protein in astrocytes may be increased by 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or more than 95%, 5-15%, 5-20%, 5-25%, 5-30%, 5-35%, 5-40%, 5-45%, 5-50%, 5-55%, 5-60%, 5-65%, 5-70%, 5-75%, 5-80%, 5-85%, 5-90%, 5-95%, 10-20%, 10-25%, 10-30%, 10-35%, 10-40%, 10-45%, 10-50%, 10-55%, 10-60%, 10-65%, 10-70%, 10-75%, 10-80%, 10-85%, 10-90%, 10-95%, 15-25%, 15-30%, 15-35%, 15-40%, 15-45%, 15-50%, 15-55%, 15-60%, 15-65%, 15-70%, 15-75%, 15-80%, 15-85%, 15-90%, 15-95%, 20-30%, 20-35%, 20-40%, 20-45%, 20-50%, 20-55%, 20-60%, 20-65%, 20-70%, 20-75%, 20-80%, 20-85%, 20-90%, 20-95%, 25-35%, 25-40%, 25-45%, 25-50%, 25-55%, 25-60%, 25-65%, 25-70%, 25-75%, 25-80%, 25-85%, 25-90%, 25-95%, 30-40%, 30-45%, 30-50%, 30-55%, 30-60%, 30-65%, 30-70%, 30-75%, 30-80%, 30-85%, 30-90%, 30-95%, 35-45%, 35-50%, 35-55%, 35-60%, 35-65%, 35-70%, 35-75%, 35-80%, 35-85%, 35-90%, 35-95%, 40-50%, 40-55%, 40-60%, 40-65%, 40-70%, 40-75%, 40-80%, 40-85%, 40-90%, 40-95%, 45-55%, 45-60%, 45-65%, 45-70%, 45-75%, 45-80%,

45-85%, 45-90%, 45-95%, 50-60%, 50-65%, 50-70%, 50-75%, 50-80%, 50-85%, 50-90%, 50-95%, 55-65%, 55-70%, 55-75%, 55-80%, 55-85%, 55-90%, 55-95%, 60-70%, 60-75%, 60-80%, 60-85%, 60-90%, 60-95%, 65-75%, 65-80%, 65-85%, 65-90%, 65-95%, 70-80%, 70-85%, 70-90%, 70-95%, 75-85%, 75-90%, 75-95%, 80-90%, 80-95%, or 90-95%.

[0356] In some embodiments, the AAV particles may be used to increase target protein in microglia. The increase of target protein in microglia may be, independently, increased by 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or more than 95%, 5-15%, 5-20%, 5-25%, 5-30%, 5-35%, 5-40%, 5-45%, 5-50%, 5-55%, 5-60%, 5-65%, 5-70%, 5-75%, 5-80%, 5-85%, 5-90%, 5-95%, 10-20%, 10-25%, 10-30%, 10-35%, 10-40%, 10-45%, 10-50%, 10-55%, 10-60%, 10-65%, 10-70%, 10-75%, 10-80%, 10-85%, 10-90%, 10-95%, 15-25%, 15-30%, 15-35%, 15-40%, 15-45%, 15-50%, 15-55%, 15-60%, 15-65%, 15-70%, 15-75%, 15-80%, 15-85%, 15-90%, 15-95%, 20-30%, 20-35%, 20-40%, 20-45%, 20-50%, 20-55%, 20-60%, 20-65%, 20-70%, 20-75%, 20-80%, 20-85%, 20-90%, 20-95%, 25-35%, 25-40%, 25-45%, 25-50%, 25-55%, 25-60%, 25-65%, 25-70%, 25-75%, 25-80%, 25-85%, 25-90%, 25-95%, 30-40%, 30-45%, 30-50%, 30-55%, 30-60%, 30-65%, 30-70%, 30-75%, 30-80%, 30-85%, 30-90%, 30-95%, 35-45%, 35-50%, 35-55%, 35-60%, 35-65%, 35-70%, 35-75%, 35-80%, 35-85%, 35-90%, 35-95%, 40-50%, 40-55%, 40-60%, 40-65%, 40-70%, 40-75%, 40-80%, 40-85%, 40-90%, 40-95%, 45-55%, 45-60%, 45-65%, 45-70%, 45-75%, 45-80%, 45-85%, 45-90%, 45-95%, 50-60%, 50-65%, 50-70%, 50-75%, 50-80%, 50-85%, 50-90%, 50-95%, 55-65%, 55-70%, 55-75%, 55-80%, 55-85%, 55-90%, 55-95%, 60-70%, 60-75%, 60-80%, 60-85%, 60-90%, 60-95%, 65-75%, 65-80%, 65-85%, 65-90%, 65-95%, 70-80%, 70-85%, 70-90%, 70-95%, 75-85%, 75-90%, 75-95%, 80-90%, 80-95%, or 90-95%.

[0357] In some embodiments, the AAV particles may be used to increase target protein in cortical neurons. The increase of target protein in the cortical neurons may be, independently, increased by 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or more than 95%, 5-15%, 5-20%, 5-25%, 5-30%, 5-35%, 5-40%, 5-45%, 5-50%, 5-55%, 5-60%, 5-65%, 5-70%, 5-75%, 5-80%, 5-85%, 5-90%, 5-95%, 10-20%, 10-25%, 10-30%, 10-35%, 10-40%, 10-45%, 10-50%, 10-55%, 10-60%, 10-65%, 10-70%, 10-75%, 10-80%, 10-85%, 10-90%, 10-95%, 15-25%, 15-30%, 15-35%, 15-40%, 15-45%, 15-50%, 15-55%, 15-60%, 15-65%, 15-70%, 15-75%, 15-80%, 15-85%, 15-90%, 15-95%, 20-30%, 20-35%, 20-40%, 20-45%, 20-50%, 20-55%, 20-60%, 20-65%, 20-70%, 20-75%, 20-80%, 20-85%, 20-90%, 20-95%, 25-35%, 25-40%, 25-45%, 25-50%, 25-55%, 25-60%, 25-65%, 25-70%, 25-75%, 25-80%, 25-85%, 25-90%, 25-95%, 30-40%, 30-45%,

30-50%, 30-55%, 30-60%, 30-65%, 30-70%, 30-75%, 30-80%, 30-85%, 30-90%, 30-95%, 35-45%, 35-50%, 35-55%, 35-60%, 35-65%, 35-70%, 35-75%, 35-80%, 35-85%, 35-90%, 35-95%, 40-50%, 40-55%, 40-60%, 40-65%, 40-70%, 40-75%, 40-80%, 40-85%, 40-90%, 40-95%, 45-55%, 45-60%, 45-65%, 45-70%, 45-75%, 45-80%, 45-85%, 45-90%, 45-95%, 50-60%, 50-65%, 50-70%, 50-75%, 50-80%, 50-85%, 50-90%, 50-95%, 55-65%, 55-70%, 55-75%, 55-80%, 55-85%, 55-90%, 55-95%, 60-70%, 60-75%, 60-80%, 60-85%, 60-90%, 60-95%, 65-75%, 65-80%, 65-85%, 65-90%, 65-95%, 70-80%, 70-85%, 70-90%, 70-95%, 75-85%, 75-90%, 75-95%, 80-90%, 80-95%, or 90-95%.

[0358] In some embodiments, the AAV particles may be used to increase target protein in hippocampal neurons. The increase of target protein in the hippocampal neurons may be, independently, increased by 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or more than 95%, 5-15%, 5-20%, 5-25%, 5-30%, 5-35%, 5-40%, 5-45%, 5-50%, 5-55%, 5-60%, 5-65%, 5-70%, 5-75%, 5-80%, 5-85%, 5-90%, 5-95%, 10-20%, 10-25%, 10-30%, 10-35%, 10-40%, 10-45%, 10-50%, 10-55%, 10-60%, 10-65%, 10-70%, 10-75%, 10-80%, 10-85%, 10-90%, 10-95%, 15-25%, 15-30%, 15-35%, 15-40%, 15-45%, 15-50%, 15-55%, 15-60%, 15-65%, 15-70%, 15-75%, 15-80%, 15-85%, 15-90%, 15-95%, 20-30%, 20-35%, 20-40%, 20-45%, 20-50%, 20-55%, 20-60%, 20-65%, 20-70%, 20-75%, 20-80%, 20-85%, 20-90%, 20-95%, 25-35%, 25-40%, 25-45%, 25-50%, 25-55%, 25-60%, 25-65%, 25-70%, 25-75%, 25-80%, 25-85%, 25-90%, 25-95%, 30-40%, 30-45%, 30-50%, 30-55%, 30-60%, 30-65%, 30-70%, 30-75%, 30-80%, 30-85%, 30-90%, 30-95%, 35-45%, 35-50%, 35-55%, 35-60%, 35-65%, 35-70%, 35-75%, 35-80%, 35-85%, 35-90%, 35-95%, 40-50%, 40-55%, 40-60%, 40-65%, 40-70%, 40-75%, 40-80%, 40-85%, 40-90%, 40-95%, 45-55%, 45-60%, 45-65%, 45-70%, 45-75%, 45-80%, 45-85%, 45-90%, 45-95%, 50-60%, 50-65%, 50-70%, 50-75%, 50-80%, 50-85%, 50-90%, 50-95%, 55-65%, 55-70%, 55-75%, 55-80%, 55-85%, 55-90%, 55-95%, 60-70%, 60-75%, 60-80%, 60-85%, 60-90%, 60-95%, 65-75%, 65-80%, 65-85%, 65-90%, 65-95%, 70-80%, 70-85%, 70-90%, 70-95%, 75-85%, 75-90%, 75-95%, 80-90%, 80-95%, or 90-95%.

[0359] In some embodiments, the AAV particles may be used to increase target protein in DRG and/or sympathetic neurons. The increase of target protein in the DRG and/or sympathetic neurons may be, independently, increased by 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or more than 95%, 5-15%, 5-20%, 5-25%, 5-30%, 5-35%, 5-40%, 5-45%, 5-50%, 5-55%, 5-60%, 5-65%, 5-70%, 5-75%, 5-80%, 5-85%, 5-90%, 5-95%, 10-20%, 10-25%, 10-30%, 10-35%, 10-40%, 10-45%, 10-50%, 10-55%, 10-60%, 10-65%, 10-70%, 10-75%, 10-80%, 10-85%, 10-90%,

10-95%, 15-25%, 15-30%, 15-35%, 15-40%, 15-45%, 15-50%, 15-55%, 15-60%, 15-65%, 15-70%, 15-75%, 15-80%, 15-85%, 15-90%, 15-95%, 20-30%, 20-35%, 20-40%, 20-45%, 20-50%, 20-55%, 20-60%, 20-65%, 20-70%, 20-75%, 20-80%, 20-85%, 20-90%, 20-95%, 25-35%, 25-40%, 25-45%, 25-50%, 25-55%, 25-60%, 25-65%, 25-70%, 25-75%, 25-80%, 25-85%, 25-90%, 25-95%, 30-40%, 30-45%, 30-50%, 30-55%, 30-60%, 30-65%, 30-70%, 30-75%, 30-80%, 30-85%, 30-90%, 30-95%, 35-45%, 35-50%, 35-55%, 35-60%, 35-65%, 35-70%, 35-75%, 35-80%, 35-85%, 35-90%, 35-95%, 40-50%, 40-55%, 40-60%, 40-65%, 40-70%, 40-75%, 40-80%, 40-85%, 40-90%, 40-95%, 45-55%, 45-60%, 45-65%, 45-70%, 45-75%, 45-80%, 45-85%, 45-90%, 45-95%, 50-60%, 50-65%, 50-70%, 50-75%, 50-80%, 50-85%, 50-90%, 50-95%, 55-65%, 55-70%, 55-75%, 55-80%, 55-85%, 55-90%, 55-95%, 60-70%, 60-75%, 60-80%, 60-85%, 60-90%, 60-95%, 65-75%, 65-80%, 65-85%, 65-90%, 65-95%, 70-80%, 70-85%, 70-90%, 70-95%, 75-85%, 75-90%, 75-95%, 80-90%, 80-95%, or 90-95%.

[0360] In some embodiments, the AAV particles of the present disclosure may be used to increase target protein in sensory neurons in order to treat neurological disease. Target protein in sensory neurons may be increased by 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or more than 95%, 5-15%, 5-20%, 5-25%, 5-30%, 5-35%, 5-40%, 5-45%, 5-50%, 5-55%, 5-60%, 5-65%, 5-70%, 5-75%, 5-80%, 5-85%, 5-90%, 5-95%, 10-20%, 10-25%, 10-30%, 10-35%, 10-40%, 10-45%, 10-50%, 10-55%, 10-60%, 10-65%, 10-70%, 10-75%, 10-80%, 10-85%, 10-90%, 10-95%, 15-25%, 15-30%, 15-35%, 15-40%, 15-45%, 15-50%, 15-55%, 15-60%, 15-65%, 15-70%, 15-75%, 15-80%, 15-85%, 15-90%, 15-95%, 20-30%, 20-35%, 20-40%, 20-45%, 20-50%, 20-55%, 20-60%, 20-65%, 20-70%, 20-75%, 20-80%, 20-85%, 20-90%, 20-95%, 25-35%, 25-40%, 25-45%, 25-50%, 25-55%, 25-60%, 25-65%, 25-70%, 25-75%, 25-80%, 25-85%, 25-90%, 25-95%, 30-40%, 30-45%, 30-50%, 30-55%, 30-60%, 30-65%, 30-70%, 30-75%, 30-80%, 30-85%, 30-90%, 30-95%, 35-45%, 35-50%, 35-55%, 35-60%, 35-65%, 35-70%, 35-75%, 35-80%, 35-85%, 35-90%, 35-95%, 40-50%, 40-55%, 40-60%, 40-65%, 40-70%, 40-75%, 40-80%, 40-85%, 40-90%, 40-95%, 45-55%, 45-60%, 45-65%, 45-70%, 45-75%, 45-80%, 45-85%, 45-90%, 45-95%, 50-60%, 50-65%, 50-70%, 50-75%, 50-80%, 50-85%, 50-90%, 50-95%, 55-65%, 55-70%, 55-75%, 55-80%, 55-85%, 55-90%, 55-95%, 60-70%, 60-75%, 60-80%, 60-85%, 60-90%, 60-95%, 65-75%, 65-80%, 65-85%, 65-90%, 65-95%, 70-80%, 70-85%, 70-90%, 70-95%, 75-85%, 75-90%, 75-95%, 80-90%, 80-95%, or 90-95%.

[0361] In some embodiments, the AAV particles of the present disclosure may be used to increase target protein and reduce symptoms of neurological disease in a subject. The

increase of target protein and/or the reduction of symptoms of neurological disease may be, independently, altered (increased for the production of target protein and reduced for the symptoms of neurological disease) by 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or more than 95%, 5-15%, 5-20%, 5-25%, 5-30%, 5-35%, 5-40%, 5-45%, 5-50%, 5-55%, 5-60%, 5-65%, 5-70%, 5-75%, 5-80%, 5-85%, 5-90%, 5-95%, 10-20%, 10-25%, 10-30%, 10-35%, 10-40%, 10-45%, 10-50%, 10-55%, 10-60%, 10-65%, 10-70%, 10-75%, 10-80%, 10-85%, 10-90%, 10-95%, 15-25%, 15-30%, 15-35%, 15-40%, 15-45%, 15-50%, 15-55%, 15-60%, 15-65%, 15-70%, 15-75%, 15-80%, 15-85%, 15-90%, 15-95%, 20-30%, 20-35%, 20-40%, 20-45%, 20-50%, 20-55%, 20-60%, 20-65%, 20-70%, 20-75%, 20-80%, 20-85%, 20-90%, 20-95%, 25-35%, 25-40%, 25-45%, 25-50%, 25-55%, 25-60%, 25-65%, 25-70%, 25-75%, 25-80%, 25-85%, 25-90%, 25-95%, 30-40%, 30-45%, 30-50%, 30-55%, 30-60%, 30-65%, 30-70%, 30-75%, 30-80%, 30-85%, 30-90%, 30-95%, 35-45%, 35-50%, 35-55%, 35-60%, 35-65%, 35-70%, 35-75%, 35-80%, 35-85%, 35-90%, 35-95%, 40-50%, 40-55%, 40-60%, 40-65%, 40-70%, 40-75%, 40-80%, 40-85%, 40-90%, 40-95%, 45-55%, 45-60%, 45-65%, 45-70%, 45-75%, 45-80%, 45-85%, 45-90%, 45-95%, 50-60%, 50-65%, 50-70%, 50-75%, 50-80%, 50-85%, 50-90%, 50-95%, 55-65%, 55-70%, 55-75%, 55-80%, 55-85%, 55-90%, 55-95%, 60-70%, 60-75%, 60-80%, 60-85%, 60-90%, 60-95%, 65-75%, 65-80%, 65-85%, 65-90%, 65-95%, 70-80%, 70-85%, 70-90%, 70-95%, 75-85%, 75-90%, 75-95%, 80-90%, 80-95%, or 90-95%.

[0362] In certain embodiments, the AAV particles of the present disclosure may be used to reduce the decline of functional capacity and activities of daily living as measured by a standard evaluation system such as, but not limited to, the total functional capacity (TFC) scale.

[0363] In certain embodiments, the AAV particles of the present disclosure may be used to improve performance on any assessment used to measure symptoms of neurological disease. Such assessments include, but are not limited to ADAS-cog (Alzheimer Disease Assessment Scale – cognitive), MMSE (Mini-Mental State Examination), GDS (Geriatric Depression Scale), FAQ (Functional Activities Questionnaire), ADL (Activities of Daily Living), GPCOG (General Practitioner Assessment of Cognition), Mini-Cog, AMTS (Abbreviated Mental Test Score), Clock-drawing test, 6-CIT (6-item Cognitive Impairment Test), TYM (Test Your Memory), MoCa (Montreal Cognitive Assessment), ACE-R (Addenbrookes Cognitive Assessment), MIS (Memory Impairment Screen), BADLS (Bristol Activities of Daily Living Scale), Barthel Index, Functional Independence Measure, Instrumental Activities of Daily Living, IQCODE (Informant Questionnaire on Cognitive

Decline in the Elderly), Neuropsychiatric Inventory, The Cohen-Mansfield Agitation Inventory, BEHAVE-AD, EuroQol, Short Form-36 and/or MBR Caregiver Strain Instrument, or any of the other tests as described in Sheehan B (Ther Adv Neurol Disord. 5(6):349-358 (2012)), the contents of which are herein incorporated by reference in their entirety.

[0364] In some embodiments, the present composition is administered as a solo therapeutic or as combination therapeutic for the treatment of neurological disease.

[0365] The AAV particles encoding the target protein may be used in combination with one or more other therapeutic agents. By "in combination with," it is not intended to imply that the agents must be administered at the same time and/or formulated for delivery together, although these methods of delivery are within the scope of the present disclosure. Compositions can be administered concurrently with, prior to, or subsequent to, one or more other desired therapeutics or medical procedures. In general, each agent will be administered at a dose and/or on a time schedule determined for that agent.

[0366] Therapeutic agents that may be used in combination with the AAV particles of the present disclosure can be small molecule compounds which are antioxidants, anti-inflammatory agents, anti-apoptosis agents, calcium regulators, antiglutamatergic agents, structural protein inhibitors, compounds involved in muscle function, and compounds involved in metal ion regulation. As a non-limiting example, the combination therapy may be in combination with one or more neuroprotective agents such as small molecule compounds, growth factors and hormones which have been tested for their neuroprotective effect on motor neuron degeneration.

[0367] Compounds tested for treating neurological disease which may be used in combination with the AAV particles described herein include, but are not limited to, cholinesterase inhibitors (donepezil, rivastigmine, galantamine), NMDA receptor antagonists such as memantine, anti-psychotics, anti-depressants, anti-convulsants (e.g., sodium valproate and levetiracetam for myoclonus), secretase inhibitors, amyloid aggregation inhibitors, copper or zinc modulators, BACE inhibitors, inhibitors of tau aggregation, such as Methylene blue, phenothiazines, anthraquinones, n-phenylamines or rhodamines, microtubule stabilizers such as NAP, taxol or paclitaxel, kinase or phosphatase inhibitors such as those targeting GSK3β (lithium) or PP2A, immunization with Aβ peptides or tau phospho-epitopes, anti-tau or anti-amyloid antibodies, dopamine-depleting agents (e.g., tetrabenazine for chorea), benzodiazepines (e.g., clonazepam for myoclonus, chorea, dystonia, rigidity, and/or spasticity), , amino acid precursors of dopamine (e.g., levodopa for rigidity), skeletal muscle relaxants (e.g., baclofen, tizanidine for rigidity and/or spasticity), inhibitors for acetylcholine

release at the neuromuscular junction to cause muscle paralysis (e.g., botulinum toxin for bruxism and/or dystonia), atypical neuroleptics (e.g., olanzapine and quetiapine for psychosis and/or irritability, risperidone, sulpiride and haloperidol for psychosis, chorea and/or irritability, clozapine for treatment-resistant psychosis, aripiprazole for psychosis with prominent negative symptoms), selective serotonin reuptake inhibitors (SSRIs) (e.g., citalopram, fluoxetine, paroxetine, sertraline, mirtazapine, venlafaxine for depression, anxiety, obsessive compulsive behavior and/or irritability), hypnotics (e.g., xopiclone and/or zolpidem for altered sleep-wake cycle), anticonvulsants (e.g., sodium valproate and carbamazepine for mania or hypomania) and mood stabilizers (e.g., lithium for mania or hypomania).

[0368] Neurotrophic factors may be used in combination therapy with the AAV particles of the present disclosure for treating neurological disease. Generally, a neurotrophic factor is defined as a substance that promotes survival, growth, differentiation, proliferation and/or maturation of a neuron, or stimulates increased activity of a neuron. In some embodiments, the present methods further comprise delivery of one or more trophic factors into the subject in need of treatment. Trophic factors may include, but are not limited to, IGF-I, GDNF, BDNF, CTNF, VEGF, Colivelin, Xaliproden, Thyrotrophin-releasing hormone and ADNF, and variants thereof.

[0369] In one aspect, the AAV particle described herein may be co-administered with AAV particles expressing neurotrophic factors such as AAV-IGF-I (See e.g., Vincent et al., *Neuromolecular medicine*, 2004, 6, 79-85; the contents of which are incorporated herein by reference in their entirety) and AAV-GDNF (See e.g., Wang et al., *J Neurosci*., 2002, 22, 6920-6928; the contents of which are incorporated herein by reference in their entirety).

[0370] In certain embodiments, administration of the AAV particles to a subject will increase the expression of a target protein in a subject and the increase of the expression of the target protein will reduce the effects and/or symptoms of neurological disease in a subject.

[0371] As a non-limiting example, the target protein may be an antibody, or fragment thereof.

AAV Particles Comprising RNAi agents or Modulatory Polynucleotides

[0372] Provided in the present disclosure are methods for introducing the AAV particles of the disclosure, comprising a viral genome with a nucleic acid sequence encoding one or more siRNA molecules into cells, the method comprising introducing into said cells any of the vectors in an amount sufficient for degradation of a target mRNA to occur, thereby

activating target-specific RNAi in the cells. In some aspects, the cells may be neurons such as but not limited to, motor, hippocampal, entorhinal, thalamic, cortical, sensory, sympathetic, or parasympathetic neurons, and glial cells such as astrocytes, microglia, and/or oligodendrocytes.

[0373] Disclosed herein are methods for treating neurological diseases associated with dysfunction of a target protein in a subject in need of treatment. The method optionally comprises administering to the subject a therapeutically effective amount of a composition comprising AAV particles comprising a viral genome with a nucleic acid sequence encoding one or more siRNA molecules. As a non-limiting example, the siRNA molecules can silence target gene expression, inhibit target protein production, and reduce one or more symptoms of neurological disease in the subject such that the subject is therapeutically treated.

[0374] In some embodiments, the composition comprising the AAV particles of the present disclosure comprising a viral genome encoding one or more siRNA molecules comprise an AAV capsid that allows for enhanced transduction of CNS and/or PNS cells after intravenous administration.

[0375] In some embodiments, the composition comprising the AAV particles of the present disclosure with a viral genome encoding at least one siRNA molecule is administered to the central nervous system of the subject. In other embodiments, the composition comprising the AAV particles of the present disclosure is administered to a tissue of a subject (e.g., putamen, thalamus or cortex of the subject).

[0376] In certain embodiments, the composition comprising the AAV particles of the disclosure, comprising a viral genome with a nucleic acid sequence encoding one or more siRNA molecules is administered to the central nervous system of the subject via systemic administration. In certain embodiments, the systemic administration is intravenous injection.

[0377] In certain embodiments, the composition comprising the AAV particles of the disclosure comprising a viral genome with a nucleic acid sequence encoding one or more siRNA molecules is administered to the central nervous system of the subject via intraparenchymal injection. Non-limiting examples of intraparenchymal injections include intraputamenal, intracortical, intrathalamic, intrastriatal, intrahippocampal or into the entorhinal cortex.

[0378] In certain embodiments, the composition comprising the AAV particles comprising a viral genome with a nucleic acid sequence encoding one or more siRNA molecules is administered to the central nervous system of the subject via intraparenchymal injection and intravenous injection.

[0379] In certain embodiments, the AAV particles comprising a viral genome with a nucleic acid sequence encoding one or more siRNA molecules may be delivered into specific types or targeted cells, including, but not limited to, thalamic, hippocampal, entorhinal, cortical, motor, sensory, excitatory, inhibitory, sympathetic, or parasympathetic neurons; glial cells including oligodendrocytes, astrocytes and microglia; and/or other cells surrounding neurons such as T cells.

[0380] In certain embodiments, the AAV particles comprising a viral genome with a nucleic acid sequence encoding one or more siRNA molecules may be delivered to neurons in the putamen, thalamus, and/or cortex.

[0381] In certain embodiments, the AAV particles comprising a viral genome with a nucleic acid sequence encoding one or more siRNA molecules may be used as a therapy for neurological disease.

[0382] In certain embodiments, the AAV particles comprising a viral genome with a nucleic acid sequence encoding one or more siRNA molecules may be used as a therapy for tauopathies.

[0383] In certain embodiments, the AAV particles comprising a viral genome with a nucleic acid sequence encoding one or more siRNA molecules may be used as a therapy for Alzheimer's Disease.

[0384] In certain embodiments, the AAV particles comprising a viral genome with a nucleic acid sequence encoding one or more siRNA molecules may be used as a therapy for Amyotrophic Lateral Sclerosis.

[0385] In certain embodiments, the AAV particles comprising a viral genome with a nucleic acid sequence encoding one or more siRNA molecules may be used as a therapy for Huntington's Disease.

[0386] In certain embodiments, the AAV particles comprising a viral genome with a nucleic acid sequence encoding one or more siRNA molecules may be used as a therapy for Parkinson's Disease.

[0387] In certain embodiments, the AAV particles comprising a viral genome with a nucleic acid sequence encoding one or more siRNA molecules may be used as a therapy for Friedreich's Ataxia.

[0388] In certain embodiments, the administration of AAV particles comprising a viral genome with a nucleic acid sequence encoding one or more siRNA molecules to a subject may lower target protein levels in a subject. The target protein levels may be lowered by about 30%, 40%, 50%, 60%, 70%, 80%, 85%, 90%, 95% and 100%, or at least 20-30%, 20-

40%, 20-50%, 20-60%, 20-70%, 20-80%, 20-90%, 20-95%, 20-100%, 30-40%, 30-50%, 30-60%, 30-70%, 30-80%, 30-90%, 30-95%, 30-100%, 40-50%, 40-60%, 40-70%, 40-80%, 40-90%, 40-95%, 40-100%, 50-60%, 50-70%, 50-80%, 50-90%, 50-95%, 50-100%, 60-70%, 60-80%, 60-90%, 60-95%, 60-100%, 70-80%, 70-90%, 70-95%, 70-100%, 80-90%, 80-95%, 80-100%, 90-95%, 90-100% or 95-100% in a subject such as, but not limited to, the CNS, a region of the CNS, or a specific cell of the CNS of a subject. As a non-limiting example, the AAV particles may lower the protein levels of a target protein by at least 50%. As a non-limiting example, the AAV particles may lower the proteins levels of a target protein by at least 40%.

[0389] In certain embodiments, the administration of AAV particles comprising a viral genome with a nucleic acid sequence encoding one or more siRNA molecules to a subject may lower the expression of a target protein in a subject. The expression of a target protein may be lowered by about 30%, 40%, 50%, 60%, 70%, 80%, 85%, 90%, 95% and 100%, or at least 20-30%, 20-40%, 20-50%, 20-60%, 20-70%, 20-80%, 20-90%, 20-95%, 20-100%, 30-40%, 30-50%, 30-60%, 30-70%, 30-80%, 30-90%, 30-95%, 30-100%, 40-50%, 40-60%, 40-70%, 40-80%, 40-90%, 40-95%, 40-100%, 50-60%, 50-70%, 50-80%, 50-90%, 50-95%, 50-100%, 60-70%, 60-80%, 60-90%, 60-95%, 60-100%, 70-80%, 70-90%, 70-95%, 70-100%, 80-90%, 80-95%, 80-100%, 90-95%, 90-100% or 95-100% in a subject such as, but not limited to, the CNS, a region of the CNS, or a specific cell of the CNS of a subject. As a non-limiting example, the AAV particles may lower the expression of a target protein by at least 50%. As a non-limiting example, the AAV particles may lower the expression of a target protein by at least 40%.

[0390] In certain embodiments, the administration of AAV particles comprising a viral genome with a nucleic acid sequence encoding one or more siRNA molecules to a subject may lower the expression of a target protein in the CNS of a subject. The expression of a target protein may be lowered by about 30%, 40%, 50%, 60%, 70%, 80%, 85%, 90%, 95% and 100%, or at least 20-30%, 20-40%, 20-50%, 20-60%, 20-70%, 20-80%, 20-90%, 20-95%, 20-100%, 30-40%, 30-50%, 30-60%, 30-70%, 30-80%, 30-90%, 30-95%, 30-100%, 40-50%, 40-60%, 40-70%, 40-80%, 40-90%, 40-95%, 40-100%, 50-60%, 50-70%, 50-80%, 50-90%, 50-95%, 50-100%, 60-70%, 60-80%, 60-90%, 60-95%, 60-100%, 70-80%, 70-90%, 70-95%, 70-100%, 80-90%, 80-95%, 80-100%, 90-95%, 90-100% or 95-100% in a subject such as, but not limited to, the CNS, a region of the CNS, or a specific cell of the CNS of a subject. As a non-limiting example, the AAV particles may lower the expression of a target

protein by at least 50%. As a non-limiting example, the AAV particles may lower the expression of a target protein by at least 40%.

[0391] In certain embodiments, the AAV particles comprising a viral genome with a nucleic acid sequence encoding one or more siRNA molecules may be used to suppress a target protein in astrocytes in order to treat neurological disease. Target protein in astrocytes may be suppressed by 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or more than 95%, 5-15%, 5-20%, 5-25%, 5-30%, 5-35%, 5-40%, 5-45%, 5-50%, 5-55%, 5-60%, 5-65%, 5-70%, 5-75%, 5-80%, 5-85%, 5-90%, 5-95%, 10-20%, 10-25%, 10-30%, 10-35%, 10-40%, 10-45%, 10-50%, 10-55%, 10-60%, 10-65%, 10-70%, 10-75%, 10-80%, 10-85%, 10-90%, 10-95%, 15-25%, 15-30%, 15-35%, 15-40%, 15-45%, 15-50%, 15-55%, 15-60%, 15-65%, 15-70%, 15-75%, 15-80%, 15-85%, 15-90%, 15-95%, 20-30%, 20-35%, 20-40%, 20-45%, 20-50%, 20-55%, 20-60%, 20-65%, 20-70%, 20-75%, 20-80%, 20-85%, 20-90%, 20-95%, 25-35%, 25-40%, 25-45%, 25-50%, 25-55%, 25-60%, 25-65%, 25-70%, 25-75%, 25-80%, 25-85%, 25-90%, 25-95%, 30-40%, 30-45%, 30-50%, 30-55%, 30-60%, 30-65%, 30-70%, 30-75%, 30-80%, 30-85%, 30-90%, 30-95%, 35-45%, 35-50%, 35-55%, 35-60%, 35-65%, 35-70%, 35-75%, 35-80%, 35-85%, 35-90%, 35-95%, 40-50%, 40-55%, 40-60%, 40-65%, 40-70%, 40-75%, 40-80%, 40-85%, 40-90%, 40-95%, 45-55%, 45-60%, 45-65%, 45-70%, 45-75%, 45-80%, 45-85%, 45-90%, 45-95%, 50-60%, 50-65%, 50-70%, 50-75%, 50-80%, 50-85%, 50-90%, 50-95%, 55-65%, 55-70%, 55-75%, 55-80%, 55-85%, 55-90%, 55-95%, 60-70%, 60-75%, 60-80%, 60-85%, 60-90%, 60-95%, 65-75%, 65-80%, 65-85%, 65-90%, 65-95%, 70-80%, 70-85%, 70-90%, 70-95%, 75-85%, 75-90%, 75-95%, 80-90%, 80-95%, or 90-95%. Target protein in astrocytes may be reduced may be 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or more than 95%, 5-15%, 5-20%, 5-25%, 5-30%, 5-35%, 5-40%, 5-45%, 5-50%, 5-55%, 5-60%, 5-65%, 5-70%, 5-75%, 5-80%, 5-85%, 5-90%, 5-95%, 10-20%, 10-25%, 10-30%, 10-35%, 10-40%, 10-45%, 10-50%, 10-55%, 10-60%, 10-65%, 10-70%, 10-75%, 10-80%, 10-85%, 10-90%, 10-95%, 15-25%, 15-30%, 15-35%, 15-40%, 15-45%, 15-50%, 15-55%, 15-60%, 15-65%, 15-70%, 15-75%, 15-80%, 15-85%, 15-90%, 15-95%, 20-30%, 20-35%, 20-40%, 20-45%, 20-50%, 20-55%, 20-60%, 20-65%, 20-70%, 20-75%, 20-80%, 20-85%, 20-90%, 20-95%, 25-35%, 25-40%, 25-45%, 25-50%, 25-55%, 25-60%, 25-65%, 25-70%, 25-75%, 25-80%, 25-85%, 25-90%, 25-95%, 30-40%, 30-45%, 30-50%, 30-55%, 30-60%, 30-65%, 30-70%, 30-75%, 30-80%, 30-85%, 30-90%, 30-95%, 35-45%, 35-50%, 35-55%, 35-60%, 35-65%, 35-70%, 35-75%, 35-80%, 35-85%, 35-90%, 35-95%, 40-50%, 40-55%, 40-60%, 40-65%, 40-70%, 40-75%, 40-80%, 40-85%, 40-

90%, 40-95%, 45-55%, 45-60%, 45-65%, 45-70%, 45-75%, 45-80%, 45-85%, 45-90%, 45-95%, 50-60%, 50-65%, 50-70%, 50-75%, 50-80%, 50-85%, 50-90%, 50-95%, 55-65%, 55-70%, 55-75%, 55-80%, 55-85%, 55-90%, 55-95%, 60-70%, 60-75%, 60-80%, 60-85%, 60-90%, 60-95%, 65-75%, 65-80%, 65-85%, 65-90%, 65-95%, 70-80%, 70-85%, 70-90%, 70-95%, 75-85%, 75-90%, 75-95%, 80-90%, 80-95%, or 90-95%.

[0392] In certain embodiments, the AAV particles comprising a viral genome with a nucleic acid sequence encoding one or more siRNA molecules may be used to suppress a target protein in microglia. The suppression of the target protein in microglia may be, independently, suppressed by 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or more than 95%, 5-15%, 5-20%, 5-25%, 5-30%, 5-35%, 5-40%, 5-45%, 5-50%, 5-55%, 5-60%, 5-65%, 5-70%, 5-75%, 5-80%, 5-85%, 5-90%, 5-95%, 10-20%, 10-25%, 10-30%, 10-35%, 10-40%, 10-45%, 10-50%, 10-55%, 10-60%, 10-65%, 10-70%, 10-75%, 10-80%, 10-85%, 10-90%, 10-95%, 15-25%, 15-30%, 15-35%, 15-40%, 15-45%, 15-50%, 15-55%, 15-60%, 15-65%, 15-70%, 15-75%, 15-80%, 15-85%, 15-90%, 15-95%, 20-30%, 20-35%, 20-40%, 20-45%, 20-50%, 20-55%, 20-60%, 20-65%, 20-70%, 20-75%, 20-80%, 20-85%, 20-90%, 20-95%, 25-35%, 25-40%, 25-45%, 25-50%, 25-55%, 25-60%, 25-65%, 25-70%, 25-75%, 25-80%, 25-85%, 25-90%, 25-95%, 30-40%, 30-45%, 30-50%, 30-55%, 30-60%, 30-65%, 30-70%, 30-75%, 30-80%, 30-85%, 30-90%, 30-95%, 35-45%, 35-50%, 35-55%, 35-60%, 35-65%, 35-70%, 35-75%, 35-80%, 35-85%, 35-90%, 35-95%, 40-50%, 40-55%, 40-60%, 40-65%, 40-70%, 40-75%, 40-80%, 40-85%, 40-90%, 40-95%, 45-55%, 45-60%, 45-65%, 45-70%, 45-75%, 45-80%, 45-85%, 45-90%, 45-95%, 50-60%, 50-65%, 50-70%, 50-75%, 50-80%, 50-85%, 50-90%, 50-95%, 55-65%, 55-70%, 55-75%, 55-80%, 55-85%, 55-90%, 55-95%, 60-70%, 60-75%, 60-80%, 60-85%, 60-90%, 60-95%, 65-75%, 65-80%, 65-85%, 65-90%, 65-95%, 70-80%, 70-85%, 70-90%, 70-95%, 75-85%, 75-90%, 75-95%, 80-90%, 80-95%, or 90-95%. The reduction may be 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or more than 95%, 5-15%, 5-20%, 5-25%, 5-30%, 5-35%, 5-40%, 5-45%, 5-50%, 5-55%, 5-60%, 5-65%, 5-70%, 5-75%, 5-80%, 5-85%, 5-90%, 5-95%, 10-20%, 10-25%, 10-30%, 10-35%, 10-40%, 10-45%, 10-50%, 10-55%, 10-60%, 10-65%, 10-70%, 10-75%, 10-80%, 10-85%, 10-90%, 10-95%, 15-25%, 15-30%, 15-35%, 15-40%, 15-45%, 15-50%, 15-55%, 15-60%, 15-65%, 15-70%, 15-75%, 15-80%, 15-85%, 15-90%, 15-95%, 20-30%, 20-35%, 20-40%, 20-45%, 20-50%, 20-55%, 20-60%, 20-65%, 20-70%, 20-75%, 20-80%, 20-85%, 20-90%, 20-95%, 25-35%, 25-40%, 25-45%, 25-50%, 25-55%, 25-60%, 25-65%, 25-70%, 25-75%, 25-80%, 25-85%, 25-90%, 25-95%, 30-40%, 30-45%, 30-50%,

30-55%, 30-60%, 30-65%, 30-70%, 30-75%, 30-80%, 30-85%, 30-90%, 30-95%, 35-45%, 35-50%, 35-55%, 35-60%, 35-65%, 35-70%, 35-75%, 35-80%, 35-85%, 35-90%, 35-95%, 40-50%, 40-55%, 40-60%, 40-65%, 40-70%, 40-75%, 40-80%, 40-85%, 40-90%, 40-95%, 45-55%, 45-60%, 45-65%, 45-70%, 45-75%, 45-80%, 45-85%, 45-90%, 45-95%, 50-60%, 50-65%, 50-70%, 50-75%, 50-80%, 50-85%, 50-90%, 50-95%, 55-65%, 55-70%, 55-75%, 55-80%, 55-85%, 55-90%, 55-95%, 60-70%, 60-75%, 60-80%, 60-85%, 60-90%, 60-95%, 65-75%, 65-80%, 65-85%, 65-90%, 65-95%, 70-80%, 70-85%, 70-90%, 70-95%, 75-85%, 75-90%, 75-95%, 80-90%, 80-95%, or 90-95%.

[0393] In certain embodiments, the AAV particles comprising a viral genome with a nucleic acid sequence encoding one or more siRNA molecules may be used to suppress target protein in cortical neurons. The suppression of a target protein in cortical neurons may be, independently, suppressed by 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or more than 95%, 5-15%, 5-20%, 5-25%, 5-30%, 5-35%, 5-40%, 5-45%, 5-50%, 5-55%, 5-60%, 5-65%, 5-70%, 5-75%, 5-80%, 5-85%, 5-90%, 5-95%, 10-20%, 10-25%, 10-30%, 10-35%, 10-40%, 10-45%, 10-50%, 10-55%, 10-60%, 10-65%, 10-70%, 10-75%, 10-80%, 10-85%, 10-90%, 10-95%, 15-25%, 15-30%, 15-35%, 15-40%, 15-45%, 15-50%, 15-55%, 15-60%, 15-65%, 15-70%, 15-75%, 15-80%, 15-85%, 15-90%, 15-95%, 20-30%, 20-35%, 20-40%, 20-45%, 20-50%, 20-55%, 20-60%, 20-65%, 20-70%, 20-75%, 20-80%, 20-85%, 20-90%, 20-95%, 25-35%, 25-40%, 25-45%, 25-50%, 25-55%, 25-60%, 25-65%, 25-70%, 25-75%, 25-80%, 25-85%, 25-90%, 25-95%, 30-40%, 30-45%, 30-50%, 30-55%, 30-60%, 30-65%, 30-70%, 30-75%, 30-80%, 30-85%, 30-90%, 30-95%, 35-45%, 35-50%, 35-55%, 35-60%, 35-65%, 35-70%, 35-75%, 35-80%, 35-85%, 35-90%, 35-95%, 40-50%, 40-55%, 40-60%, 40-65%, 40-70%, 40-75%, 40-80%, 40-85%, 40-90%, 40-95%, 45-55%, 45-60%, 45-65%, 45-70%, 45-75%, 45-80%, 45-85%, 45-90%, 45-95%, 50-60%, 50-65%, 50-70%, 50-75%, 50-80%, 50-85%, 50-90%, 50-95%, 55-65%, 55-70%, 55-75%, 55-80%, 55-85%, 55-90%, 55-95%, 60-70%, 60-75%, 60-80%, 60-85%, 60-90%, 60-95%, 65-75%, 65-80%, 65-85%, 65-90%, 65-95%, 70-80%, 70-85%, 70-90%, 70-95%, 75-85%, 75-90%, 75-95%, 80-90%, 80-95%, or 90-95%. The reduction may be 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or more than 95%, 5-15%, 5-20%, 5-25%, 5-30%, 5-35%, 5-40%, 5-45%, 5-50%, 5-55%, 5-60%, 5-65%, 5-70%, 5-75%, 5-80%, 5-85%, 5-90%, 5-95%, 10-20%, 10-25%, 10-30%, 10-35%, 10-40%, 10-45%, 10-50%, 10-55%, 10-60%, 10-65%, 10-70%, 10-75%, 10-80%, 10-85%, 10-90%, 10-95%, 15-25%, 15-30%, 15-35%, 15-40%, 15-45%, 15-50%, 15-55%, 15-60%, 15-65%, 15-70%, 15-75%, 15-80%, 15-85%, 15-90%, 15-95%,

20-30%, 20-35%, 20-40%, 20-45%, 20-50%, 20-55%, 20-60%, 20-65%, 20-70%, 20-75%, 20-80%, 20-85%, 20-90%, 20-95%, 25-35%, 25-40%, 25-45%, 25-50%, 25-55%, 25-60%, 25-65%, 25-70%, 25-75%, 25-80%, 25-85%, 25-90%, 25-95%, 30-40%, 30-45%, 30-50%, 30-55%, 30-60%, 30-65%, 30-70%, 30-75%, 30-80%, 30-85%, 30-90%, 30-95%, 35-45%, 35-50%, 35-55%, 35-60%, 35-65%, 35-70%, 35-75%, 35-80%, 35-85%, 35-90%, 35-95%, 40-50%, 40-55%, 40-60%, 40-65%, 40-70%, 40-75%, 40-80%, 40-85%, 40-90%, 40-95%, 45-55%, 45-60%, 45-65%, 45-70%, 45-75%, 45-80%, 45-85%, 45-90%, 45-95%, 50-60%, 50-65%, 50-70%, 50-75%, 50-80%, 50-85%, 50-90%, 50-95%, 55-65%, 55-70%, 55-75%, 55-80%, 55-85%, 55-90%, 55-95%, 60-70%, 60-75%, 60-80%, 60-85%, 60-90%, 60-95%, 65-75%, 65-80%, 65-85%, 65-90%, 65-95%, 70-80%, 70-85%, 70-90%, 70-95%, 75-85%, 75-90%, 75-95%, 80-90%, 80-95%, or 90-95%.

[0394] In certain embodiments, the AAV particles comprising a viral genome with a nucleic acid sequence encoding one or more siRNA molecules may be used to suppress a target protein in hippocampal neurons. The suppression of a target protein in the hippocampal neurons may be, independently, suppressed by 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or more than 95%, 5-15%, 5-20%, 5-25%, 5-30%, 5-35%, 5-40%, 5-45%, 5-50%, 5-55%, 5-60%, 5-65%, 5-70%, 5-75%, 5-80%, 5-85%, 5-90%, 5-95%, 10-20%, 10-25%, 10-30%, 10-35%, 10-40%, 10-45%, 10-50%, 10-55%, 10-60%, 10-65%, 10-70%, 10-75%, 10-80%, 10-85%, 10-90%, 10-95%, 15-25%, 15-30%, 15-35%, 15-40%, 15-45%, 15-50%, 15-55%, 15-60%, 15-65%, 15-70%, 15-75%, 15-80%, 15-85%, 15-90%, 15-95%, 20-30%, 20-35%, 20-40%, 20-45%, 20-50%, 20-55%, 20-60%, 20-65%, 20-70%, 20-75%, 20-80%, 20-85%, 20-90%, 20-95%, 25-35%, 25-40%, 25-45%, 25-50%, 25-55%, 25-60%, 25-65%, 25-70%, 25-75%, 25-80%, 25-85%, 25-90%, 25-95%, 30-40%, 30-45%, 30-50%, 30-55%, 30-60%, 30-65%, 30-70%, 30-75%, 30-80%, 30-85%, 30-90%, 30-95%, 35-45%, 35-50%, 35-55%, 35-60%, 35-65%, 35-70%, 35-75%, 35-80%, 35-85%, 35-90%, 35-95%, 40-50%, 40-55%, 40-60%, 40-65%, 40-70%, 40-75%, 40-80%, 40-85%, 40-90%, 40-95%, 45-55%, 45-60%, 45-65%, 45-70%, 45-75%, 45-80%, 45-85%, 45-90%, 45-95%, 50-60%, 50-65%, 50-70%, 50-75%, 50-80%, 50-85%, 50-90%, 50-95%, 55-65%, 55-70%, 55-75%, 55-80%, 55-85%, 55-90%, 55-95%, 60-70%, 60-75%, 60-80%, 60-85%, 60-90%, 60-95%, 65-75%, 65-80%, 65-85%, 65-90%, 65-95%, 70-80%, 70-85%, 70-90%, 70-95%, 75-85%, 75-90%, 75-95%, 80-90%, 80-95%, or 90-95%. The reduction may be 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or more than 95%, 5-15%, 5-20%, 5-25%, 5-30%, 5-35%, 5-40%, 5-45%, 5-50%, 5-55%, 5-60%, 5-65%, 5-70%, 5-75%, 5-80%, 5-85%, 5-90%,

5-95%, 10-20%, 10-25%, 10-30%, 10-35%, 10-40%, 10-45%, 10-50%, 10-55%, 10-60%, 10-65%, 10-70%, 10-75%, 10-80%, 10-85%, 10-90%, 10-95%, 15-25%, 15-30%, 15-35%, 15-40%, 15-45%, 15-50%, 15-55%, 15-60%, 15-65%, 15-70%, 15-75%, 15-80%, 15-85%, 15-90%, 15-95%, 20-30%, 20-35%, 20-40%, 20-45%, 20-50%, 20-55%, 20-60%, 20-65%, 20-70%, 20-75%, 20-80%, 20-85%, 20-90%, 20-95%, 25-35%, 25-40%, 25-45%, 25-50%, 25-55%, 25-60%, 25-65%, 25-70%, 25-75%, 25-80%, 25-85%, 25-90%, 25-95%, 30-40%, 30-45%, 30-50%, 30-55%, 30-60%, 30-65%, 30-70%, 30-75%, 30-80%, 30-85%, 30-90%, 30-95%, 35-45%, 35-50%, 35-55%, 35-60%, 35-65%, 35-70%, 35-75%, 35-80%, 35-85%, 35-90%, 35-95%, 40-50%, 40-55%, 40-60%, 40-65%, 40-70%, 40-75%, 40-80%, 40-85%, 40-90%, 40-95%, 45-55%, 45-60%, 45-65%, 45-70%, 45-75%, 45-80%, 45-85%, 45-90%, 45-95%, 50-60%, 50-65%, 50-70%, 50-75%, 50-80%, 50-85%, 50-90%, 50-95%, 55-65%, 55-70%, 55-75%, 55-80%, 55-85%, 55-90%, 55-95%, 60-70%, 60-75%, 60-80%, 60-85%, 60-90%, 60-95%, 65-75%, 65-80%, 65-85%, 65-90%, 65-95%, 70-80%, 70-85%, 70-90%, 70-95%, 75-85%, 75-90%, 75-95%, 80-90%, 80-95%, or 90-95%.

[0395] In certain embodiments, the AAV particles comprising a viral genome with a nucleic acid sequence encoding one or more siRNA molecules may be used to suppress a target protein in DRG and/or sympathetic neurons. The suppression of a target protein in the DRG and/or sympathetic neurons may be, independently, suppressed by 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or more than 95%, 5-15%, 5-20%, 5-25%, 5-30%, 5-35%, 5-40%, 5-45%, 5-50%, 5-55%, 5-60%, 5-65%, 5-70%, 5-75%, 5-80%, 5-85%, 5-90%, 5-95%, 10-20%, 10-25%, 10-30%, 10-35%, 10-40%, 10-45%, 10-50%, 10-55%, 10-60%, 10-65%, 10-70%, 10-75%, 10-80%, 10-85%, 10-90%, 10-95%, 15-25%, 15-30%, 15-35%, 15-40%, 15-45%, 15-50%, 15-55%, 15-60%, 15-65%, 15-70%, 15-75%, 15-80%, 15-85%, 15-90%, 15-95%, 20-30%, 20-35%, 20-40%, 20-45%, 20-50%, 20-55%, 20-60%, 20-65%, 20-70%, 20-75%, 20-80%, 20-85%, 20-90%, 20-95%, 25-35%, 25-40%, 25-45%, 25-50%, 25-55%, 25-60%, 25-65%, 25-70%, 25-75%, 25-80%, 25-85%, 25-90%, 25-95%, 30-40%, 30-45%, 30-50%, 30-55%, 30-60%, 30-65%, 30-70%, 30-75%, 30-80%, 30-85%, 30-90%, 30-95%, 35-45%, 35-50%, 35-55%, 35-60%, 35-65%, 35-70%, 35-75%, 35-80%, 35-85%, 35-90%, 35-95%, 40-50%, 40-55%, 40-60%, 40-65%, 40-70%, 40-75%, 40-80%, 40-85%, 40-90%, 40-95%, 45-55%, 45-60%, 45-65%, 45-70%, 45-75%, 45-80%, 45-85%, 45-90%, 45-95%, 50-60%, 50-65%, 50-70%, 50-75%, 50-80%, 50-85%, 50-90%, 50-95%, 55-65%, 55-70%, 55-75%, 55-80%, 55-85%, 55-90%, 55-95%, 60-70%, 60-75%, 60-80%, 60-85%, 60-90%, 60-95%, 65-75%, 65-80%, 65-85%, 65-90%, 65-95%, 70-80%, 70-85%, 70-90%, 70-95%, 75-85%, 75-90%, 75-95%, 80-

90%, 80-95%, or 90-95%. The reduction may be 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or more than 95%, 5-15%, 5-20%, 5-25%, 5-30%, 5-35%, 5-40%, 5-45%, 5-50%, 5-55%, 5-60%, 5-65%, 5-70%, 5-75%, 5-80%, 5-85%, 5-90%, 5-95%, 10-20%, 10-25%, 10-30%, 10-35%, 10-40%, 10-45%, 10-50%, 10-55%, 10-60%, 10-65%, 10-70%, 10-75%, 10-80%, 10-85%, 10-90%, 10-95%, 15-25%, 15-30%, 15-35%, 15-40%, 15-45%, 15-50%, 15-55%, 15-60%, 15-65%, 15-70%, 15-75%, 15-80%, 15-85%, 15-90%, 15-95%, 20-30%, 20-35%, 20-40%, 20-45%, 20-50%, 20-55%, 20-60%, 20-65%, 20-70%, 20-75%, 20-80%, 20-85%, 20-90%, 20-95%, 25-35%, 25-40%, 25-45%, 25-50%, 25-55%, 25-60%, 25-65%, 25-70%, 25-75%, 25-80%, 25-85%, 25-90%, 25-95%, 30-40%, 30-45%, 30-50%, 30-55%, 30-60%, 30-65%, 30-70%, 30-75%, 30-80%, 30-85%, 30-90%, 30-95%, 35-45%, 35-50%, 35-55%, 35-60%, 35-65%, 35-70%, 35-75%, 35-80%, 35-85%, 35-90%, 35-95%, 40-50%, 40-55%, 40-60%, 40-65%, 40-70%, 40-75%, 40-80%, 40-85%, 40-90%, 40-95%, 45-55%, 45-60%, 45-65%, 45-70%, 45-75%, 45-80%, 45-85%, 45-90%, 45-95%, 50-60%, 50-65%, 50-70%, 50-75%, 50-80%, 50-85%, 50-90%, 50-95%, 55-65%, 55-70%, 55-75%, 55-80%, 55-85%, 55-90%, 55-95%, 60-70%, 60-75%, 60-80%, 60-85%, 60-90%, 60-95%, 65-75%, 65-80%, 65-85%, 65-90%, 65-95%, 70-80%, 70-85%, 70-90%, 70-95%, 75-85%, 75-90%, 75-95%, 80-90%, 80-95%, or 90-95%.

[0396] In certain embodiments, the AAV particles comprising a viral genome with a nucleic acid sequence encoding one or more siRNA molecules may be used to suppress a target protein in sensory neurons in order to treat neurological disease. Target protein in sensory neurons may be suppressed by 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or more than 95%, 5-15%, 5-20%, 5-25%, 5-30%, 5-35%, 5-40%, 5-45%, 5-50%, 5-55%, 5-60%, 5-65%, 5-70%, 5-75%, 5-80%, 5-85%, 5-90%, 5-95%, 10-20%, 10-25%, 10-30%, 10-35%, 10-40%, 10-45%, 10-50%, 10-55%, 10-60%, 10-65%, 10-70%, 10-75%, 10-80%, 10-85%, 10-90%, 10-95%, 15-25%, 15-30%, 15-35%, 15-40%, 15-45%, 15-50%, 15-55%, 15-60%, 15-65%, 15-70%, 15-75%, 15-80%, 15-85%, 15-90%, 15-95%, 20-30%, 20-35%, 20-40%, 20-45%, 20-50%, 20-55%, 20-60%, 20-65%, 20-70%, 20-75%, 20-80%, 20-85%, 20-90%, 20-95%, 25-35%, 25-40%, 25-45%, 25-50%, 25-55%, 25-60%, 25-65%, 25-70%, 25-75%, 25-80%, 25-85%, 25-90%, 25-95%, 30-40%, 30-45%, 30-50%, 30-55%, 30-60%, 30-65%, 30-70%, 30-75%, 30-80%, 30-85%, 30-90%, 30-95%, 35-45%, 35-50%, 35-55%, 35-60%, 35-65%, 35-70%, 35-75%, 35-80%, 35-85%, 35-90%, 35-95%, 40-50%, 40-55%, 40-60%, 40-65%, 40-70%, 40-75%, 40-80%, 40-85%, 40-90%, 40-95%, 45-55%, 45-60%, 45-65%, 45-70%, 45-75%, 45-80%, 45-85%, 45-90%, 45-95%, 50-60%, 50-65%, 50-70%, 50-75%, 50-80%, 50-85%, 50-90%,

50-95%, 55-65%, 55-70%, 55-75%, 55-80%, 55-85%, 55-90%, 55-95%, 60-70%, 60-75%, 60-80%, 60-85%, 60-90%, 60-95%, 65-75%, 65-80%, 65-85%, 65-90%, 65-95%, 70-80%, 70-85%, 70-90%, 70-95%, 75-85%, 75-90%, 75-95%, 80-90%, 80-95%, or 90-95%. Target protein in the sensory neurons may be reduced may be 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or more than 95%, 5-15%, 5-20%, 5-25%, 5-30%, 5-35%, 5-40%, 5-45%, 5-50%, 5-55%, 5-60%, 5-65%, 5-70%, 5-75%, 5-80%, 5-85%, 5-90%, 5-95%, 10-20%, 10-25%, 10-30%, 10-35%, 10-40%, 10-45%, 10-50%, 10-55%, 10-60%, 10-65%, 10-70%, 10-75%, 10-80%, 10-85%, 10-90%, 10-95%, 15-25%, 15-30%, 15-35%, 15-40%, 15-45%, 15-50%, 15-55%, 15-60%, 15-65%, 15-70%, 15-75%, 15-80%, 15-85%, 15-90%, 15-95%, 20-30%, 20-35%, 20-40%, 20-45%, 20-50%, 20-55%, 20-60%, 20-65%, 20-70%, 20-75%, 20-80%, 20-85%, 20-90%, 20-95%, 25-35%, 25-40%, 25-45%, 25-50%, 25-55%, 25-60%, 25-65%, 25-70%, 25-75%, 25-80%, 25-85%, 25-90%, 25-95%, 30-40%, 30-45%, 30-50%, 30-55%, 30-60%, 30-65%, 30-70%, 30-75%, 30-80%, 30-85%, 30-90%, 30-95%, 35-45%, 35-50%, 35-55%, 35-60%, 35-65%, 35-70%, 35-75%, 35-80%, 35-85%, 35-90%, 35-95%, 40-50%, 40-55%, 40-60%, 40-65%, 40-70%, 40-75%, 40-80%, 40-85%, 40-90%, 40-95%, 45-55%, 45-60%, 45-65%, 45-70%, 45-75%, 45-80%, 45-85%, 45-90%, 45-95%, 50-60%, 50-65%, 50-70%, 50-75%, 50-80%, 50-85%, 50-90%, 50-95%, 55-65%, 55-70%, 55-75%, 55-80%, 55-85%, 55-90%, 55-95%, 60-70%, 60-75%, 60-80%, 60-85%, 60-90%, 60-95%, 65-75%, 65-80%, 65-85%, 65-90%, 65-95%, 70-80%, 70-85%, 70-90%, 70-95%, 75-85%, 75-90%, 75-95%, 80-90%, 80-95%, or 90-95%.

[0397] In certain embodiments, the AAV particles comprising a viral genome with a nucleic acid sequence encoding one or more siRNA molecules may be used to suppress a target protein and reduce symptoms of neurological disease in a subject. The suppression of target protein and/or the reduction of symptoms of neurological disease may be, independently, reduced or suppressed by 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or more than 95%, 5-15%, 5-20%, 5-25%, 5-30%, 5-35%, 5-40%, 5-45%, 5-50%, 5-55%, 5-60%, 5-65%, 5-70%, 5-75%, 5-80%, 5-85%, 5-90%, 5-95%, 10-20%, 10-25%, 10-30%, 10-35%, 10-40%, 10-45%, 10-50%, 10-55%, 10-60%, 10-65%, 10-70%, 10-75%, 10-80%, 10-85%, 10-90%, 10-95%, 15-25%, 15-30%, 15-35%, 15-40%, 15-45%, 15-50%, 15-55%, 15-60%, 15-65%, 15-70%, 15-75%, 15-80%, 15-85%, 15-90%, 15-95%, 20-30%, 20-35%, 20-40%, 20-45%, 20-50%, 20-55%, 20-60%, 20-65%, 20-70%, 20-75%, 20-80%, 20-85%, 20-90%, 20-95%, 25-35%, 25-40%, 25-45%, 25-50%, 25-55%, 25-60%, 25-65%, 25-70%, 25-75%, 25-80%, 25-85%, 25-90%,

25-95%, 30-40%, 30-45%, 30-50%, 30-55%, 30-60%, 30-65%, 30-70%, 30-75%, 30-80%, 30-85%, 30-90%, 30-95%, 35-45%, 35-50%, 35-55%, 35-60%, 35-65%, 35-70%, 35-75%, 35-80%, 35-85%, 35-90%, 35-95%, 40-50%, 40-55%, 40-60%, 40-65%, 40-70%, 40-75%, 40-80%, 40-85%, 40-90%, 40-95%, 45-55%, 45-60%, 45-65%, 45-70%, 45-75%, 45-80%, 45-85%, 45-90%, 45-95%, 50-60%, 50-65%, 50-70%, 50-75%, 50-80%, 50-85%, 50-90%, 50-95%, 55-65%, 55-70%, 55-75%, 55-80%, 55-85%, 55-90%, 55-95%, 60-70%, 60-75%, 60-80%, 60-85%, 60-90%, 60-95%, 65-75%, 65-80%, 65-85%, 65-90%, 65-95%, 70-80%, 70-85%, 70-90%, 70-95%, 75-85%, 75-90%, 75-95%, 80-90%, 80-95%, or 90-95%.

[0398] In certain embodiments, the AAV particles comprising a viral genome with a nucleic acid sequence encoding one or more siRNA molecules may be used to reduce the decline of functional capacity and activities of daily living as measured by a standard evaluation system such as, but not limited to, the total functional capacity (TFC) scale.

[0399] In some embodiments, the present composition is administered as a solo therapeutic or as combination therapeutic for the treatment of neurological disease.

[0400] The AAV particles comprising a viral genome with a nucleic acid sequence encoding one or more siRNA molecules may be used in combination with one or more other therapeutic agents. By "in combination with," it is not intended to imply that the agents must be administered at the same time and/or formulated for delivery together, although these methods of delivery are within the scope of the present disclosure. Compositions can be administered concurrently with, prior to, or subsequent to, one or more other desired therapeutics or medical procedures. In general, each agent will be administered at a dose and/or on a time schedule determined for that agent.

[0401] Therapeutic agents that may be used in combination with the AAV particles comprising a viral genome with a nucleic acid sequence encoding one or more siRNA molecules can be small molecule compounds which are antioxidants, anti-inflammatory agents, anti-apoptosis agents, calcium regulators, antiglutamatergic agents, structural protein inhibitors, compounds involved in muscle function, and compounds involved in metal ion regulation.

[0402] Compounds tested for treating neurological disease which may be used in combination with the AAV particles comprising a viral genome with a nucleic acid sequence encoding one or more siRNA molecules include, but are not limited to, cholinesterase inhibitors (donepezil, rivastigmine, galantamine), NMDA receptor antagonists such as memantine, anti-psychotics, anti-depressants, anti-convulsants (e.g., sodium valproate and levetiracetam for myoclonus), secretase inhibitors, amyloid aggregation inhibitors, copper or

zinc modulators, BACE inhibitors, inhibitors of tau aggregation, such as Methylene blue, phenothiazines, anthraquinones, n-phenylamines or rhodamines, microtubule stabilizers such as NAP, taxol or paclitaxel, kinase or phosphatase inhibitors such as those targeting GSK3β (lithium) or PP2A, immunization with Aβ peptides or tau phospho-epitopes, anti-tau or anti-amyloid antibodies, dopamine-depleting agents (e.g., tetrabenazine for chorea), benzodiazepines (e.g., clonazepam for myoclonus, chorea, dystonia, rigidity, and/or spasticity), , amino acid precursors of dopamine (e.g., levodopa for rigidity), skeletal muscle relaxants (e.g., baclofen, tizanidine for rigidity and/or spasticity), inhibitors for acetylcholine release at the neuromuscular junction to cause muscle paralysis (e.g., botulinum toxin for bruxism and/or dystonia), atypical neuroleptics (e.g., olanzapine and quetiapine for psychosis and/or irritability, risperidone, sulpiride and haloperidol for psychosis, chorea and/or irritability, clozapine for treatment-resistant psychosis, aripiprazole for psychosis with prominent negative symptoms), selective serotonin reuptake inhibitors (SSRIs) (e.g., citalopram, fluoxetine, paroxetine, sertraline, mirtazapine, venlafaxine for depression, anxiety, obsessive compulsive behavior and/or irritability), hypnotics (e.g., xopiclone and/or zolpidem for altered sleep-wake cycle), anticonvulsants (e.g., sodium valproate and carbamazepine for mania or hypomania) and mood stabilizers (e.g., lithium for mania or hypomania).

[0403] Neurotrophic factors may be used in combination therapy with the AAV particles comprising a viral genome with a nucleic acid sequence encoding one or more siRNA molecules for treating neurological disease. Generally, a neurotrophic factor is defined as a substance that promotes survival, growth, differentiation, proliferation and/or maturation of a neuron, or stimulates increased activity of a neuron. In some embodiments, the present methods further comprise delivery of one or more trophic factors into the subject in need of treatment. Trophic factors may include, but are not limited to, IGF-I, GDNF, BDNF, CTNF, VEGF, Colivelin, Xaliproden, Thyrotrophin-releasing hormone and ADNF, and variants thereof.

[0404] In one aspect, the AAV particle encoding the nucleic acid sequence for the at least one siRNA duplex targeting the gene of interest may be co-administered with AAV particles expressing neurotrophic factors such as AAV-IGF-I (See e.g., Vincent et al., *Neuromolecular medicine*, 2004, 6, 79-85; the content of which is incorporated herein by reference in its entirety) and AAV-GDNF (See e.g., Wang et al., *J Neurosci*., 2002, 22, 6920-6928; the contents of which are incorporated herein by reference in their entirety).

[0405] In certain embodiments, administration of the AAV particles to a subject will reduce the expression of a target protein in a subject and the reduction of expression of the target protein will reduce the effects and/or symptoms of neurological disease in a subject.

IV. FORMULATION

Pharmaceutical compositions

[0406] According to the present disclosure the AAV particles may be prepared as pharmaceutical compositions. As used herein the term "pharmaceutical composition" refers to compositions comprising at least one active ingredient and optionally, one or more pharmaceutically acceptable excipients.

[0407] Relative amounts of the active ingredient (e.g. AAV particle), a pharmaceutically acceptable excipient, and/or any additional ingredients in a pharmaceutical composition in accordance with the present disclosure may vary. Differences in the constitution of a pharmaceutical composition may depend upon the identity, size, and/or condition of the subject being treated, the route by which the composition is to be administered, the nature of the AAV particle composition or the excipient, and/or any other factor. The composition may comprise between 0.0001% and 99% (w/w) of the active ingredient. By way of example, the composition may comprise between 0.0001% and 100%, e.g., between .5 and 50%, between 1-30%, between 5-80%, or at least 80% (w/w) active ingredient.

[0408] In certain embodiments, the pharmaceutical composition comprises AAV particles having one type of AAV capsid protein. In another embodiment, the pharmaceutical composition comprises a mixture of AAV particles, having different AAV capsid proteins.

[0409] In some embodiments, the pharmaceutical compositions described herein may comprise at AAV particles comprising a viral genome encoding at least one payload. As a non-limiting example, the pharmaceutical compositions may contain an AAV particle with 1, 2, 3, 4, 5, or more payloads.

[0410] Although the descriptions of pharmaceutical compositions provided herein are principally directed to pharmaceutical compositions which are suitable for administration to humans, it will be understood by the skilled artisan that such compositions are generally suitable for administration to any other animal, e.g., to non-human animals, e.g. non-human mammals. Modification of pharmaceutical compositions suitable for administration to humans in order to render the compositions suitable for administration to various animals is well understood, and the ordinarily skilled veterinary pharmacologist can design and/or perform such modification with merely ordinary, if any, experimentation. Subjects to which administration of the pharmaceutical compositions is contemplated include, but are not

limited to, humans and/or other primates; mammals, including commercially relevant mammals such as cattle, pigs, horses, sheep, cats, dogs, mice, rats, birds, including commercially relevant birds such as poultry, chickens, ducks, geese, and/or turkeys.

[0411] In some embodiments, pharmaceutical compositions are administered to humans, human patients or subjects.

[0412] In certain embodiments, the pharmaceutical composition is administered to the human, human patient, and/or subject by intravenous delivery. The pharmaceutical composition may be prepared in a manner optimized for administration by intravenous delivery.

Formulation

[0413] Formulations of the present disclosure can include, without limitation, one or more AAV particles, saline, liposomes, lipid nanoparticles, polymers, peptides, proteins, cells transfected with viral vectors (e.g., for transfer or transplantation into a subject) and combinations thereof.

[0414] Formulations of the pharmaceutical compositions described herein may be prepared by any method known or hereafter developed in the art of pharmacology.

[0415] In general, such preparatory methods include the step of associating the active ingredient with an excipient and/or one or more other accessory ingredients. As used herein, the phrase "active ingredient" generally refers either to an AAV particle with a viral genome encoding a payload or to the end product, or payload itself.

[0416] A pharmaceutical composition in accordance with the present disclosure may be prepared, packaged, and/or sold in bulk, as a single unit dose, and/or as a plurality of single unit doses. As used herein, a "unit dose" refers to a discrete amount of the pharmaceutical composition comprising a predetermined amount of the active ingredient. The amount of the active ingredient is generally equal to the dosage of the active ingredient which would be administered to a subject and/or a convenient fraction of such a dosage such as, for example, one-half or one-third of such a dosage.

[0417] In some embodiments, the AAV formulations described herein may contain sufficient AAV particles for expression of at least one expressed functional payload. As a non-limiting example, the AAV particles may contain viral genomes encoding 1, 2, 3, 4 or 5 functional payloads.

[0418] In some embodiments, the formulations described herein may contain at least one AAV particle comprising a viral genome with a nucleic acid sequence encoding a protein of interest. The protein of interest may include but is not limited to an antibody, aromatic L-

amino acid decarboxylase (AADC), survival motor neuron 1 (SMN1), frataxin (FXN), APOE (APOE2, APOE3, or APOE4), GBA1, GRN, ASPA, CLN2, GLB1, SGSH, NAGLU, IDS, NPC1, or GAN.

[0419] In some embodiments, the formulations described herein may contain at least one AAV particle comprising a viral genome with a nucleic acid sequence encoding the siRNA molecules described herein. In certain embodiments, the siRNA molecules may target a gene of interest at one target site. In another embodiment, the formulation comprises a plurality of AAV particles, each AAV particle comprising a viral genome with a nucleic acid sequence encoding a siRNA molecule targeting the gene of interest at a different target site. The target gene may be targeted at 1, 2, 3, 4, 5 or more than 5 sites. In certain embodiments, the target gene may include, but is not limited to, SOD1, MAPT, APOE, HTT, C9ORF72, TDP-43, APP, BACE, SNCA, ATXN1, ATXN2, ATXN3, ATXN7, SCN1A-SCN5A, or SCN8A-SCN11A.

[0420] According to the present disclosure AAV particles may be formulated for systemic delivery. In another embodiment, AAV particles may be formulated for CNS delivery. The formulation of AAV particles may be optimized for delivery to any target tissue by any administration route described herein. As a non-limiting example, the formulation of AAV particles may be optimized for CNS as the target tissue and intravenous administration as the method of delivery. Alternatively, the formulation of AAV particles may be optimized for DRG as the target tissue and intravenous administration as the method of delivery.

[0421] The AAV particles of the disclosure can be formulated using one or more excipients to: (1) increase stability; (2) increase cell transfection or transduction; (3) permit the sustained or delayed expression of the payload; (4) alter the biodistribution (e.g., target the viral particle to specific tissues or cell types); (5) increase the translation of encoded protein; (6) alter the release profile of encoded protein; and/or (7) allow for regulatable expression of the payload.

[0422] In some embodiments, a pharmaceutically acceptable excipient may be at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% pure. In some embodiments, an excipient is approved for use for humans and for veterinary use. In some embodiments, an excipient may be approved by United States Food and Drug Administration. In some embodiments, an excipient may be of pharmaceutical grade. In some embodiments, an excipient may meet the standards of the United States Pharmacopoeia (USP), the European Pharmacopoeia (EP), the British Pharmacopoeia, and/or the International Pharmacopoeia.

[0423] Excipients, as used herein, include, but are not limited to, any and all solvents, dispersion media, diluents, or other liquid vehicles, dispersion or suspension aids, surface active agents, isotonic agents, thickening or emulsifying agents, preservatives, and the like, as suited to the particular dosage form desired. Various excipients for formulating pharmaceutical compositions and techniques for preparing the composition are known in the art (see Remington: The Science and Practice of Pharmacy, 21st Edition, A. R. Gennaro, Lippincott, Williams & Wilkins, Baltimore, MD, 2006; incorporated herein by reference in its entirety). The use of a conventional excipient medium may be contemplated within the scope of the present disclosure, except insofar as any conventional excipient medium may be incompatible with a substance or its derivatives, such as by producing any undesirable biological effect or otherwise interacting in a deleterious manner with any other component(s) of the pharmaceutical composition.

[0424] Exemplary diluents include, but are not limited to, calcium carbonate, sodium carbonate, calcium phosphate, dicalcium phosphate, calcium sulfate, calcium hydrogen phosphate, sodium phosphate lactose, sucrose, cellulose, microcrystalline cellulose, kaolin, mannitol, sorbitol, inositol, sodium chloride, dry starch, cornstarch, powdered sugar, *etc.*, and/or combinations thereof.

[0425] In some embodiments, AAV particle formulations may comprise at least one inactive ingredient. As used herein, the term "inactive ingredient" refers to one or more agents that do not contribute to the activity of the active ingredient of the pharmaceutical composition included in formulations. In some embodiments, all, none or some of the inactive ingredients which may be used in the formulations of the present disclosure may be approved by the US Food and Drug Administration (FDA). Inactive ingredients and their use are well known in the art.

[0426] Pharmaceutical composition formulations of AAV particles disclosed herein may include cations or anions. In certain embodiments, the formulations include metal cations such as, but not limited to, Zn2+, Ca2+, Cu2+, Mn2+, Mg+ and combinations thereof. As a non-limiting example, formulations may include polymers and complexes with a metal cation (*See e.g.*, U.S. Pat. Nos. 6265389 and 6555525, each of which is herein incorporated by reference in its entirety).

[0427] Formulations of the disclosure may also include one or more pharmaceutically acceptable salts. As used herein, "pharmaceutically acceptable salts" refers to derivatives of the disclosed compounds wherein the parent compound is modified by converting an existing acid or base moiety to its salt form (e.g., by reacting the free base group with a suitable

organic acid). Examples of pharmaceutically acceptable salts include, but are not limited to, mineral or organic acid salts of basic residues such as amines; alkali or organic salts of acidic residues such as carboxylic acids; and the like. Representative acid addition salts include acetate, acetic acid, adipate, alginate, ascorbate, aspartate, benzenesulfonate, benzene sulfonic acid, benzoate, bisulfate, borate, butyrate, camphorate, camphor sulfonate, citrate, cyclopentane propionate, digluconate, dodecyl sulfate, ethane sulfonate, fumarate, glucoheptonate, glycerophosphate, hemi sulfate, heptonate, hexanoate, hydrobromide, hydrochloride, hydroiodide, 2-hydroxy-ethanesulfonate, lactobionate, lactate, laurate, lauryl sulfate, malate, maleate, malonate, methane sulfonate, 2-naphthalenesulfonate, nicotinate, nitrate, oleate, oxalate, palmitate, pamoate, pectinate, persulfate, 3-phenylpropionate, phosphate, picrate, pivalate, propionate, stearate, succinate, sulfate, tartrate, thiocyanate, toluene sulfonate, undecanoate, valerate salts, and the like. Representative alkali or alkaline earth metal salts include sodium, lithium, potassium, calcium, magnesium, and the like, as well as nontoxic ammonium, quaternary ammonium, and amine cations, including, but not limited to ammonium, tetramethylammonium, tetraethylammonium, methylamine, dimethylamine, trimethylamine, triethylamine, ethylamine, and the like. The pharmaceutically acceptable salts of the present disclosure include the conventional non-toxic salts of the parent compound formed, for example, from non-toxic inorganic or organic acids.

[0428] Solvates may be prepared by crystallization, recrystallization, or precipitation from a solution that includes organic solvents, water, or a mixture thereof. Examples of suitable solvents are ethanol, water (for example, mono-, di-, and tri-hydrates), *N*-methylpyrrolidinone (NMP), dimethyl sulfoxide (DMSO), *N*,*N*'-dimethylformamide (DMF), *N*,*N*'-dimethylacetamide (DMAC), 1,3-dimethyl-2-imidazolidinone (DMEU), 1,3-dimethyl-3,4,5,6-tetrahydro-2-(1H)-pyrimidinone (DMPU), acetonitrile (ACN), propylene glycol, ethyl acetate, benzyl alcohol, 2-pyrrolidone, benzyl benzoate, and the like. When water is the solvent, the solvate is referred to as a "hydrate."

[0429] In certain embodiments, the AAV particles of the disclosure may be formulated in phosphate buffered saline (PBS), in combination with an ethylene oxide/propylene oxide copolymer (also known as pluronic or poloxamer).

[0430] In certain embodiments, the AAV particles of the disclosure may be formulated in PBS with 0.001% pluronic acid (F-68) (poloxamer 188) at a pH of about 7.0.

[0431] In certain embodiments, the AAV particles of the disclosure may be formulated in PBS with 0.001% pluronic acid (F-68) (poloxamer 188) at a pH of about 7.3.

[0432] In certain embodiments, the AAV particles of the disclosure may be formulated in PBS with 0.001% pluronic acid (F-68) (poloxamer 188) at a pH of about 7.4.

[0433] In certain embodiments, the AAV particles of the disclosure may be formulated in a solution comprising sodium chloride, sodium phosphate and an ethylene oxide/propylene oxide copolymer.

[0434] In certain embodiments, the AAV particles of the disclosure may be formulated in a solution comprising sodium chloride, sodium phosphate dibasic, sodium phosphate monobasic and poloxamer 188/pluronic acid (F-68).

[0435] In certain embodiments, the AAV particles of the disclosure may be formulated in a solution comprising sodium chloride, potassium phosphate monobasic, sodium phosphate dibasic, and poloxamer 188/pluronic acid (F-68).

[0436] In certain embodiments, AAV particles are formulated in a solution comprising about 200mM sodium chloride (NaCl), about 1mM potassium phosphate monobasic (KH_2PO_4), about 3mM sodium phosphate dibasic (Na_2HPO_4), and about 0.001% Pluronic F-68/poloxamer 188 at a pH of about 7.4. The concentration of sodium chloride in the final solution may be 150mM-250mM. As non-limiting examples, the concentration of sodium chloride in the final solution may be 150mM, 160mM, 170mM, 180mM, 190mM, 200mM, 210mM, 220mM, 230mM, 240mM, 250mM, or any concentration in between. The concentration of potassium phosphate monobasic in the final solution may be 0.01mM-3mM. As non-limiting examples, the concentration of potassium phosphate monobasic in the final solution may be 0.01mM, 0.5mM, 1mM, 2mM, 3mM, or any concentration in between. The concentration of sodium phosphate dibasic in the final solution may be 1mM-10mM. As non-limiting examples, the concentration of sodium phosphate dibasic in the final solution may be 1mM, 2mM, 3mM, 4mM, 5mM, 6mM, 7mM, 8mM, 9mM, 10mM or any concentration in between. The concentration of pluronic F-68 (poloxamer 188) may be 0.0001%-1%. As non-limiting examples, the concentration of pluronic F-68 (poloxamer 188) may be 0.0001%, 0.0005%, 0.001%, 0.005%, 0.01%, 0.05%, 0.1%, 0.5%, or 1%. The final solution may have a pH of 6.8-7.7. Non-limiting examples for the pH of the final solution include a pH of 6.8, 6.9, 7.0, 7.1, 7.2, 7.3, 7.4, 7.5, 7.6, or 7.7.

V. DOSING AND ADMINISTRATION

[0437] In certain embodiments, the AAV particles may be administered to a subject in a therapeutically effective amount to reduce the symptoms of disease, such as a neurological disease (affecting either the CNS or PNS), of a subject (e.g., determined using a known

evaluation method). In some embodiments the subject is a mammal. A mammal may include, a mouse, a non-human primate, and/or a human.

Administration

[0438] The AAV particles of the present disclosure may be administered by any delivery route which results in a therapeutically effective outcome. These include, but are not limited to, intravenous (into a vein), intraparenchymal (CNS), intraparenchymal (brain), intraparenchymal (spinal cord), intraparenchymal (DRG), intracranial, intrastriatal, intrathalamic, enteral (into the intestine), gastroenteral, epidural (into the dura mater), oral (by way of the mouth), transdermal, intracerebral (into the cerebrum), intracerebroventricular (into the cerebral ventricles), sub-pial (between pia and CNS parenchyma), intracarotid arterial (into the intracarotid artery), epicutaneous (application onto the skin), intradermal, (into the skin itself), subcutaneous (under the skin), nasal administration (through the nose), intravenous bolus, intravenous drip, intra-arterial (into an artery), systemic, intramuscular (into a muscle), intracardiac (into the heart), intraosseous infusion (into the bone marrow), intrathecal (into the spinal canal), intraperitoneal, (infusion or injection into the peritoneum), intravesical infusion, intravitreal, (through the eye), intracavernous injection (into a pathologic cavity) intracavitary (into the base of the penis), intravaginal administration, intrauterine, extra-amniotic administration, transdermal (diffusion through the intact skin for systemic distribution), transmucosal (diffusion through a mucous membrane), transvaginal, insufflation (snorting), sublingual, sublabial, enema, eye drops (onto the conjunctiva), or in ear drops, auricular (in or by way of the ear), buccal (directed toward the cheek), conjunctival, cutaneous, dental (to a tooth or teeth), electro-osmosis, endocervical, endosinusial, endotracheal, extracorporeal, hemodialysis, infiltration, interstitial, intra-abdominal, intra-amniotic, intra-articular, intrabiliary, intrabronchial, intrabursal, intracartilaginous (within a cartilage), intracaudal (within the cauda equine), intracisternal (within the cisterna magna cerebellomedularis), intracorneal (within the cornea), dental intracoronal, intracoronary (within the coronary arteries), intracorporus cavernosum (within the dilatable spaces of the corporus cavernosa of the penis), intradiscal (within a disc), intraductal (within a duct of a gland), intraduodenal (within the duodenum), intradural (within or beneath the dura), intraepidermal (to the epidermis), intraesophageal (to the esophagus), intragastric (within the stomach), intragingival (within the gingivae), intraileal (within the distal portion of the small intestine), intralesional (within or introduced directly to a localized lesion), intraluminal (within a lumen of a tube), intralymphatic (within the lymph), intramedullary (within the marrow cavity of a bone), intrameningeal (within the meninges),

intramyocardial (within the myocardium), intraocular (within the eye), intraovarian (within the ovary), intrapericardial (within the pericardium), intrapleural (within the pleura), intraprostatic (within the prostate gland), intrapulmonary (within the lungs or its bronchi), intrasinal (within the nasal or periorbital sinuses), intraspinal (within the vertebral column), intrasynovial (within the synovial cavity of a joint), intratendinous (within a tendon), intratesticular (within the testicle), intrathecal (within the cerebrospinal fluid at any level of the cerebrospinal axis), intrathoracic (within the thorax), intratubular (within the tubules of an organ), intratumor (within a tumor), intratympanic (within the aurus media), intravascular (within a vessel or vessels), intraventricular (within a ventricle), iontophoresis (by means of electric current where ions of soluble salts migrate into the tissues of the body), irrigation (to bathe or flush open wounds or body cavities), laryngeal (directly upon the larynx), nasogastric (through the nose and into the stomach), occlusive dressing technique (topical route administration which is then covered by a dressing which occludes the area), ophthalmic (to the external eye), oropharyngeal (directly to the mouth and pharynx), parenteral, percutaneous, periarticular, peridural, perineural, periodontal, rectal, respiratory (within the respiratory tract by inhaling orally or nasally for local or systemic effect), retrobulbar (behind the pons or behind the eyeball), soft tissue, subarachnoid, subconjunctival, submucosal, topical, transplacental (through or across the placenta), transtracheal (through the wall of the trachea), transtympanic (across or through the tympanic cavity), ureteral (to the ureter), urethral (to the urethra), vaginal, caudal block, diagnostic, nerve block, biliary perfusion, cardiac perfusion, photopheresis and spinal.

[0439] In certain embodiments, the AAV particles of the disclosure are administered by intraparenchymal injection. In other words, the AAV particles are delivered directly to the target tissue. AAV particles of the disclosure may be administered by intraparenchymal delivery to central nervous system tissue, such as but not limited to, the putamen, the thalamus, and/or the cortex. AAV particles of the disclosure may be administered by intraparenchymal delivery to the peripheral nervous system tissue, such as, but not limited to, the dorsal root ganglia.

[0440] In some embodiments, the AAV particles that may be administered to a subject by peripheral injections. AAV particles may be administered systemically. In certain embodiments, AAV particles are administered intravenously.

[0441] Intravenous administration encompasses the use of any vein of the subject for the delivery of the AAV particles of the disclosure. Non-limiting examples of target veins include, median cubital vein, orbital veins (superior or inferior ophthalmic, saphenous veins

(greater or lesser), internal jugular, and/or femoral vein. When the subject is a mouse, the target vein may be the tail vein or the orbital veins.

[0442] In certain embodiments, the AAV particles of the present disclosure may be administered via intravenous delivery to cells of the central nervous system (CNS), such as, but not limited to, neurons, astrocytes, microglia and/or oligodendrocytes.

[0443] In certain embodiments, the AAV particles of the present disclosure may be administered via intravenous delivery to cells of the peripheral nervous system (PNS), such as, but not limited to, neurons and/or Schwann cells.

[0444] In certain embodiments, the AAV particles of the present disclosure may be administered via intravenous delivery to DRG neurons.

[0445] In certain embodiments, the AAV particles may be delivered by injection into a CSF pathway (e.g., intrathecal or intraventricular).

[0446] In certain embodiments, the AAV particles of the present disclosure may be administered to a subject by intracranial delivery (See, e.g., U. S. Pat. No. 8,119,611; the contents of which are incorporated herein by reference in their entirety).

[0447] In certain embodiments, the AAV particle may be administered to the CNS or PNS in a therapeutically effective amount to improve function and/or survival for a subject with a neurological disease. As a non-limiting example, the vector may be administered intravenously.

[0448] The AAV particles of the present disclosure may be administered in any suitable form, either as a liquid solution or suspension, as a solid form suitable for liquid solution or suspension in a liquid solution. The AAV particles may be formulated with any appropriate and pharmaceutically acceptable excipient.

[0449] In some embodiments, the AAV particles of the present disclosure may be delivered to a subject via a single route of administration. In other embodiments, the AAV particles may be delivered to a subject via more than one route of administration.

[0450] In some embodiments, the AAV particles of the present disclosure may be delivered to a subject via a multi-site route of administration. AAV particles may be administered at 2, 3, 4, 5 or more than 5 sites.

[0451] In some embodiments, two or more compositions comprising AAV particles may be administered to the same subject. In some embodiments, the two or more AAV particle compositions may be administered via the same route. In some embodiments, the two or more AAV particle compositions may be administered via different routes. Two or more compositions comprising AAV particles may be administered simultaneously, or at different

times. In some embodiments, one composition comprising AAV particles may be administered by an intraparenchymal route, while another composition comprising AAV particles may be administered by an intravenous route.

[0452] In some embodiments, AAV particles may be administered by injection. In some embodiments, AAV particles are administered by infusion. In some embodiments, AAVs may be administered as a bolus.

[0453] Injection sites for AAV particle administration may include, but are not limited to, the putamen, thalamus, cortex, hippocampus, dorsal root ganglia, and deep cerebellar nuclei.

[0454] In certain embodiments, administration of the AAV particles of the present disclosure occurs only once, and serves as a one-time treatment. In other embodiments, administration of the AAV particles of the present disclosure occurs more than once.

Dosing

[0455] The present disclosure provides methods of administering AAV particles in accordance with the disclosure to a subject in need thereof. The pharmaceutical, diagnostic, or prophylactic AAV particles and compositions of the present disclosure may be administered to a subject using any amount and any route of administration effective for preventing, treating, managing, or diagnosing diseases, disorders and/or conditions. The exact amount required will vary from subject to subject, depending on the species, age, and general condition of the subject, the severity of the disease, the particular composition, its mode of administration, its mode of activity, and the like. The subject may be a human, a mammal, or an animal.

[0456] Compositions in accordance with the disclosure are typically formulated in unit dosage form for ease of administration and uniformity of dosage. It will be understood, however, that the total daily usage of the compositions of the present disclosure may be decided by the attending physician within the scope of sound medical judgment. The specific therapeutically effective, prophylactically effective, or appropriate diagnostic dose level for any particular individual will depend upon a variety of factors including the disorder being treated and the severity of the disorder; the activity of the specific payload employed; the specific composition employed; the age, body weight, general health, sex and diet of the patient; the time of administration, route of administration, and rate of excretion of the specific AAV particle employed; the duration of the treatment; drugs used in combination or coincidental with the specific AAV particle employed; and like factors well known in the medical arts.

[0457] In certain embodiments, AAV particle pharmaceutical compositions in accordance with the present disclosure may be administered at dosage levels sufficient to deliver from about 0.0001 mg/kg to about 100 mg/kg, from about 0.001 mg/kg to about 0.05 mg/kg, from about 0.005 mg/kg to about 0.05 mg/kg, from about 0.001 mg/kg to about 0.005 mg/kg, from about 0.05 mg/kg to about 0.5 mg/kg, from about 0.01 mg/kg to about 50 mg/kg, from about 0.1 mg/kg to about 40 mg/kg, from about 0.5 mg/kg to about 30 mg/kg, from about 0.01 mg/kg to about 10 mg/kg, from about 0.1 mg/kg to about 10 mg/kg, or from about 1 mg/kg to about 25 mg/kg, of subject body weight to obtain the desired therapeutic, diagnostic, or prophylactic effect. It will be understood that the above dosing concentrations may be converted to vg or viral genomes per kg or into total viral genomes administered by one of skill in the art.

[0458] In certain embodiments, AAV particle pharmaceutical compositions in accordance with the present disclosure may be administered at about 0.1-600 µl/site, or about 0.1 to about 0.5 µl/site, about 0.5 to about 1 µl/site, about 1 to about 10 µl/site, about 10 to about 600 µl/site, about 50 to about 500 µl/site, about 100 to about 400 µl/site, about 120 to about 300 µl/site, about 140 to about 200 µl/site, about 160 µl/site. As non-limiting examples, AAV particles may be administered at 0.5 µl/site, 50 µl/site, 150 µl/site, 160 µl/site or 250 µl/site.

[0459] In certain embodiments, delivery of the compositions in accordance with the present disclosure to cells comprises a rate of delivery defined by [VG/hour = mL/hour * VG/mL] wherein VG is viral genomes, VG/mL is composition concentration, and mL/hour is rate of delivery.

[0460] In certain embodiments, delivery of AAV particle compositions to cells may comprise a total concentration per subject between about $1x10^6$ VG (viral genome) and about $1x10^{16}$ VG. In some embodiments, delivery may comprise a composition concentration of about $1x10^6$, $2x10^6$, $3x10^6$, $4x10^6$, $5x10^6$, $6x10^6$, $7x10^6$, $8x10^6$, $9x10^6$, $1x10^7$, $2x10^7$, $3x10^7$, $4x10^7$, $5x10^7$, $6x10^7$, $7x10^7$, $8x10^7$, $9x10^7$, $1x10^8$, $2x10^8$, $3x10^8$, $4x10^8$, $5x10^8$, $6x10^8$, $7x10^8$, $8x10^8$, $9x10^8$, $1x10^9$, $2x10^9$, $3x10^9$, $4x10^9$, $5x10^9$, $6x10^9$, $7x10^9$, $8x10^9$, $9x10^9$, $1x10^{10}$, $1.5x10^{10}$, $2x10^{10}$, $2.5x10^{10}$, $3x10^{10}$, $4x10^{10}$, $5x10^{10}$, $6x10^{10}$, $7x10^{10}$, $7.5x10^{10}$, $8x10^{10}$, $9x10^{10}$, $1x10^{11}$, $1.25x10^{11}$, $2x10^{11}$, $2.1x10^{11}$, $2.2x10^{11}$, $2.3x10^{11}$, $2.4x10^{11}$, $2.5x10^{11}$, $2.6x10^{11}$, $2.7x10^{11}$, $2.8x10^{11}$, $2.9x10^{11}$, $3x10^{11}$, $3.75x10^{11}$, $4x10^{11}$, $5x10^{11}$, $6x10^{11}$, $6.25x10^{11}$, $6.75x10^{11}$, $7x10^{11}$, $7.1x10^{11}$, $7.2x10^{11}$, $7.3x10^{11}$, $7.4x10^{11}$, $7.5x10^{11}$, $7.6x10^{11}$, $7.7x10^{11}$, $7.8x10^{11}$, $7.9x10^{11}$, $8x10^{11}$, $9x10^{11}$, $1x10^{12}$, $1.1\ x10^{12}$, $1.2x10^{12}$, $1.3x10^{12}$, $1.4x10^{12}$, $1.5x10^{12}$, $1.6x10^{12}$, $1.7x10^{12}$, $1.8x10^{12}$, $1.9x10^{12}$, $2x10^{12}$, $3x10^{12}$, $4x10^{12}$, $4.1x10^{12}$, $4.2x10^{12}$, $4.3x10^{12}$, $4.4x10^{12}$, $4.5x10^{12}$,$4.6x10^{12}$, $4.7x10^{12}$, $4.8x10^{12}$, $4.9x10^{12}$, $5x10^{12}$, $6x10^{12}$, $6.1x10^{12}$, $6.2x10^{12}$, $6.3x10^{12}$,

$6.4x10^{12}$, $6.5x10^{12}$, $6.6x10^{12}$, $6.7x10^{12}$, $6.8x10^{12}$, $6.9x10^{12}$, $7x10^{12}$, $8x10^{12}$, $8.1x10^{12}$, $8.2x10^{12}$, $8.3x10^{12}$, $8.4x10^{12}$, $8.5x10^{12}$, $8.6x10^{12}$, $8.7x10^{12}$, $8.8\ x10^{12}$, $8.9x10^{12}$, $9x10^{12}$, $1x10^{13}$, $2x10^{13}$, $3x10^{13}$, $4x10^{13}$, $5x10^{13}$, $6x10^{13}$, $6.7x10^{13}$, $7x10^{13}$, $8x10^{13}$, $9x10^{13}$, $1x10^{14}$, $2x10^{14}$, $3x10^{14}$, $4x10^{14}$, $5x10^{14}$, $6x10^{14}$, $7x10^{14}$, $8x10^{14}$, $9x10^{14}$, $1x10^{15}$, $2x10^{15}$, $3x10^{15}$, $4x10^{15}$, $5x10^{15}$, $6x10^{15}$, $7x10^{15}$, $8x10^{15}$, $9x10^{15}$, or $1x10^{16}$ VG/subject.

[0461] In certain embodiments, delivery of AAV particle compositions to cells may comprise a total concentration per subject between about $1x10^{6}$ VG/kg and about $1x10^{16}$ VG/kg. In some embodiments, delivery may comprise a composition concentration of about $1x10^{6}$, $2x10^{6}$, $3x10^{6}$, $4x10^{6}$, $5x10^{6}$, $6x10^{6}$, $7x10^{6}$, $8x10^{6}$, $9x10^{6}$, $1x10^{7}$, $2x10^{7}$, $3x10^{7}$, $4x10^{7}$, $5x10^{7}$, $6x10^{7}$, $7x10^{7}$, $8x10^{7}$, $9x10^{7}$, $1x10^{8}$, $2x10^{8}$, $3x10^{8}$, $4x10^{8}$, $5x10^{8}$, $6x10^{8}$, $7x10^{8}$, $8x10^{8}$, $9x10^{8}$, $1x10^{9}$, $2x10^{9}$, $3x10^{9}$, $4x10^{9}$, $5x10^{9}$, $6x10^{9}$, $7x10^{9}$, $8x10^{9}$, $9x10^{9}$, $1x10^{10}$, $2x10^{10}$, $3x10^{10}$, $4x10^{10}$, $5x10^{10}$, $6x10^{10}$, $7x10^{10}$, $8x10^{10}$, $9x10^{10}$, $1x10^{11}$, $2x10^{11}$, $2.1x10^{11}$, $2.2x10^{11}$, $2.3x10^{11}$, $2.4x10^{11}$, $2.5x10^{11}$, $2.6x10^{11}$, $2.7x10^{11}$, $2.8x10^{11}$, $2.9x10^{11}$, $3x10^{11}$, $4x10^{11}$, $5x10^{11}$, $6x10^{11}$, $7x10^{11}$, $7.1x10^{11}$, $7.2x10^{11}$, $7.3x10^{11}$, $7.4x10^{11}$, $7.5x10^{11}$, $7.6x10^{11}$, $7.7x10^{11}$, $7.8x10^{11}$, $7.9x10^{11}$, $8x10^{11}$, $9x10^{11}$, $1x10^{12}$, $1.1\ x10^{12}$, $1.2x10^{12}$, $1.3x10^{12}$, $1.4x10^{12}$, $1.5x10^{12}$, $1.6x10^{12}$, $1.7x10^{12}$, $1.8x10^{12}$, $1.9x10^{12}$, $2x10^{12}$, $3x10^{12}$, $4x10^{12}$, $4.1x10^{12}$, $4.2x10^{12}$, $4.3x10^{12}$, $4.4x10^{12}$, $4.5x10^{12}$,$4.6x10^{12}$, $4.7x10^{12}$, $4.8x10^{12}$, $4.9x10^{12}$, $5x10^{12}$, $6x10^{12}$, $6.1x10^{12}$, $6.2x10^{12}$, $6.3x10^{12}$, $6.4x10^{12}$, $6.5x10^{12}$, $6.6x10^{12}$, $6.7x10^{12}$, $6.8x10^{12}$, $6.9x10^{12}$, $7x10^{12}$, $8x10^{12}$, $8.1x10^{12}$, $8.2x10^{12}$, $8.3x10^{12}$, $8.4x10^{12}$, $8.5x10^{12}$, $8.6x10^{12}$, $8.7x10^{12}$, $8.8\ x10^{12}$, $8.9x10^{12}$, $9x10^{12}$, $1x10^{13}$, $2x10^{13}$, $3x10^{13}$, $4x10^{13}$, $5x10^{13}$, $6x10^{13}$, $6.7x10^{13}$, $7x10^{13}$, $8x10^{13}$, $9x10^{13}$, $1x10^{14}$, $2x10^{14}$, $3x10^{14}$, $4x10^{14}$, $5x10^{14}$, $6x10^{14}$, $7x10^{14}$, $8x10^{14}$, $9x10^{14}$, $1x10^{15}$, $2x10^{15}$, $3x10^{15}$, $4x10^{15}$, $5x10^{15}$, $6x10^{15}$, $7x10^{15}$, $8x10^{15}$, $9x10^{15}$, or $1x10^{16}$ VG/kg. In certain embodiments, the delivery comprises a composition concentration of $1x10^{13}$ VG/kg. In certain embodiments, the delivery comprises a composition concentration of $2.1x10^{12}$ VG/kg. In certain embodiments, the delivery comprises a composition concentration of $1x10^{13}$ VG/kg. In certain embodiments, the delivery comprises a composition concentration of $6.7x10^{12}$ VG/kg. In certain embodiments, the delivery comprises a composition concentration of $7x10^{12}$ VG/kg. In certain embodiments, the delivery comprises a composition concentration of $2x10^{13}$ VG/kg. In certain embodiments, the delivery comprises a composition concentration of $3x10^{11}$ VG/kg. In certain embodiments, the delivery comprises a composition concentration of $3x10^{12}$ VG/kg. In certain embodiments, the delivery comprises a composition concentration of $3x10^{13}$ VG/kg. In certain embodiments, the delivery comprises a composition concentration of $6.3x10^{12}$ VG/kg.

[0462] In certain embodiments, delivery of AAV particle compositions to cells may comprise a total concentration per site between about $1x10^6$ VG/site and about $1x10^{16}$ VG/site. In some embodiments, delivery may comprise a composition concentration of about $1x10^6$, $2x10^6$, $3x10^6$, $4x10^6$, $5x10^6$, $6x10^6$, $7x10^6$, $8x10^6$, $9x10^6$, $1x10^7$, $2x10^7$, $3x10^7$, $4x10^7$, $5x10^7$, $6x10^7$, $7x10^7$, $8x10^7$, $9x10^7$, $1x10^8$, $2x10^8$, $3x10^8$, $4x10^8$, $5x10^8$, $6x10^8$, $7x10^8$, $8x10^8$, $9x10^8$, $1x10^9$, $2x10^9$, $3x10^9$, $4x10^9$, $5x10^9$, $6x10^9$, $7x10^9$, $8x10^9$, $9x10^9$, $1x10^{10}$, $2x10^{10}$, $3x10^{10}$, $4x10^{10}$, $5x10^{10}$, $6x10^{10}$, $7x10^{10}$, $8x10^{10}$, $9x10^{10}$, $1x10^{11}$, $2x10^{11}$, $2.1x10^{11}$, $2.2x10^{11}$, $2.3x10^{11}$, $2.4x10^{11}$, $2.5x10^{11}$, $2.6x10^{11}$, $2.7x10^{11}$, $2.8x10^{11}$, $2.9x10^{11}$, $3x10^{11}$, $4x10^{11}$, $5x10^{11}$, $6x10^{11}$, $7x10^{11}$, $7.1x10^{11}$, $7.2x10^{11}$, $7.3x10^{11}$, $7.4x10^{11}$, $7.5x10^{11}$, $7.6x10^{11}$, $7.7x10^{11}$, $7.8x10^{11}$, $7.9x10^{11}$, $8x10^{11}$, $9x10^{11}$, $1x10^{12}$, $1.1\ x10^{12}$, $1.2x10^{12}$, $1.3x10^{12}$, $1.4x10^{12}$, $1.5x10^{12}$, $1.6x10^{12}$, $1.7x10^{12}$, $1.8x10^{12}$, $1.9x10^{12}$, $2x10^{12}$, $3x10^{12}$, $4x10^{12}$, $4.1x10^{12}$, $4.2x10^{12}$, $4.3x10^{12}$, $4.4x10^{12}$, $4.5x10^{12}$,$4.6x10^{12}$, $4.7x10^{12}$, $4.8x10^{12}$, $4.9x10^{12}$, $5x10^{12}$, $6x10^{12}$, $6.1x10^{12}$, $6.2x10^{12}$, $6.3x10^{12}$, $6.4x10^{12}$, $6.5x10^{12}$, $6.6x10^{12}$, $6.7x10^{12}$, $6.8x10^{12}$, $6.9x10^{12}$, $7x10^{12}$, $8x10^{12}$, $8.1x10^{12}$, $8.2x10^{12}$, $8.3x10^{12}$, $8.4x10^{12}$, $8.5x10^{12}$, $8.6x10^{12}$, $8.7x10^{12}$, $8.8\ x10^{12}$, $8.9x10^{12}$, $9x10^{12}$, $1x10^{13}$, $2x10^{13}$, $3x10^{13}$, $4x10^{13}$, $5x10^{13}$, $6x10^{13}$, $6.7x10^{13}$, $7x10^{13}$, $8x10^{13}$, $9x10^{13}$, $1x10^{14}$, $2x10^{14}$, $3x10^{14}$, $4x10^{14}$, $5x10^{14}$, $6x10^{14}$, $7x10^{14}$, $8x10^{14}$, $9x10^{14}$, $1x10^{15}$, $2x10^{15}$, $3x10^{15}$, $4x10^{15}$, $5x10^{15}$, $6x10^{15}$, $7x10^{15}$, $8x10^{15}$, $9x10^{15}$, or $1x10^{16}$ VG/site.

[0463] In certain embodiments, delivery of AAV particles to cells of the central nervous system may comprise a total dose between about $1x10^6$ VG and about $1x10^{16}$ VG. In some embodiments, delivery may comprise a total dose of about $1x10^6$, $2x10^6$, $3x10^6$, $4x10^6$, $5x10^6$, $6x10^6$, $7x10^6$, $8x10^6$, $9x10^6$, $1x10^7$, $2x10^7$, $3x10^7$, $4x10^7$, $5x10^7$, $6x10^7$, $7x10^7$, $8x10^7$, $9x10^7$, $1x10^8$, $2x10^8$, $3x10^8$, $4x10^8$, $5x10^8$, $6x10^8$, $7x10^8$, $8x10^8$, $9x10^8$, $1x10^9$, $2x10^9$, $3x10^9$, $4x10^9$, $5x10^9$, $6x10^9$, $7x10^9$, $8x10^9$, $9x10^9$, $1x10^{10}$, $1.9x10^{10}$, $2x10^{10}$, $3x10^{10}$, $3.73x10^{10}$, $4x10^{10}$, $5x10^{10}$, $6x10^{10}$, $7x10^{10}$, $8x10^{10}$, $9x10^{10}$, $1x10^{11}$, $2x10^{11}$, $2.5x10^{11}$, $3x10^{11}$, $4x10^{11}$, $5x10^{11}$, $6x10^{11}$, $7x10^{11}$, $8x10^{11}$, $9x10^{11}$, $1x10^{12}$, $2x10^{12}$, $3x10^{12}$, $4x10^{12}$, $5x10^{12}$, $6x10^{12}$, $6.1x10^{12}$, $6.2x10^{12}$, $6.3x10^{12}$, $6.4x10^{12}$, $6.5x10^{12}$, $6.6x10^{12}$, $6.7x10^{12}$, $6.8x10^{12}$, $6.9x10^{12}$, $7x10^{12}$, $8x10^{12}$, $9x10^{12}$, $1x10^{13}$, $2x10^{13}$, $3x10^{13}$, $4x10^{13}$, $5x10^{13}$, $6x10^{13}$, $7x10^{13}$, $8x10^{13}$, $9x10^{13}$, $1x10^{14}$, $2x10^{14}$, $3x10^{14}$, $4x10^{14}$, $5x10^{14}$, $6x10^{14}$, $7x10^{14}$, $8x10^{14}$, $9x10^{14}$, $1x10^{15}$, $2x10^{15}$, $3x10^{15}$, $4x10^{15}$, $5x10^{15}$, $6x10^{15}$, $7x10^{15}$, $8x10^{15}$, $9x10^{15}$, or $1x10^{16}$ VG. As a non-limiting example, the total dose is $1x10^{13}$ VG. As another non-limiting example, the total dose is $2.1x10^{12}$ VG. As another non-limiting example, the total dose is $6.3x10^{12}$ VG.

[0464] In certain embodiments, about 10^5 to 10^6 viral genome (unit) may be administered per dose.

[0465] In certain embodiments, delivery of the compositions comprising the AAV particles in accordance with the present disclosure to cells may comprise a total concentration between about $1x10^6$ VG/mL and about $1x10^{16}$ VG/mL. In some embodiments, delivery may comprise a composition concentration of about $1x10^6$, $2x10^6$, $3x10^6$, $4x10^6$, $5x10^6$, $6x10^6$, $7x10^6$, $8x10^6$, $9x10^6$, $1x10^7$, $2x10^7$, $3x10^7$, $4x10^7$, $5x10^7$, $6x10^7$, $7x10^7$, $8x10^7$, $9x10^7$, $1x10^8$, $2x10^8$, $3x10^8$, $4x10^8$, $5x10^8$, $6x10^8$, $7x10^8$, $8x10^8$, $9x10^8$, $1x10^9$, $2x10^9$, $3x10^9$, $4x10^9$, $5x10^9$, $6x10^9$, $7x10^9$, $8x10^9$, $9x10^9$, $1x10^{10}$, $2x10^{10}$, $3x10^{10}$, $4x10^{10}$, $5x10^{10}$, $6x10^{10}$, $7x10^{10}$, $8x10^{10}$, $9x10^{10}$, $1x10^{11}$, $2x10^{11}$, $3x10^{11}$, $4x10^{11}$, $5x10^{11}$, $6x10^{11}$, $7x10^{11}$, $8x10^{11}$, $9x10^{11}$, $1x10^{12}$, $1.1x10^{12}$, $1.2x10^{12}$, $1.3x10^{12}$, $1.4x10^{12}$, $1.5x10^{12}$, $1.6x10^{12}$, $1.7x10^{12}$, $1.8x10^{12}$, $1.9x10^{12}$, $2x10^{12}$, $2.1x10^{12}$, $2.2x10^{12}$, $2.3x10^{12}$, $2.4x10^{12}$, $2.5x10^{12}$, $2.6x10^{12}$, $2.7x10^{12}$, $2.8x10^{12}$, $2.9x10^{12}$, $3x10^{12}$, $3.1x10^{12}$, $3.2x10^{12}$, $3.3x10^{12}$, $3.4x10^{12}$, $3.5x10^{12}$, $3.6x10^{12}$, $3.7x10^{12}$, $3.8x10^{12}$, $3.9x10^{12}$, $4x10^{12}$, $4.1x10^{12}$, $4.2x10^{12}$, $4.3x10^{12}$, $4.4x10^{12}$, $4.5x10^{12}$, $4.6x10^{12}$, $4.7x10^{12}$, $4.8x10^{12}$, $4.9x10^{12}$, $5x10^{12}$, $6x10^{12}$, $6.1x10^{12}$, $6.2x10^{12}$, $6.3x10^{12}$, $6.4x10^{12}$, $6.5x10^{12}$, $6.6x10^{12}$, $6.7x10^{12}$, $6.8x10^{12}$, $6.9x10^{12}$, $7x10^{12}$, $8x10^{12}$, $9x10^{12}$, $1x10^{13}$, $2x10^{13}$, $3x10^{13}$, $4x10^{13}$, $5x10^{13}$, $6x10^{13}$, $6.7x10^{13}$, $7x10^{13}$, $8x10^{13}$, $9x10^{13}$, $1x10^{14}$, $2x10^{14}$, $3x10^{14}$, $4x10^{14}$, $5x10^{14}$, $6x10^{14}$, $7x10^{14}$, $8x10^{14}$, $9x10^{14}$, $1x10^{15}$, $2x10^{15}$, $3x10^{15}$, $4x10^{15}$, $5x10^{15}$, $6x10^{15}$, $7x10^{15}$, $8x10^{15}$, $9x10^{15}$, or $1x10^{16}$ VG/mL.

[0466] In certain embodiments, delivery of AAV particles to cells of the central nervous system may comprise a composition concentration between about $1x10^6$ VG/mL and about $1x10^{16}$ VG/mL. In some embodiments, delivery may comprise a composition concentration of about $1x10^6$, $2x10^6$, $3x10^6$, $4x10^6$, $5x10^6$, $6x10^6$, $7x10^6$, $8x10^6$, $9x10^6$, $1x10^7$, $2x10^7$, $3x10^7$, $4x10^7$, $5x10^7$, $6x10^7$, $7x10^7$, $8x10^7$, $9x10^7$, $1x10^8$, $2x10^8$, $3x10^8$, $4x10^8$, $5x10^8$, $6x10^8$, $7x10^8$, $8x10^8$, $9x10^8$, $1x10^9$, $2x10^9$, $3x10^9$, $4x10^9$, $5x10^9$, $6x10^9$, $7x10^9$, $8x10^9$, $9x10^9$, $1x10^{10}$, $2x10^{10}$, $3x10^{10}$, $4x10^{10}$, $5x10^{10}$, $6x10^{10}$, $7x10^{10}$, $8x10^{10}$, $9x10^{10}$, $1x10^{11}$, $2x10^{11}$, $3x10^{11}$, $4x10^{11}$, $5x10^{11}$, $6x10^{11}$, $7x10^{11}$, $8x10^{11}$, $9x10^{11}$, $1x10^{12}$, $2x10^{12}$, $3x10^{12}$, $4x10^{12}$, $5x10^{12}$, $6x10^{12}$, $6.1x10^{12}$, $6.2x10^{12}$, $6.3x10^{12}$, $6.4x10^{12}$, $6.5x10^{12}$, $6.6x10^{12}$, $6.7x10^{12}$, $6.8x10^{12}$, $6.9x10^{12}$, $7x10^{12}$, $8x10^{12}$, $9x10^{12}$, $1x10^{13}$, $2x10^{13}$, $3x10^{13}$, $4x10^{13}$, $5x10^{13}$, $6x10^{13}$, $7x10^{13}$, $8x10^{13}$, $9x10^{13}$, $1x10^{14}$, $2x10^{14}$, $3x10^{14}$, $4x10^{14}$, $5x10^{14}$, $6x10^{14}$, $7x10^{14}$, $8x10^{14}$, $9x10^{14}$, $1x10^{15}$, $2x10^{15}$, $3x10^{15}$, $4x10^{15}$, $5x10^{15}$, $6x10^{15}$, $7x10^{15}$, $8x10^{15}$, $9x10^{15}$, or $1x10^{16}$ VG/mL. In certain embodiments, the delivery comprises a composition concentration of $1x10^{13}$ VG/mL. In certain embodiments, the delivery comprises a composition concentration of $2.1x10^{12}$ VG/mL. In certain embodiments, the delivery comprises a composition concentration of $1x10^{13}$ VG/mL. In certain embodiments, the delivery comprises a composition concentration of $2x10^{13}$ VG/mL. In certain embodiments, the delivery comprises a composition

concentration of $3x10^{11}$ VG/mL. In certain embodiments, the delivery comprises a composition concentration of $3x10^{12}$ VG/mL. In certain embodiments, the delivery comprises a composition concentration of $6.3x10^{12}$ VG/mL. In certain embodiments, the delivery comprises a composition concentration of $3x10^{13}$ VG/mL.

[0467] In certain embodiments, the desired dosage may be delivered using multiple administrations (*e.g.*, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, or more administrations). When multiple administrations are employed, split dosing regimens such as those described herein may be used. As used herein, a "split dose" is the division of "single unit dose" or total daily dose into two or more doses, *e.g.*, two or more administrations of the "single unit dose". As used herein, a "single unit dose" is a dose of any therapeutic administered in one dose/at one time/single route/single point of contact, i.e., single administration event.

[0468] The desired dosage of the AAV particles of the present disclosure may be administered as a "pulse dose" or as a "continuous flow". As used herein, a "pulse dose" is a series of single unit doses of any therapeutic administered with a set frequency over a period of time. As used herein, a "continuous flow" is a dose of therapeutic administered continuously for a period of time in a single route/single point of contact, i.e., continuous administration event. A total daily dose, an amount given or prescribed in 24 hour period, may be administered by any of these methods, or as a combination of these methods, or by any other methods suitable for a pharmaceutical administration.

[0469] In certain embodiments, delivery of the AAV particles of the present disclosure to a subject provides regulating activity of a target gene in a subject. The regulating activity may be an increase in the production of the target protein in a subject or the decrease of the production of target protein in a subject. The regulating activity can be for at least 1 month, 2 months, 3 months, 4 months, 5 months, 6 months, 7 months, 8 months, 9 months, 10 months, 11 months, 1 year, 13 months, 14 months, 15 months, 16 months, 17 months, 18 months, 19 months, 20 months, 20 months, 21 months, 22 months, 23 months, 2 years, 3 years, 4 years, 5 years, 6 years, 7 years, 8 years, 9 years, 10 years or more than 10 years.

[0470] In some embodiments, the AAV particle of the present disclosure may be administered to a subject using a single dose, one-time treatment. The dose of the one-time treatment may be administered by any methods known in the art and/or described herein. As used herein, a "one-time treatment" refers to a composition which is only administered one time. If needed, a booster dose may be administered to the subject to ensure the appropriate efficacy is reached. A booster may be administered 1 month, 2 months, 3 months, 4 months,

5 months, 6 months, 7 months, 8 months, 9 months, 10 months, 11 months, 12 months, 1 year, 13 months, 14 months, 15 months, 16 months, 17 months, 18 months, 19 months, 20 months, 21 months, 22 months, 23 months, 24 months, 2 years, 3 years, 4 years, 5 years, 6 years, 7 years, 8 years, 9 years, 10 years, or more than 10 years after the one-time treatment.

Delivery

[0471] In certain embodiments, the AAV particles or pharmaceutical compositions of the disclosure are delivered by intravenous injection.

[0472] In certain embodiments, the AAV particles or pharmaceutical compositions of the present disclosure may be administered or delivered using the methods for treatment of disease described in US Patent No. 8,999,948, or International Publication No. WO2014178863, the contents of each of which are herein incorporated by reference in their entirety.

[0473] In certain embodiments, the AAV particles or pharmaceutical compositions of the present disclosure may be administered or delivered using the methods for delivering gene therapy in Alzheimer's Disease or other neurodegenerative conditions as described in US Application No. 20150126590, the contents of which are herein incorporated by reference in their entirety.

[0474] In certain embodiments, the AAV particles or pharmaceutical compositions of the present disclosure may be administered or delivered using the methods for delivery of a CNS gene therapy as described in US Patent Nos. 6,436,708, and 8,946,152, and International Publication No. WO2015168666, the contents of each of which are herein incorporated by reference in their entirety.

[0475] In certain embodiments, the AAV particle or pharmaceutical compositions of the present disclosure may be administered or delivered using the methods for delivering proteins using AAV vectors described in European Patent Application No. EP2678433, the contents of which are herein incorporated by reference in their entirety.

[0476] In certain embodiments, the AAV particle or pharmaceutical compositions of the present disclosure may be administered or delivered using the methods for delivering DNA to the bloodstream described in US Patent No. US 6,211,163, the contents of which are herein incorporated by reference in their entirety.

[0477] In certain embodiments, the AAV particle or pharmaceutical compositions of the present disclosure may be administered or delivered using the methods for delivering a payload to the central nervous system described in US Patent No. US 7,588,757, the contents of which are herein incorporated by reference in their entirety.

[0478] In certain embodiments, the AAV particle or pharmaceutical compositions of the present disclosure may be administered or delivered using the methods for delivering a payload described in US Patent No. US 8,283,151, the contents of which are herein incorporated by reference in their entirety.

[0479] In certain embodiments, the AAV particle or pharmaceutical compositions of the present disclosure may be administered or delivered using the methods for delivering a payload using a glutamic acid decarboxylase (GAD) delivery vector described in International Patent Publication No. WO2001089583, the contents of which are herein incorporated by reference in their entirety.

[0480] In certain embodiments, the AAV particle or pharmaceutical compositions of the present disclosure may be administered or delivered using the methods for delivering a payload to neural cells described in International Patent Publication No. WO2012057363, the contents of which are herein incorporated by reference in their entirety.

Delivery to Cells

[0481] The present disclosure provides a method of delivering to a cell or tissue any of the above-described AAV particles, comprising contacting the cell or tissue with said AAV particle or contacting the cell or tissue with a formulation comprising said AAV particle, or contacting the cell or tissue with any of the described compositions, including pharmaceutical compositions. The method of delivering the AAV particle to a cell or tissue can be accomplished in *vitro, ex vivo*, or *in vivo*.

Delivery to Subjects

[0482] The present disclosure additionally provides a method of delivering to a subject, including a mammalian subject, any of the above-described AAV particles comprising administering to the subject said AAV particle, or administering to the subject a formulation comprising said AAV particle, or administering to the subject any of the described compositions, including pharmaceutical compositions.

[0483] In certain embodiments, the subject is a human. In some aspects, the human subject is a patient with a disease, for example, a neurological disease, or a disease associated with the central or peripheral nervous system or components thereof.

Combinations

[0484] The AAV particles may be used in combination with one or more other therapeutic, prophylactic, research or diagnostic agents. By "in combination with," it is not intended to imply that the agents must be administered at the same time and/or formulated for delivery together, although these methods of delivery are within the scope of the present

disclosure. Compositions can be administered concurrently with, prior to, or subsequent to, one or more other desired therapeutics or medical procedures. In general, each agent will be administered at a dose and/or on a time schedule determined for that agent. In some embodiments, the present disclosure encompasses the delivery of pharmaceutical, prophylactic, research, or diagnostic compositions in combination with agents that may improve their bioavailability, reduce and/or modify their metabolism, inhibit their excretion, and/or modify their distribution within the body.

VI. KITS AND DEVICES

Kits

[0485] In certain embodiments, the disclosure provides a variety of kits for conveniently and/or effectively carrying out the methods described herein. Typically, kits will comprise sufficient amounts and/or numbers of components to allow a user to perform multiple treatments of a subject(s) and/or to perform multiple experiments.

[0486] Any of the targeting peptides and/or associated AAV particles of the present disclosure may be comprised in a kit. In some embodiments, kits may further include reagents and/or instructions for creating and/or synthesizing compounds and/or compositions of the present disclosure. In some embodiments, kits may also include one or more buffers. In some embodiments, kits of the disclosure may include components for making protein or nucleic acid arrays or libraries and thus, may include, for example, solid supports.

[0487] In some embodiments, kit components may be packaged either in aqueous media or in lyophilized form. The container means of the kits will generally include at least one vial, test tube, flask, bottle, syringe or other container means, into which a component may be placed, and preferably, suitably aliquoted. Where there is more than one kit component, (labeling reagent and label may be packaged together), kits may also generally contain second, third or other additional containers into which additional components may be separately placed. In some embodiments, kits may also comprise second container means for containing sterile, pharmaceutically acceptable buffers and/or other diluents. In some embodiments, various combinations of components may be comprised in one or more vial. Kits of the present disclosure may also typically include means for containing compounds and/or compositions of the present disclosure, e.g., proteins, nucleic acids, and any other reagent containers in close confinement for commercial sale. Such containers may include injection or blow-molded plastic containers into which desired vials are retained.

[0488] In some embodiments, kit components are provided in one and/or more liquid solutions. In some embodiments, liquid solutions are aqueous solutions, with sterile aqueous

solutions being particularly preferred. In some embodiments, kit components may be provided as dried powder(s). When reagents and/or components are provided as dry powders, such powders may be reconstituted by the addition of suitable volumes of solvent. In some embodiments, it is envisioned that solvents may also be provided in another container means. In some embodiments, labeling dyes are provided as dried powders. In some embodiments, it is contemplated that 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 120, 130, 140, 150, 160, 170, 180, 190, 200, 300, 400, 500, 600, 700, 800, 900, 1000 micrograms or at least or at most those amounts of dried dye are provided in kits of the disclosure. In such embodiments, dye may then be resuspended in any suitable solvent, such as DMSO.

[0489] In some embodiments, kits may include instructions for employing kit components as well the use of any other reagent not included in the kit. Instructions may include variations that may be implemented.

Devices

[0490] In certain embodiments, the AAV particles of the disclosure are delivered by catheter.

[0491] In certain embodiments, the AAV particles of the disclosure are delivered by syringe and/or syringe pump.

[0492] In certain embodiments, the AAV particles of the disclosure are delivered by cannula.

[0493] In certain embodiments, the AAV particles of the disclosure are delivered by a device, wherein the device is further placed in a mechanism to direct or target the trajectory.

[0494] In certain embodiments, the AAV particles may be delivered to a subject using a device to deliver the AAV particles and a head fixation assembly. The head fixation assembly may be, but is not limited to, any of the head fixation assemblies sold by MRI interventions. As a non-limiting example, the head fixation assembly may be any of the assemblies described in US Patent Nos. 8099150, 8548569, and 9031636 and International Patent Publication Nos. WO201108495 and WO2014014585, the contents of each of which are incorporated by reference in their entireties. A head fixation assembly may be used in combination with an MRI compatible drill such as, but not limited to, the MRI compatible drills described in International Patent Publication No. WO2013181008 and US Patent Publication No. US20130325012, the contents of which are herein incorporated by reference in its entirety.

[0495] In certain embodiments, the AAV particles may be delivered using a method, system and/or computer program for positioning of an apparatus to a target point on a subject

to deliver the AAV particles. As a non-limiting example, the method, system and/or computer program may be the methods, systems and/or computer programs described in US Patent No. 8340743, the contents of which are herein incorporated by reference in their entirety. The method may include: determining a target point in the body and a reference point, wherein the target point and the reference point define a planned trajectory line (PTL) extending through each; determining a visualization plane, wherein the PTL intersects the visualization plane at a sighting point; mounting the guide device relative to the body to move with respect to the PTL, wherein the guide device does not intersect the visualization plane; determining a point of intersection (GPP) between the guide axis and the visualization plane; and aligning the GPP with the sighting point in the visualization plane.

[0496] In certain embodiments, the AAV particles may be delivered to a subject using a convention-enhanced delivery device. Non-limiting examples of targeted delivery of drugs using convection are described in US Patent Publication Nos. US20100217228, US20130035574, and US 20130035660 and International Patent Publication No. WO2013019830 and WO2008144585, the contents of each of which are herein incorporated by reference in their entireties.

[0497] In certain embodiments, a subject may be imaged prior to, during and/or after delivery of the AAV particles. The imaging method may be a method known in the art and/or described herein, such as but not limited to, magnetic resonance imaging (MRI). As a non-limiting example, imaging may be used to assess therapeutic effect. As another non-limiting example, imaging may be used for assisted delivery of AAV particles.

[0498] In certain embodiments, the AAV particles may be delivered using an MRI-guided device. Non-limiting examples of MRI-guided devices are described in US Patent Nos. 9055884, 9042958, 8886288, 8768433, 8396532, 8369930, 8374677, and 8175677 and US Patent Application No. US20140024927 the contents of each of which are herein incorporated by reference in their entireties. As a non-limiting example, the MRI-guided device may be able to provide data in real time such as those described in US Patent Nos. 8886288 and 8768433, the contents of each of which is herein incorporated by reference in its entirety. As another non-limiting example, the MRI-guided device or system may be used with a targeting cannula such as the systems described in US Patent Nos. 8175677 and 8374677, the contents of each of which are herein incorporated by reference in their entireties. As yet another non-limiting example, the MRI-guided device includes a trajectory guide frame for guiding an interventional device as described, for example, in US Patent No.

9055884 and US Patent Application No. US20140024927, the contents of each of which are herein incorporated by reference in their entireties.

[0499] In certain embodiments, the AAV particles may be delivered using an MRI-compatible tip assembly. Non-limiting examples of MRI-compatible tip assemblies are described in US Patent Publication No. US20140275980, the contents of which is herein incorporated by reference in its entirety.

[0500] In certain embodiments, the AAV particles may be delivered using a cannula which is MRI-compatible. Non-limiting examples of MRI-compatible cannulas include those taught in International Patent Publication No. WO2011130107, the contents of which are herein incorporated by reference in its entirety.

[0501] In certain embodiments, the AAV particles may be delivered using a catheter which is MRI-compatible. Non-limiting examples of MRI-compatible catheters include those taught in International Patent Publication No. WO2012116265, US Patent No. 8825133 and US Patent Publication No. US20140024909, the contents of each of which are herein incorporated by reference in their entireties.

[0502] In certain embodiments, the AAV particles may be delivered using a device with an elongated tubular body and a diaphragm as described in US Patent Publication Nos. US20140276582 and US20140276614, the contents of each of which are herein incorporated by reference in their entireties.

[0503] In certain embodiments, the AAV particles may be delivered using an MRI compatible localization and/or guidance system such as, but not limited to, those described in US Patent Publication Nos. US20150223905 and US20150230871, the contents of each of which are herein incorporated by reference in their entireties. As a non-limiting example, the MRI compatible localization and/or guidance systems may comprise a mount adapted for fixation to a patient, a targeting cannula with a lumen configured to attach to the mount so as to be able to controllably translate in at least three dimensions, and an elongate probe configured to snugly advance via slide and retract in the targeting cannula lumen, the elongate probe comprising at least one of a stimulation or recording electrode.

[0504] In certain embodiments, the AAV particles may be delivered to a subject using a trajectory frame as described in US Patent Publication Nos. US20150031982 and US20140066750 and International Patent Publication Nos. WO2015057807 and WO2014039481, the contents of each of which are herein incorporated by reference in their entireties.

[0505] In certain embodiments, the AAV particles may be delivered to a subject using a gene gun.

VII. DEFINITIONS

[0506] *Adeno-associated virus:* As used herein, the term "adeno-associated virus" or "AAV" refers to members of the dependovirus genus comprising any particle, sequence, gene, protein, or component derived therefrom.

[0507] *AAV Particle*: As used herein, an "AAV particle" is a virus which comprises a capsid and a viral genome with at least one payload region and at least one ITR. As used herein "AAV particles of the disclosure" are AAV particles comprising a parent capsid sequence with at least one targeting peptide insert. AAV particles of the present disclosure may be produced recombinantly and may be based on adeno-associated virus (AAV) parent or reference sequences. AAV particle may be derived from any serotype, described herein or known in the art, including combinations of serotypes (i.e., "pseudotyped" AAV) or from various genomes (e.g., single stranded or self-complementary). In addition, the AAV particle may be replication defective and/or targeted. In certain embodiments, the AAV particle may have a targeting peptide inserted into the capsid to enhance tropism for a desired target tissue. It is to be understood that reference to the AAV particles of the disclosure also includes pharmaceutical compositions thereof, even if not explicitly recited.

[0508] *Administering:* As used herein, the term "administering" refers to providing a pharmaceutical agent or composition to a subject.

[0509] *Amelioration*: As used herein, the term "amelioration" or "ameliorating" refers to a lessening of severity of at least one indicator of a condition or disease. For example, in the context of neurodegeneration disorder, amelioration includes the reduction of neuron loss.

[0510] *Animal:* As used herein, the term "animal" refers to any member of the animal kingdom. In some embodiments, "animal" refers to humans at any stage of development. In some embodiments, "animal" refers to non-human animals at any stage of development. In certain embodiments, the non-human animal is a mammal (*e.g.*, a rodent, a mouse, a rat, a rabbit, a monkey, a dog, a cat, a sheep, cattle, a primate, or a pig). In some embodiments, animals include, but are not limited to, mammals, birds, reptiles, amphibians, fish, and worms. In some embodiments, the animal is a transgenic animal, genetically-engineered animal, or a clone.

[0511] *Antisense strand:* As used herein, the term "the antisense strand" or "the first strand" or "the guide strand" of a siRNA molecule refers to a strand that is substantially complementary to a section of about 10-50 nucleotides, e.g., about 15-30, 16-25, 18-23 or 19-

22 nucleotides of the mRNA of a gene targeted for silencing. The antisense strand or first strand has sequence sufficiently complementary to the desired target mRNA sequence to direct target-specific silencing, e.g., complementarity sufficient to trigger the destruction of the desired target mRNA by the RNAi machinery or process.

[0512] *Approximately:* As used herein, the term "approximately" or "about," as applied to one or more values of interest, refers to a value that is similar to a stated reference value. In certain embodiments, the term "approximately" or "about" refers to a range of values that fall within 25%, 20%, 19%, 18%, 17%, 16%, 15%, 14%, 13%, 12%, 11%, 10%, 9%, 8%, 7%, 6%, 5%, 4%, 3%, 2%, 1%, or less in either direction (greater than or less than) of the stated reference value unless otherwise stated or otherwise evident from the context (except where such number would exceed 100% of a possible value).

[0513] *Capsid*: As used herein, the term "capsid" refers to the protein shell of a virus particle.

[0514] *Complementary and substantially complementary:* As used herein, the term "complementary" refers to the ability of polynucleotides to form base pairs with one another. Base pairs are typically formed by hydrogen bonds between nucleotide units in antiparallel polynucleotide strands. Complementary polynucleotide strands can form base pairs in the Watson-Crick manner (e.g., A to T, A to U, C to G), or in any other manner that allows for the formation of duplexes. As persons skilled in the art are aware, when using RNA as opposed to DNA, uracil rather than thymine is the base that is considered to be complementary to adenine. However, when a U is denoted in the context of the present disclosure, the ability to substitute a T is implied, unless otherwise stated. Perfect complementarity or 100% complementarity refers to the situation in which each nucleotide unit of one polynucleotide strand can form a hydrogen bond with a nucleotide unit of a second polynucleotide strand. Less than perfect complementarity refers to the situation in which some, but not all, nucleotide units of two strands can form hydrogen bond with each other. For example, for two 20-mers, if only two base pairs on each strand can form a hydrogen bond with each other, the polynucleotide strands exhibit 10% complementarity. In the same example, if 18 base pairs on each strand can form hydrogen bonds with each other, the polynucleotide strands exhibit 90% complementarity. As used herein, the term "substantially complementary" means that the siRNA has a sequence (e.g., in the antisense strand) which is sufficient to bind the desired target mRNA, and to trigger the RNA silencing of the target mRNA.

[0515] *Control Elements:* As used herein, "control elements", "regulatory control elements" or "regulatory sequences" refers to promoter regions, polyadenylation signals, transcription termination sequences, upstream regulatory domains, origins of replication, internal ribosome entry sites ("IRES"), enhancers, and the like, which provide for the replication, transcription and translation of a coding sequence in a recipient cell. Not all of these control elements need always be present as long as the selected coding sequence is capable of being replicated, transcribed and/or translated in an appropriate host cell.

[0516] *Delivery:* As used herein, "delivery" refers to the act or manner of delivering an AAV particle, a compound, substance, entity, moiety, cargo or payload.

[0517] *Element:* As used herein, the term "element" refers to a distinct portion of an entity. In some embodiments, an element may be a polynucleotide sequence with a specific purpose, incorporated into a longer polynucleotide sequence.

[0518] *Encapsulate:* As used herein, the term "encapsulate" means to enclose, surround or encase. As an example, a capsid protein often encapsulates a viral genome.

[0519] *Engineered:* As used herein, embodiments of the disclosure are "engineered" when they are designed to have a feature or property, whether structural or chemical, that varies from a starting point, wild type or native molecule.

[0520] *Effective Amount:* As used herein, the term "effective amount" of an agent is that amount sufficient to effect beneficial or desired results, for example, clinical results, and, as such, an "effective amount" depends upon the context in which it is being applied. For example, in the context of administering an agent that treats cancer, an effective amount of an agent is, for example, an amount sufficient to achieve treatment, as defined herein, of cancer, as compared to the response obtained without administration of the agent.

[0521] *Expression*: As used herein, "expression" of a nucleic acid sequence refers to one or more of the following events: (1) production of an RNA template from a DNA sequence (*e.g.*, by transcription); (2) processing of an RNA transcript (*e.g.*, by splicing, editing, 5′ cap formation, and/or 3′ end processing); (3) translation of an RNA into a polypeptide or protein; and (4) post-translational modification of a polypeptide or protein.

[0522] *Feature:* As used herein, a "feature" refers to a characteristic, a property, or a distinctive element.

[0523] *Formulation*: As used herein, a "formulation" includes at least one AAV particle (active ingredient) and an excipient, and/or an inactive ingredient.

[0524] *Fragment:* A "fragment," as used herein, refers to a portion. For example, an antibody fragment may comprise a CDR, or a heavy chain variable region, or a scFv, etc.

[0525] *Functional*: As used herein, a "functional" biological molecule is a biological molecule in a form in which it exhibits a property and/or activity by which it is characterized.

[0526] *Gene expression*: The term "gene expression" refers to the process by which a nucleic acid sequence undergoes successful transcription and in most instances translation to produce a protein or peptide. For clarity, when reference is made to measurement of "gene expression", this should be understood to mean that measurements may be of the nucleic acid product of transcription, e.g., RNA or mRNA or of the amino acid product of translation, e.g., polypeptides or peptides. Methods of measuring the amount or levels of RNA, mRNA, polypeptides and peptides are well known in the art.

[0527] *Homology*: As used herein, the term "homology" refers to the overall relatedness between polymeric molecules, *e.g.* between polynucleotide molecules (*e.g.* DNA molecules and/or RNA molecules) and/or between polypeptide molecules. In some embodiments, polymeric molecules are considered to be "homologous" to one another if their sequences are at least 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 99% identical or similar. The term "homologous" necessarily refers to a comparison between at least two sequences (polynucleotide or polypeptide sequences). In accordance with the disclosure, two polynucleotide sequences are considered to be homologous if the polypeptides they encode are at least about 50%, 60%, 70%, 80%, 90%, 95%, or even 99% for at least one stretch of at least about 20 amino acids. In some embodiments, homologous polynucleotide sequences are characterized by the ability to encode a stretch of at least 4–5 uniquely specified amino acids. For polynucleotide sequences less than 60 nucleotides in length, homology is determined by the ability to encode a stretch of at least 4–5 uniquely specified amino acids. In accordance with the disclosure, two protein sequences are considered to be homologous if the proteins are at least about 50%, 60%, 70%, 80%, or 90% identical for at least one stretch of at least about 20 amino acids.

[0528] *Identity*: As used herein, the term "identity" refers to the overall relatedness between polymeric molecules, *e.g.*, between polynucleotide molecules (*e.g.* DNA molecules and/or RNA molecules) and/or between polypeptide molecules. Calculation of the percent identity of two polynucleotide sequences, for example, can be performed by aligning the two sequences for optimal comparison purposes (*e.g.*, gaps can be introduced in one or both of a first and a second nucleic acid sequences for optimal alignment and non-identical sequences can be disregarded for comparison purposes). In certain embodiments, the length of a sequence aligned for comparison purposes is at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, or 100% of the length of the

reference sequence. The nucleotides at corresponding nucleotide positions are then compared. When a position in the first sequence is occupied by the same nucleotide as the corresponding position in the second sequence, then the molecules are identical at that position. The percent identity between the two sequences is a function of the number of identical positions shared by the sequences, taking into account the number of gaps, and the length of each gap, which needs to be introduced for optimal alignment of the two sequences. The comparison of sequences and determination of percent identity between two sequences can be accomplished using a mathematical algorithm. For example, the percent identity between two nucleotide sequences can be determined using methods such as those described in Computational Molecular Biology, Lesk, A. M., ed., Oxford University Press, New York, 1988; Biocomputing: Informatics and Genome Projects, Smith, D. W., ed., Academic Press, New York, 1993; Sequence Analysis in Molecular Biology, von Heinje, G., Academic Press, 1987; Computer Analysis of Sequence Data, Part I, Griffin, A. M., and Griffin, H. G., eds., Humana Press, New Jersey, 1994; and Sequence Analysis Primer, Gribskov, M. and Devereux, J., eds., M Stockton Press, New York, 1991; the contents of each of which are incorporated herein by reference in their entirety. For example, the percent identity between two nucleotide sequences can be determined using the algorithm of Meyers and Miller (CABIOS, 1989, 4:11-17), which has been incorporated into the ALIGN program (version 2.0) using a PAM120 weight residue table, a gap length penalty of 12 and a gap penalty of 4. The percent identity between two nucleotide sequences can, alternatively, be determined using the GAP program in the GCG software package using an NWSgapdna.CMP matrix. Methods commonly employed to determine percent identity between sequences include, but are not limited to those disclosed in Carillo, H., and Lipman, D., SIAM J Applied Math., 48:1073 (1988); incorporated herein by reference. Techniques for determining identity are codified in publicly available computer programs. Exemplary computer software to determine homology between two sequences include, but are not limited to, GCG program package, Devereux, J., *et al.*, *Nucleic Acids Research*, 12(1), 387 (1984)), BLASTP, BLASTN, and FASTA Altschul, S. F. *et al.*, *J. Molec. Biol.*, 215, 403 (1990)).

[0529] *Inhibit expression of a gene:* As used herein, the phrase "inhibit expression of a gene" means to cause a reduction in the amount of an expression product of the gene. The expression product can be an RNA transcribed from the gene (*e.g.*, an mRNA) or a polypeptide translated from an mRNA transcribed from the gene. Typically, a reduction in the level of an mRNA results in a reduction in the level of a polypeptide translated therefrom.

The level of expression may be determined using standard techniques for measuring mRNA or protein.

[0530] *Insert:* As used herein the term "insert" may refer to the addition of a targeting peptide sequence to a parent AAV capsid sequence. An "insertion" may result in the replacement of one or more amino acids of the parent AAV capsid sequence. Alternatively, an insertion may result in no changes to the parent AAV capsid sequence beyond the addition of the targeting peptide sequence.

[0531] *Inverted terminal repeat:* As used herein, the term "inverted terminal repeat" or "ITR" refers to a cis-regulatory element for the packaging of polynucleotide sequences into viral capsids.

[0532] *Library:* As used herein, the term "library" refers to a diverse collection of linear polypeptides, polynucleotides, viral particles, or viral vectors. As examples, a library may be a DNA library or an AAV capsid library.

[0533] *Neurological disease:* As used herein, a "neurological disease" is any disease associated with the central or peripheral nervous system and components thereof (e.g., neurons).

[0534] *Naturally Occurring:* As used herein, "naturally occurring" or "wild-type" means existing in nature without artificial aid, or involvement of the hand of man.

[0535] *Open reading frame:* As used herein, "open reading frame" or "ORF" refers to a sequence which does not contain a stop codon in a given reading frame.

[0536] *Parent sequence:* As used herein, a "parent sequence" is a nucleic acid or amino acid sequence from which a variant is derived. In certain embodiments, a parent sequence is a sequence into which a heterologous sequence is inserted. In other words, a parent sequence may be considered an acceptor or recipient sequence. In certain embodiments, a parent sequence is an AAV capsid sequence into which a targeting sequence is inserted.

[0537] *Particle*: As used herein, a "particle" is a virus comprised of at least two components, a protein capsid and a polynucleotide sequence enclosed within the capsid.

[0538] *Patient:* As used herein, "patient" refers to a subject who may seek or be in need of treatment, requires treatment, is receiving treatment, will receive treatment, or a subject who is under care by a trained professional for a particular disease or condition.

[0539] *Payload region:* As used herein, a "payload region" is any nucleic acid sequence (e.g., within the viral genome) which encodes one or more "payloads" of the disclosure. As non-limiting examples, a payload region may be a nucleic acid sequence within the viral genome of an AAV particle, which encodes a payload, wherein the payload is an RNAi agent

or a polypeptide. Payloads of the present disclosure may be, but are not limited to, peptides, polypeptides, proteins, antibodies, RNAi agents, etc.

[0540] *Peptide:* As used herein, "peptide" is less than or equal to 50 amino acids long, e.g., about 5, 10, 15, 20, 25, 30, 35, 40, 45, or 50 amino acids long.

[0541] *Pharmaceutically acceptable*: The phrase "pharmaceutically acceptable" is employed herein to refer to those compounds, materials, compositions, and/or dosage forms which are, within the scope of sound medical judgment, suitable for use in contact with the tissues of human beings and animals without excessive toxicity, irritation, allergic response, or other problem or complication, commensurate with a reasonable benefit/risk ratio.

[0542] *Preventing*: As used herein, the term "preventing" or "prevention" refers to partially or completely delaying onset of an infection, disease, disorder and/or condition; partially or completely delaying onset of one or more symptoms, features, or clinical manifestations of a particular infection, disease, disorder, and/or condition; partially or completely delaying onset of one or more symptoms, features, or manifestations of a particular infection, disease, disorder, and/or condition; partially or completely delaying progression from an infection, a particular disease, disorder and/or condition; and/or decreasing the risk of developing pathology associated with the infection, the disease, disorder, and/or condition.

[0543] *Prophylactic*: As used herein, "prophylactic" refers to a therapeutic or course of action used to prevent the spread of disease.

[0544] *Prophylaxis:* As used herein, a "prophylaxis" refers to a measure taken to maintain health and prevent the spread of disease.

[0545] *Region:* As used herein, the term "region" refers to a zone or general area. In some embodiments, when referring to a protein or protein module, a region may comprise a linear sequence of amino acids along the protein or protein module or may comprise a three-dimensional area, an epitope and/or a cluster of epitopes. In some embodiments, regions comprise terminal regions. As used herein, the term "terminal region" refers to regions located at the ends or termini of a given agent. When referring to proteins, terminal regions may comprise N- and/or C-termini.

[0546] In some embodiments, when referring to a polynucleotide, a region may comprise a linear sequence of nucleic acids along the polynucleotide or may comprise a three-dimensional area, secondary structure, or tertiary structure. In some embodiments, regions comprise terminal regions. As used herein, the term "terminal region" refers to regions

located at the ends or termini of a given agent. When referring to polynucleotides, terminal regions may comprise 5' and/or 3' termini.

[0547] *RNA or RNA molecule*: As used herein, the term "RNA" or "RNA molecule" or "ribonucleic acid molecule" refers to a polymer of ribonucleotides; the term "DNA" or "DNA molecule" or "deoxyribonucleic acid molecule" refers to a polymer of deoxyribonucleotides. DNA and RNA can be synthesized naturally, e.g., by DNA replication and transcription of DNA, respectively; or be chemically synthesized. DNA and RNA can be single-stranded (i.e., ssRNA or ssDNA, respectively) or multi-stranded (e.g., double stranded, i.e., dsRNA and dsDNA, respectively). The term "mRNA" or "messenger RNA", as used herein, refers to a single stranded RNA that encodes the amino acid sequence of one or more polypeptide chains.

[0548] *RNA interfering or RNAi:* As used herein, the term "RNA interfering" or "RNAi" refers to a sequence specific regulatory mechanism mediated by RNA molecules which results in the inhibition or interfering or "silencing" of the expression of a corresponding protein-coding gene. RNAi has been observed in many types of organisms, including plants, animals and fungi. RNAi occurs in cells naturally to remove foreign RNAs (e.g., viral RNAs). Natural RNAi proceeds via fragments cleaved from free dsRNA which direct the degradative mechanism to other similar RNA sequences. RNAi is controlled by the RNA-induced silencing complex (RISC) and is initiated by short/small dsRNA molecules in cell cytoplasm, where they interact with the catalytic RISC component argonaute. The dsRNA molecules can be introduced into cells exogenously. Exogenous dsRNA initiates RNAi by activating the ribonuclease protein Dicer, which binds and cleaves dsRNAs to produce double-stranded fragments of 21-25 base pairs with a few unpaired overhang bases on each end. These short double stranded fragments are called small interfering RNAs (siRNAs).

[0549] *RNAi agent:* As used herein, the term "RNAi agent" refers to an RNA molecule, or its derivative, that can induce inhibition, interfering, or "silencing" of the expression of a target gene and/or its protein product. An RNAi agent may knock-out (virtually eliminate or eliminate) expression, or knock-down (lessen or decrease) expression. The RNAi agent may be, but is not limited to, dsRNA, siRNA, shRNA, pre-miRNA, pri-miRNA, miRNA, stRNA, lncRNA, piRNA, or snoRNA.

[0550] *Sample:* As used herein, the term "sample" or "biological sample" refers to a subset of its tissues, cells or component parts (e.g. body fluids, including but not limited to blood, serum, mucus, lymphatic fluid, synovial fluid, cerebrospinal fluid, saliva, amniotic fluid, amniotic cord blood, urine, vaginal fluid and semen). A sample further may include a

homogenate, lysate or extract prepared from a whole organism or a subset of its tissues, cells or component parts, or a fraction or portion thereof, including but not limited to, for example, plasma, serum, spinal fluid, lymph fluid, the external sections of the skin, respiratory, intestinal, and genitourinary tracts, tears, saliva, milk, blood cells, tumors, organs. A sample further refers to a medium, such as a nutrient broth or gel, which may contain cellular components, such as proteins or nucleic acid molecule.

[0551] *Self-complementary viral particle*: As used herein, a "self-complementary viral particle" is a particle comprised of at least two components, a protein capsid and a self-complementary viral genome enclosed within the capsid.

[0552] *Sense Strand:* As used herein, the term "the sense strand" or "the second strand" or "the passenger strand" of a siRNA molecule refers to a strand that is complementary to the antisense strand or first strand. The antisense and sense strands of a siRNA molecule are hybridized to form a duplex structure. As used herein, a "siRNA duplex" includes a siRNA strand having sufficient complementarity to a section of about 10-50 nucleotides of the mRNA of the gene targeted for silencing and a siRNA strand having sufficient complementarity to form a duplex with the other siRNA strand.

[0553] *Similarity*: As used herein, the term "similarity" refers to the overall relatedness between polymeric molecules, *e.g.* between polynucleotide molecules (*e.g.* DNA molecules and/or RNA molecules) and/or between polypeptide molecules. Calculation of percent similarity of polymeric molecules to one another can be performed in the same manner as a calculation of percent identity, except that calculation of percent similarity takes into account conservative substitutions as is understood in the art.

[0554] *Short interfering RNA or siRNA:* As used herein, the terms "short interfering RNA," "small interfering RNA" or "siRNA" refer to an RNA molecule (or RNA analog) comprising between about 5-60 nucleotides (or nucleotide analogs) which is capable of directing or mediating RNAi. Preferably, a siRNA molecule comprises between about 15-30 nucleotides or nucleotide analogs, such as between about 16-25 nucleotides (or nucleotide analogs), between about 18-23 nucleotides (or nucleotide analogs), between about 19-22 nucleotides (or nucleotide analogs) (e.g., 19, 20, 21 or 22 nucleotides or nucleotide analogs), between about 19-25 nucleotides (or nucleotide analogs), and between about 19-24 nucleotides (or nucleotide analogs). The term "short" siRNA refers to a siRNA comprising 5-23 nucleotides, preferably 21 nucleotides (or nucleotide analogs), for example, 19, 20, 21 or 22 nucleotides. The term "long" siRNA refers to a siRNA comprising 24-60 nucleotides, preferably about 24-25 nucleotides, for example, 23, 24, 25 or 26 nucleotides. Short siRNAs

may, in some instances, include fewer than 19 nucleotides, e.g., 16, 17 or 18 nucleotides, or as few as 5 nucleotides, provided that the shorter siRNA retains the ability to mediate RNAi. Likewise, long siRNAs may, in some instances, include more than 26 nucleotides, e.g., 27, 28, 29, 30, 35, 40, 45, 50, 55, or even 60 nucleotides, provided that the longer siRNA retains the ability to mediate RNAi or translational repression absent further processing, e.g., enzymatic processing, to a short siRNA. siRNAs can be single stranded RNA molecules (ss-siRNAs) or double stranded RNA molecules (ds-siRNAs) comprising a sense strand and an antisense strand which hybridized to form a duplex structure called an siRNA duplex.

[0555] *Subject:* As used herein, the term "subject" or "patient" refers to any organism to which a composition in accordance with the disclosure may be administered, *e.g.*, for experimental, diagnostic, prophylactic, and/or therapeutic purposes. Typical subjects include animals (*e.g.*, mammals such as mice, rats, rabbits, non-human primates, and humans) and/or plants.

[0556] *Substantially*: As used herein, the term "substantially" refers to the qualitative condition of exhibiting total or near-total extent or degree of a characteristic or property of interest. One of ordinary skill in the biological arts will understand that biological and chemical phenomena rarely, if ever, go to completion and/or proceed to completeness or achieve or avoid an absolute result. The term "substantially" is therefore used herein to capture the potential lack of completeness inherent in many biological and chemical phenomena.

[0557] *Targeting peptide:* As used herein, a "targeting peptide" refers to a peptide of 3-20 amino acids in length. These targeting peptides may be inserted into, or attached to, a parent amino acid sequence to alter the characteristics (e.g., tropism) of the parent protein. As a non-limiting example, the targeting peptide can be inserted into an AAV capsid sequence for enhanced targeting to a desired cell-type, tissue, organ or organism. It is to be understood that a targeting peptide is encoded by a targeting polynucleotide which may similarly be inserted into a parent polynucleotide sequence. Therefore, a "targeting sequence" refers to a peptide or polynucleotide sequence for insertion into an appropriate parent sequence (amino acid or polynucleotide, respectively).

[0558] *Target Cells:* As used herein, "target cells" or "target tissue" refers to any one or more cells of interest. The cells may be found *in vitro*, *in vivo*, *in situ* or in the tissue or organ of an organism. The organism may be an animal, preferably a mammal, more preferably a human and most preferably a patient.

[0559] *Therapeutic Agent:* The term "therapeutic agent" refers to any agent that, when administered to a subject, has a therapeutic, diagnostic, and/or prophylactic effect and/or elicits a desired biological and/or pharmacological effect.

[0560] *Therapeutically effective amount:* As used herein, the term "therapeutically effective amount" means an amount of an agent to be delivered (*e.g.*, nucleic acid, drug, therapeutic agent, diagnostic agent, prophylactic agent, *etc.*) that is sufficient, when administered to a subject suffering from or susceptible to an infection, disease, disorder, and/or condition, to treat, improve symptoms of, diagnose, prevent, and/or delay the onset of the infection, disease, disorder, and/or condition. In some embodiments, a therapeutically effective amount is provided in a single dose.

[0561] *Therapeutically effective outcome*: As used herein, the term "therapeutically effective outcome" means an outcome that is sufficient in a subject suffering from or susceptible to an infection, disease, disorder, and/or condition, to treat, improve symptoms of, diagnose, prevent, and/or delay the onset of the infection, disease, disorder, and/or condition.

[0562] *Treating*: As used herein, the term "treating" refers to partially or completely alleviating, ameliorating, improving, relieving, delaying onset of, inhibiting progression of, reducing severity of, and/or reducing incidence of one or more symptoms or features of a particular infection, disease, disorder, and/or condition. For example, "treating" cancer may refer to inhibiting survival, growth, and/or spread of a tumor. Treatment may be administered to a subject who does not exhibit signs of a disease, disorder, and/or condition and/or to a subject who exhibits only early signs of a disease, disorder, and/or condition for the purpose of decreasing the risk of developing pathology associated with the disease, disorder, and/or condition.

[0563] *Vector:* As used herein, the term "vector" refers to any molecule or moiety which transports, transduces or otherwise acts as a carrier of a heterologous molecule. In some embodiments, vectors may be plasmids. In some embodiments, vectors may be viruses. An AAV particle is an example of a vector. Vectors of the present disclosure may be produced recombinantly and may be based on and/or may comprise adeno-associated virus (AAV) parent or reference sequences. The heterologous molecule may be a polynucleotide and/or a polypeptide.

[0564] *Viral Genome:* As used herein, the terms "viral genome" or "vector genome" refer to the nucleic acid sequence(s) encapsulated in an AAV particle. A viral genome comprises a nucleic acid sequence with at least one payload region encoding a payload and at least one ITR.

[0565] The present disclosure is further illustrated by the following non-limiting examples.

EXAMPLES

Example 1. Targeting peptides identified using CREATE in mice

[0566] The CREATE method for generating libraries of targeting peptides has previously been described in Deverman et al (Nature Biotechnology 34(2):204-209 (2016), the contents of which are herein incorporated in their entirety. This method was used to identify targeting peptides for enhancing AAV tropism to desired tissues (e.g., CNS). In short, random 7-amino acid peptides were inserted between amino acids 588 and 589 of K449R AAV9 (SEQ ID NO: 3), by inserting, at the DNA level, the nucleotides coding for random 7 amino acids into the corresponding region of the K449R AAV9 nucleotide sequence, to generate a DNA library. The K449R variant of AAV9 has the same function as wild-type AAV9. The DNA library was then used to create an AAV particle library which was intravenously administered to adult GFAP-Cre mice. DNAs packaged in AAV particles transducing the Cre-expressing cells were recovered in a Cre-dependent manner a week after administration. The recovered DNAs were cloned into the K449R AAV9 backbone to create a 2nd round DNA library. A second round of in-vivo selection yielded a series of AAV variants comprising targeting peptides that enhanced tropism for CNS tissues. Examples of targeting peptides isolated in such a manner include targeting peptides PHP.B (TLAVPFK; SEQ ID NO: 43054), PHP.A (YTLSQGW; SEQ ID NO: 43055), PHP.B2 (SVSKPFL; SEQ ID NO: 43056), PHP.B3 (FTLTTPK; SEQ ID NO: 43057), PHP.S (QAVRTSL; SEQ ID NO: 43058), G2B-A7 (MNSTKNV; SEQ ID NO: 43060), and G2B5-G9 (VSGGHHS; SEQ ID NO: 43061) shown in Table 4 below.

Table 4. Exemplar Targeting Peptides

Targeting Peptide	Sequence	Reference Information	SEQ ID NO:
PHP.B	TLAVPFK	WO2015038958 SEQ ID NO: 1	43054
PHP.A	YTLSQGW	WO2015038958 SEQ ID NO: 60	43055
PHP.B2	SVSKPFL	WO2015038958 SEQ ID NO: 28	43056
PHP.B3	FTLTTPK	WO2015038958 SEQ ID NO: 29	43057
PHP.S	QAVRTSL	WO2017100671 SEQ ID NO: 37	43058
PHP.N	DGTLAVPFKAQ	WO2017100671 SEQ ID NO: 4	43059
G2B4 (G2B-A7)	MNSTKNV	WO2017100671 SEQ ID NO: 43	43060
G2B5 (G2B5-G9)	VSGGHHS	WO2017100671 SEQ ID NO: 44	43061
PHP.B-EST	ESTLAVPFKAQ	WO2017100671 SEQ ID NO: 5	43062

PHP.B-GGT	GGTLAVPFKAQ	WO2017100671 SEQ ID NO: 6	43063
PHP.B-ATP	AQTLATPFKAQ	WO2017100671 SEQ ID NO: 7	43064
PHP.B-ATT-T	ATTLATPFKAQ	WO2017100671 SEQ ID NO: 8	43065
PHP.B-DGT-T	DGTLATPFKAQ	WO2017100671 SEQ ID NO: 9	43066
PHP.B-GGT-T	GGTLATPFKAQ	WO2017100671 SEQ ID NO: 10	43067
PHP.B-SGS	SGSLAVPFKAQ	WO2017100671 SEQ ID NO: 11	43068
PHP.B-AQP	AQTLAQPFKAQ	WO2017100671 SEQ ID NO: 12	43069
PHP.B-QQP	AQTLQQPFKAQ	WO2017100671 SEQ ID NO: 13	43070
PHP.B-SNP(3)	AQTLSNPFKAQ	WO2017100671 SEQ ID NO: 14	43071
PHP.B-SNP	AQTLAVPFSNP	WO2017100671 SEQ ID NO: 15	43072

[0567] The PHP.B 7-mer and flanking sequences were further evolved through site saturation mutagenesis of sets of three consecutive amino acids, using NNK codons, wherein N = any base and K is a G or T. DNA libraries of these site saturation mutagenesis sequences were generated to then create AAV particle libraries. CREATE was used for AAV particle selection in three different CNS cell populations, 1) astrocytes (GFAP-Cre), 2) GABA-ergic (inhibitory) neurons (VGAT-IRES-Cre), and 3) a subset of glutamatergic (excitatory) neurons (Vglut2-IRES-CRE). AAV particles transducing Cre-expressing cells were subjected to two rounds of selection and were then recovered and assessed by clonal and/or next generation sequencing (NGS). An example of a targeting peptide isolated in such a manner include PHP.N (DGTLAVPFKAQ; SEQ ID NO: 43059), PHP.B-EST (ESTLAVPFKAQ; SEQ ID NO: 43062), PHP.B-GGT (GGTLAVPFKAQ; SEQ ID NO: 43063), PHP.B-ATP (AQTLATPFKAQ; SEQ ID NO: 43064), PHP.B-ATT-T (ATTLATPFKAQ; SEQ ID NO: 43065), PHP.B-DGT-T (DGTLATPFKAQ; SEQ ID NO: 43066), PHP.B-GGT-T (GGTLATPFKAQ; SEQ ID NO: 43067), PHP.B-SGS (SGSLAVPFKAQ; SEQ ID NO: 43068), PHP.B-AQP (AQTLAQPFKAQ; SEQ ID NO: 43069), PHP.B-QQP (AQTLQQPFKAQ; SEQ ID NO: 43070), PHP.B-SNP(3) (AQTLSNPFKAQ; SEQ ID NO: 43071), and PHP.B-SNP (AQTLAVPFSNP; SEQ ID NO: 43072) as shown in Table 4 above.

Example 2. Identification of improved CNS targeting peptides and AAV particles

[0568] Using CREATE in mice to isolate novel targeting peptides for enhancing tropism of AAV particles to the CNS after intravenous delivery has proven useful in identifying targeting peptides and associated AAV variants such as PHP.B and PHPN. These vectors have shown broad CNS distribution following intravenous administration when tested in mice, however, whether these vectors will show similar efficacy in NHP or humans remains

to be determined. Even if efficacy is the same, the dose necessary for CNS distribution after IV administration in a large mammal may be prohibitive. Continuing to evolve targeting peptides in systems more closely matched to humans (e.g., NHP) can help generate targeting peptides and AAV particles with more desirable CNS transduction profiles, for use in humans using intravenous delivery.

Pilot study to test co-transduction of AAV-Cre vectors and PHP.N reporter

[0569] To use CREATE in non-transgenic NHP lacking Cre expression, AAV-Cre vectors need to be delivered intraparenchymally to the target CNS tissues of the NHP. To evaluate co-transduction of intraparenchymally (IPa) administered Cre-expressing AAV particles and an intravenously administered Cre-dependent reporter packaged in an AAV particle, the system will first be tested in mice.

[0570] Four Cre-vectors will be created, 1) for ubiquitous expression using a CAG, UBC or EF1α promoter (CAG- UBC- or EF1α-Cre), 2) for neuronal expression using a human synapsin promoter (hSyn1-Cre), 3) for astrocytic expression using a truncated GFAP promoter (GfABᵢD-Cre, and 4) for oligodendrocyte expression using a myelin basic promoter (MBP-Cre), then packaged into an AAV capsid (AAV1, AAV9, AAVrh10 or AAVPHP.B) to generate AAV particles. A vector expressing a fluorescent protein can be used to mark vector spread at the injection site (e.g., CAG-mRuby2/tdTomato).

[0571] Two reporter AAV particles will be created for testing, 1) AAVPHP.N:CAG-DIO-mTurquoise2 (forward)/GFP(reverse) and 2) AAV1/9/rh10-CAG-DIO-mTurquoise2(f)/GFP(r). These reporter AAV particles will be delivered either by intravenous administration or by co-intraparenchymal administration with the Cre-vectors. Only those cells of the CNS also expressing Cre (co-transduced by a cre-vector administered intraparenchymally) will express the reporter.

[0572] Each cre-vector will be injected into two mice and each mouse will also be administered one of the two reporter AAV particles (16 mice). The reporter AAV particles may be administered intravenously or intraparenchymally. Four mice will serve as non-Cre mRuby2/tdTomato controls. Using an intracranial surgical approach, Cre-vectors (and/or a reporter AAV) will be intraparenchymally administered to the striatum, thalamus and/or cortex at a volume of 0.5μL and a concentration of $3x10^9$ to $3x10^{10}$ vg/site. The reporter AAV particles administered intravenously will be given at a concentration of $3x10^{11}$vg.

[0573] Mice will be evaluated three weeks after AAV particle administration. Co-transduction efficiency will be evaluated based on imaging of the coincidence of green and red fluorescent signals.

[0574] It is anticipated that the IV-administered reporter AAV particles will deliver the reporter to CNS tissues expressing Cre and mRuby2/tdTomato (e.g., striatum, thalamus and/or cortex). To be considered successful, the results of this pilot experiment will show a high yield of GFP (reporter) transduced neurons in the mRuby/tdTomato transduced brain region (delivered by IPa). As an example, >50% of neurons and astrocytes and 10-30% of oligodendrocytes in the mRuby/tdTomato transduced brain region may also express GFP.

[0575] It is possible that off-target cell-types will be transduced by the Cre-vectors and reporter AAV particles. In this case, miRNA binding sites complementary to miRNAs expressed in these off-target cell types, but not in the target cell type, may be introduced into the viral genomes of the AAV particles for enhanced targeting and specificity.

Pilot mouse AAV-Cre based AAV-PHP.B/N library selection

[0576] In order to test whether expected and/or novel capsid sequences comprising targeting peptides can be recovered from the brain following intraparenchymal delivery to the striatum, thalamus and/or cortex of the Cre-vectors and intravenous delivery of an AAV capsid library, a pilot study will first be performed in mice. This study can also be used to test library diversification/randomization strategies.

[0577] Four DNA libraries based on PHP.B/PHP.N will be generated by PCR, with mixed bases at the desired positions. PCR fragments will be cloned into the library acceptor AAV genome (e.g., AAV9) by Gibson assembly and processed to remove unassembled DNA. The AAV DNA libraries will then be transfected directly into HEK293 cells for AAV particle production. The libraries will be built into an AAV vector with rep/cap in cis and a floxed element. Libraries of AAV particles will be generated based on these DNA libraries.

[0578] Library 1 will extend the targeting peptide sequence to include the 2-3 amino acids immediately upstream and/or downstream of the 7-mer peptide insert. These amino acids will be replaced with random amino acids generated by NNK-containing primers. This library will comprise site saturation mutagenesis at 5-6 amino acids of the targeting peptide sequence and produce a library diversity of $3.2x10^6$ to $6.4x10^7$ sequences.

[0579] Library 2 will be a mixed library of PHP.B/N, PHP.B2 and PHP.B3 targeting peptides mutated 3-amino acids at a time, creating 21 combined libraries with approximately $1.6x10^5$ variants. This library is based on the same strategy as was used for generation of PHP.N from PHP.B, described above.

[0580] Library 3 will be a mixture of two novel 7-mer peptide libraries inserted between amino acids 588 and 589 of AAV9 (SEQ ID NO: 2), K449R AAV9 (SEQ ID NO: 3) and/or AAV-DJ8 and/or AAV5.

[0581] Library 4 will include capsid sequences modified at a distinct surface site (e.g., loop IV and/or VIII).

[0582] Cell-type specific Cre-vectors (as described above) and AAV particle libraries will be injected into mice (2 mice per Cre-vector, per library and 2 Cre-control mice; 18 mice total). Cre-vectors will be delivered to the striatum and cortex via intraparenchymal administration, whereas the AAV particle libraries will be administered intravenously.

[0583] Libraries may optionally be spiked with a small amount of AAV9 or AAVPHP.B to serve as a normalization control.

[0584] Tissue samples (e.g., brain) will be collected 3 weeks after administration of Cre-vectors and AAV libraries. The total DNA will be isolated and capsid sequences recovered. For recovery, Cre-dependent amplification strategies may be used. Capsid sequences will be prepared for NGS using standard methods known in the art.

[0585] DNA libraries will be sequenced by NGS at a depth of 50M, 100bp reads. Virus libraries will be sequenced at a depth of 20M, 100bp reads. Samples recovered from one CNS region and one liver sample per mouse will be sequenced at a depth of 5M reads.

[0586] Capsid sequences comprising targeting peptides that show evidence of enrichment across CNS cell-types will be isolated and cloned. If no clearly enriched variants arise from the first round library, a second-round capsid library may be generated. Capsid sequences comprising targeting peptides that show evidence of enrichment across CNS cell-types from a second round library will be isolated and cloned.

[0587] Isolated variants will be screened in adult mice. Each capsid variant will be used to package a ubiquitous reporter vector (e.g., ssAAV-CAG-GFP) and transduction efficiency to CNS tissues (brain and spinal cord) subsequent to intravenous administration will be evaluated by immunofluorescence imaging, as compared to parental capsids PHP.B, PHP.N and/or AAV9. Vector genome quantification in target tissues (e.g., brain, spinal cord, liver, heart, spleen, skeletal muscle) will be determined by qPCR.

[0588] It is anticipated that intraparenchymal delivery of AAV-Cre vectors will allow for the adaptation of the CREATE method to non-transgenic animals. A successful outcome of this pilot study would be the identification of one or more capsid variants (and targeting peptides) with enhanced tropism for CNS tissue after intravenous administration. As a positive control, it is anticipated that PHP.B, PHP.N, PHP.B2, and PHP.B3 or other AAV variants (see Table 4) will be identified again in Library 2.

Pilot testing of NHP injection strategy

[0589] AAV-Cre vectors will need to be delivered directly to the CNS tissue of the non-transgenic NHP. The injection strategy will be validated with a pilot study in NHP. The pilot study will assess spacing of injection sites for separation between areas of vector spread based on differing promoters (promoters described above). Further, the pilot study will address toxicity or immune responses to the modified CREATE system, by assessing markers of cell death, glial reactivity (Iba1 and GFAP immunostaining), T cell infiltration, and/or H&E staining. Simultaneously, expression of IV administered AAV-PHP.B delivered at a concentration of about $2x10^{13}$ vg/kg can be assessed for transduction efficiency based on the Cre-dependent reporter. Transduction efficiency of AAV particles comprising reporter constructs delivered by co-intraparenchymal administration may also be determined.

Selection of AAV capsid variants in NHP

[0590] AAVPHP.B/N based capsid libraries are generated as described above, however prior to injection into NHP, the libraries will be titred and assessed by NGS. Cell-type specific Cre-vectors will be stereotactically delivered to the CNS tissue of three NHP, while the AAV capsid libraries will be injected intravenously, one week prior to injection of Cre vector. Stereotactic delivery to CNS tissue, may include intraparenchymal delivery to the putamen, thalamus, cortex, hippocampus and/or deep cerebellar nuclei.

[0591] Two-three weeks post-Cre-vectors stereotactical administration, tissue samples (e.g., brain, spinal cord, peripheral organs) are collected for analysis. Total vector DNA is isolated from the desired tissue sample(s) and a Cre-dependent amplification strategy is used to recover capsid sequences from each animal and each tissue region of interest. Samples are then prepared for NGS and sequenced as described previously.

[0592] AAV capsid variants showing enrichment across CNS cell types will be cloned for further examination and tested in adult mice/NHP for transduction efficiency to tissues of interest.

[0593] It is anticipated that AAV capsid sequences comprising targeting peptides with enhanced tropism to CNS tissues after IV administration, as compared to AAV9, PHP.B or PHP.A will be identified through these NHP experiments.

[0594] The methods for selection of AAV capsid variants in NHP as described above can be repeated, and a second round library generated to further narrow the number of lead AAV capsid sequence candidates with enhanced tropism to the CNS and/or to enhance reliability. AAV capsid variants showing enrichment across CNS cell types in the second round library will also be cloned for further examination and testing in mice/NHP.

[0595] A second evolution step may optionally be included for the AAV capsid candidates generated in the aforementioned NHP selection process. AAV capsid variant sequences with targeting peptides inserted at amino acid position 588-589 of the parent capsid sequence, are further modified at a second surface site. Modifications at more than one surface site may increase CNS tropism of the AAV capsid variants.

[0596] The top ten AAV capsid variants identified in these experiments will be cloned for further testing, and a viral genome encoding a reporter construct will be packaged inside. Variants will be identified based on total read number recovered from each sample, enrichment over the previous round or the starting library, and predicted high level of virus production. AAV particles will be titred and injected IV into adult mice at a dose of $1x10^{11}$ vg/mouse. Three weeks after injection, the mouse is perfused and tissues collected and processed for assessment of fluorescence by confocal microscopy. The top three candidates after further examination in mice will be tested individually in NHP to identify an AAV variant capsid with the best NHP CNS transduction profile following IV administration. Alternatively, AAV particles may be tested immediately in NHP and/or in parallel with the mouse studies described above.

Example 3. Identification of dorsal root ganglion targeting peptides and AAV particles

[0597] The dorsal root ganglia are clusters of neuronal cell bodies that lie just outside the spinal cord along the dorsal roots. Neurons of the dorsal root, with cell bodies in the DRG, convey sensory information from the periphery back to the spinal cord and central nervous system. Neurons of the DRG can be difficult to target with efficiency and selectivity for delivery of, for example, a therapeutic agent. Pathological conditions associated with DRG and their component neurons (e.g., neuropathic pain) could potentially be more easily treated if targeting peptides and associated AAV particles are identified for specific and efficient transduction of DRG following intravenous administration of AAV particles.

Mouse sensory neuron selection, first round of evolution

[0598] One of the targeting peptides (PHP.S; SEQ ID NO: 43058) identified using CREATE in mice (as described above), has previously demonstrated efficient transduction of peripheral neurons of the dorsal root, nodose, sympathetic, parasympathetic and cardiac ganglia. To identify targeting peptides and associated AAV particles with enhanced specificity for neurons of the DRG and subpopulations thereof, libraries based on this PHP.S targeting peptide will be generated and screened in transgenic mice.

[0599] Three AAV capsid libraries will be created and screened. Each library will be generated by site-saturation mutagenesis of different subsets of amino acids of the parent PHP.S amino acid sequence or flanking sequences of the parent AAV capsid.

[0600] Library 1 will involve site-saturation mutagenesis of the amino acids flanking the PHP.S 7-mer on both the 5' and 3' end in the parent AAV capsid sequence. This mutagenesis may include 4 or 5 amino acids flanking the 7-mer, yielding approximately $1.6x10^5$ to $3.2x10^6$ unique sequences.

[0601] For Library 2, sets of three amino acids of the PHP.S 7-mer and/or flanking regions will be evolved together, to generate six, 3 amino acid libraries with approximately $4.8x10^4$ unique amino acid sequences.

[0602] Library 3 will be a mixture of two novel 7-mer peptide libraries inserted between amino acids 588 and 589 of AAV9 (SEQ ID NO: 2), K449R AAV9 (SEQ ID NO: 3) and/or AAV-DJ8, giving approximately $1.3x10^9$ unique amino acid sequences each.

[0603] The three DNA libraries will be used to generate AAV particle libraries. Both DNA and AAV particle libraries will be titered by qPCR and assessed by NGS. AAV particle libraries will be given to transgenic mice via intravenous administration at a dose of approximately $1x10^{11}$vg/mouse.

[0604] Five transgenic mouse lines will be used, as follows; 1) Vglut-Cre for selection of targeting peptides for total sensory neuron transduction, 2) $Na_v1.8$-Cre for selection of targeting peptides for nociceptive neuron transduction, 3) Parvalbumin (PV)-Cre for selection of targeting peptides for parvalbumin neuron transduction, 4) TH-Cre for selection of targeting peptides for sympathetic/adrenergic neuron transduction and 5) Chat-Cre for selection of targeting peptides for parasympathetic/cholinergic neuron transduction.

[0605] One to two weeks after intravenous delivery, AAV particles will be recovered from neurons of the dorsal root, nodose, and cardiac ganglia, sympathetic and parasympathetic neurons including those of the myenteric ganglia and submucosal plexus of the intestines, and olfactory sensory neurons. DNA and AAV particle libraries associated with a desired transduction profile (e.g., transduction of a particular neuronal subset) will be sequenced and further characterized.

[0606] Fluorescence imaging will be used to determine transgene expression in the DRG and other peripheral ganglia. Immunostaining can be used to co-localize transgene expression to particular neuronal subtypes of the DRG. Transgene/reporter expression can be driven by either ubiquitous or neuron-specific promoter(s).

[0607] It is anticipated that several rounds of evolution may be necessary in order to identify a targeting peptide and associated AAV particle with a transduction profile for a specific neuronal subset, such as nociceptive neurons of the DRG. Negative selection may also be applied, wherein targeting peptides and associated AAV particles are eliminated from consideration if the transduction profile is considered undesirable.

Mouse sensory neuron selection, second round of evolution

[0608] One or more of the targeting peptides with enhanced specificity and efficiency of transduction of neurons of the DRG will be further evolved to increase specificity. Evolution strategies may include site-saturation mutagenesis of loop IV (e.g., amino acids 452-458) or mutation of known receptor binding sites.

[0609] Fluorescence imaging will be used to determine transgene expression in the DRG and other peripheral ganglia. Immunostaining can be used to co-localize transgene expression to particular neuronal subtypes of the DRG. Biodistribution of vector genomes can be determined by qPCR.

Example 4. Targeting of AAVPHP.B and AAVPHP.A to the CNS and DRG

[0610] To determine the tropism of AAV particles comprising the PHP.B or PHP.A targeting peptide to CNS and to the dorsal root ganglia after intravenous administration, the following study design was executed in adult (6-7 weeks) male C57BL/6 mice.

Table 5: Study design for PHP.B/PHP.A targeting to DRG

Test Article	Dose (vg)	Route (Tail vein)	Volume (uL)	N (IHC)	End of Study
Vehicle	0	IV	160	2	D28
AAV9-ssGFP	$5x10^{11}$	IV	160	4	D28
PHP.B-ssGFP	$5x10^{11}$	IV	160	4	D28
PHP.A-ssGFP	$5x10^{11}$	IV	160	4	D28

[0611] Targeting peptides PHP.B (TLAVPFK; SEQ ID NO: 43054) or PHP.A (YTLSQGW; SEQ ID NO: 43055) were inserted into an AAV9 (SEQ ID NO: 2) capsid sequence between amino acid positions 588 and 589. AAV9 without a targeting insert was used as a comparison vector, and PBS used as a control. A single stranded viral genome encoding GFP was used, yielding AAV particles AAV9-ssGFP, PHP.B-ssGFP and PHP.A-ssGFP. AAV particles (or PBS) were administered intravenously via the tail vein at a dose of $5x10^{11}$ and volume of 160µL.

[0612] Twenty eight days after intravenous delivery of the AAV particles, the animals were sacrificed and tissues collected for immunohistochemical and immunofluorescent analyses. Tissues from the dorsal root ganglion, brain (striatum, cortex, hippocampus), spinal cord (ventral horn), liver, heart and muscle were collected for processing by standard methods known in the art.

[0613] Analysis of tissue sections of brain, striatum, cortex, hippocampus and ventral horn showed that vectors comprising PHP.B or PHP.A targeting peptides mediate greater gene delivery throughout the CNS than AAV9 following intravenous injection in adult mice.

[0614] Similar analysis of tissue sections of the DRG demonstrated that after intravenous administration of the AAV particles, the greatest transduction of sensory neurons (most GFP signal) was seen with the use of targeting peptide PHP.B. Both AAV9 and PHP.A yielded transduced sensory neurons in the DRG following intravenous delivery, though to a lesser extent to that seen with PHP.B. As expected, intravenous delivery of PBS showed no transduction of sensory neurons of the DRG. These results demonstrate that targeting peptide PHP.B can be used for enhanced targeting to the CNS and of the sensory neurons of the dorsal root ganglia.

Example 5. Seven-mer targeting peptide libraries for selection in NHP

[0615] DNA libraries and associated AAV capsid libraries of 7-mer targeting peptides were generated and tested in mice and NHP. Targeting peptides were inserted into an AAV9 (SEQ ID NO: 2) parent capsid sequence between amino acid positions 588 and 589 (loop VIII).

[0616] AAV1-Cre vectors were administered intraparenchymally to the striatum and thalamus of three adult (2-11yr, 4-8kg) non-human primates (macaca mulatta or rhesus macaque), while the AAV capsid library was administered intravenously as shown in the study design of Table 6, below. The AAV particles were delivered in an excipient comprising 200mM NaCl, 1mM KH_2PO_4, 3mM Na_2HPO_4, 0.001% Pluronic F-68 at pH 7.4.

Table 6: Study design for AAV9-7mer library in NHP

Group	N	Day 1 Dosing (IV)		Day 11±1 Dosing (MRI-CED)				
		Material	Dose & Volume	Material	Dose & Volume			
					Putamen		Thalamus	
					Left	Right	Left	Right
1A	1	AAV9-7mer	$5.0x10^{12}$ vg/kg (1 mL/kg)	AAV1-Cre	$3.75x10^{11}$ vg (150µL)	$7.5x10^{10}$ vg (150µL)	$6.25x10^{11}$ vg (250µL)	$1.25x10^{11}$ vg (250µL)
1B	1	AAV9-7mer	$5.0x10^{12}$ vg/kg (1 mL/kg)	AAV1-Cre	$7.5x10^{10}$ vg (150µL)	$1.5x10^{10}$ vg (150µL)	$1.25x10^{11}$ vg (250µL)	$2.5x10^{10}$ vg (250µL)
1C	1	AAV9-7mer	$5.0x10^{12}$ vg/kg (1 mL/kg)	AAV1-Cre	$3.75x10^{11}$ vg (150µL)	$1.5x10^{10}$ vg (150µL)	$6.75x10^{11}$ vg (250µL)	$2.5x10^{10}$ vg (250µL)

[0617] Five animals were selected based on results of neutralizing antibody assays for anti-AAV antibodies to AAV1 and AAV9. Minimal or no detectable capsid specific antibodies was required for selection. Two of these five animals served as alternate study animals. Study subjects underwent a pre-project physical examination.

[0618] On Day 1 of the study, each animal received intravenous infusion of the AAV9-7mer library. On Day 7±1, animals had bilateral intracranial infusion of AAV1-Cre vectors to the putamen and thalamus, using MRI-guided convection enhanced delivery.

[0619] On the day of dosing, AAV9-7mer libraries or AAV1-Cre containing compositions were thawed at 2-8C. The excipient detailed above was used as a vehicle control. Dosing solutions were gently centrifuged to collect material from the vial cap then transferred to the syringe/needle for delivery. Dosing solutions were kept at room temperature until administration, but not longer than for 2 hours. On Day 7±1, for the MRI-CED dosing, Gadoteridol (ProHance, Bracco Diagnostics Inc) was added at a 1:250 ratio and mixed carefully by tube inversion prior to loading into dosing syringes.

[0620] For intravenous administration of the AAV9-7mer libraries on Day 1, animals were immobilized with ketamine (10mg/kg, administered intramuscularly (IM)) and dexmedetomidine (15µg/kg, IM) and given a single intravenous infusion (dose volume of 1 mL/kg) via the saphenous vein, using a syringe pump. After dosing, a 0.2mL flush of vehicle/excipient was administered. Animals were allowed to recover and returned to home cages.

[0621] On Day 7±1, for the MRI-CED of AAV1-Cre vectors, animals were anesthetized with ketamine (10 mg/kg) and dexmedetomidine (15µg/kg) via intramuscular injection, weighed, shaved on the head and neck, intubated and maintained on 1-5% isoflurane. The head was secured in a stereotaxic frame and the overlying skin cleaned and prepared for implantation procedures. Aseptic techniques were used to expose the skull by opening the wound site by anatomical layers. Bilateral craniotomies were performed at entry sites located above the frontal/parietal and occipital lobes. A skull mounted cannula guide ball array was temporarily secured to the skull with titanium screws over each burr hole. After implantation of the cannula guides, animals were transferred to the MRI suite. MRI was used to align the cannula guides with putamen and thalamus targets ipsilateral (same side of the brain/body) to each cannula guide. Repeat MRI was used to visually monitor infusions.

[0622] Dosing solutions were delivered via an adjustable tip 16G cannula (MRI Interventions Inc) primed with the dosing solution then guided into each target site through the skull mounted cannula arrays. Cannula were connected via microbore extension lines

(Smiths Medical) to a syringe mounted on a syringe pump (Harvard apparatus). Ascending infusion rates (up to 10 µL/min) were used to deliver dose volumes (150 µL/putamen; 250µL/thalamus) to the putamen and thalamus. Serial MRI scans were used to monitor infusate distribution.

[0623] Immediately after MRI-CED dosing, animals were transferred back to the operating room where the cannula guide system was removed and the wound site closed, using a vicryl suture. Animals were provided pre- and post-operative medications, allowed to recover from anesthesia and returned to their home cages.

[0624] Fourteen days after MRI-CED dosing to the putamen and thalamus (Day 21±2) animals were euthanized and tissue samples collected. Euthanasia was performed using intravenous delivery of a pentobarbital sodium solution (100mg/kg), followed by a bilateral thoracotomy. A transcardial perfusion using ice-cold saline was performed via left cardiac ventricle, with approximately 2.5 L of ice-cold saline with heparin (100 U/mL) using a perfusion pump set to 200-400 mL/min over about 10min. Samples were collected from brain, spinal cord, 12 dorsal root ganglia and associated roots (4 each from cervical, thoracic and lumbar spinal cord), liver, heart (left ventricle and right atrium), gastrocnemius muscle, soleus muscle, pancreas, kidney, spleen, lung, adrenal glands, stomach, sciatic nerve, saphenous nerve, thyroid gland, eyes (with optic nerve), pituitary gland, skeletal muscle (rectus femoris), colon, duodenum, ileum, jejunum, skin of the leg, superior cervical ganglia, urinary bladder, ovaries, uterus, prostate gland, testes, and/or any sites identified as having a lesion, and fresh frozen for biochemical analysis.

[0625] At the time of collection, all samples were photographed alongside a ruler for scale. The brain was cut coronally in a matrix at 3mm slice thickness, then alphabetically annotated rostral (nose) to caudal (tail). A small punch (1mm diameter) was created in the white matter of the right cortex for orientation purposes. Brain samples were frozen on dry ice. The spinal cord was cut into segments corresponding to each vertebral level, then transferred to a chilled cryovial tube and snap frozen on dry ice. DRG and associated roots were collected from C1, C3, C5, C7, T3, T5, T7, T9, L1, L3, L5 and L7. These were transferred into a chilled cryovial and frozen on dry ice. For the other organ samples collected, two samples per organ, approximately 1.0x1.0x0.5cm (or the entire organ if smaller) were collected, transferred to a chilled cryovial tube and snap-frozen on dry ice. All samples were stored frozen at -60C or below.

[0626] Blood and cerebrospinal fluid (CSF) samples were collected on Day 1, prior to IV dosing, on Day 7±1, prior to MRI-CED dosing, and on Day 21±2 prior to termination. Time

points and descriptions of sample collection are shown below in Table 7. Whole blood samples were collected in tubes containing EDTA, mixed by inversion and aliquoted into 2 sub-samples, then stored at -60C or below. Sample volumes listed in the Serum column, refer to the volume of whole blood which was then processed to serum and split to 2 aliquots and stored at -60C or below. CSF samples were collected after animals were immobilized with ketamine (10mg/kg; IM) and dexmedetomidine (15ug/kg; IM). The neck was shaved and flexed and skin prepared. A 23G needle was manually advanced through the skin and the atlanto-occipital membrane into the cerebellomedullary cistern space. Once CSF flow was confirmed in the needle hub, CSF collection began. Collected CSF was centrifuged (4,500g for 5 min at 4C), the supernatant filtered through a 0.8µm low protein binding syringe filter, and the filtrate split into 4 aliquots for analysis. At necropsy, all available CSF was collected, processed, and aliquoted to approximately 1.0mL samples. CSF samples were stored at -60C or below.

Table 7. Time points for sample collection

Time point	Fasted	N	Sample Volume (mL)		
			Serum	Whole blood	CSF
Pre-screening	Yes	18	2.0	N/A	N/A
Day 1: prior to IV dosing	Yes	3	2.0	0.5	1.5
Day 7±1: prior to intraparenchymal MRI-CED dosing	Yes	3	2.0	0.5	1.5
Day 21±2: prior to necropsy	Yes	3	2.0	0.5	All available

[0627] Animals were monitored throughout the study with twice daily clinical observations assessing mortality, neurological signs or other abnormalities and/or signs of pain or distress. Food consumption was also monitored daily. Body weights were measured once weekly, beginning prior to IV dosing on Day 1.

[0628] After this first round of selection in NHP, targeting peptides with amino acid sequences as represented by SEQ ID NO: 4-14326 (shown in Table 2) were recovered from CNS tissues. DNA libraries comprising SEQ ID NO: 14327-42972 have been prepared for second round selection in NHP.

Example 6. Three-mer targeting peptide library for selection in NHP

[0629] A DNA library and associated AAV capsid library was generated based on a 9-mer of the PHP.N targeting peptide. The 9-mer PHP.N amino acid sequence was further evolved through site saturation mutagenesis of sets of three consecutive amino acids, to generate the targeting peptides represented by SEQ ID NO: 42973-42999, as shown in Table 3. Amino

acids at positions 1, 2, and 6-9 of the parent PHP.N 9-mer remained the same, with site saturation mutagenesis of only amino acids at positions 3, 4, and 5, yielding 27 targeting peptide sequences for screening and characterization.

Equivalents and Scope

[0630] Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments in accordance with the disclosure. The scope of the present disclosure is not intended to be limited to the above Description, but rather is as set forth in the appended claims.

[0631] In the claims, articles such as "a," "an," and "the" may mean one or more than one unless indicated to the contrary or otherwise evident from the context. Claims or descriptions that include "or" between one or more members of a group are considered satisfied if one, more than one, or all of the group members are present in, employed in, or otherwise relevant to a given product or process unless indicated to the contrary or otherwise evident from the context. The disclosure includes embodiments in which exactly one member of the group is present in, employed in, or otherwise relevant to a given product or process. The disclosure includes embodiments in which more than one, or the entire group members are present in, employed in, or otherwise relevant to a given product or process.

[0632] It is also noted that the term "comprising" is intended to be open and permits but does not require the inclusion of additional elements or steps. When the term "comprising" is used herein, the term "consisting of" is thus also encompassed and disclosed.

[0633] Where ranges are given, endpoints are included. Furthermore, it is to be understood that unless otherwise indicated or otherwise evident from the context and understanding of one of ordinary skill in the art, values that are expressed as ranges can assume any specific value or subrange within the stated ranges in different embodiments of the disclosure, to the tenth of the unit of the lower limit of the range, unless the context clearly dictates otherwise.

[0634] In addition, it is to be understood that any particular embodiment of the present disclosure that falls within the prior art may be explicitly excluded from any one or more of the claims. Since such embodiments are deemed to be known to one of ordinary skill in the art, they may be excluded even if the exclusion is not set forth explicitly herein. Any particular embodiment of the compositions of the disclosure (e.g., any antibiotic, therapeutic or active ingredient; any method of production; any method of use; etc.) can be excluded from any one or more claims, for any reason, whether or not related to the existence of prior art.

[0635] It is to be understood that the words which have been used are words of description rather than limitation, and that changes may be made within the purview of the appended claims without departing from the true scope and spirit of the disclosure in its broader aspects.

[0636] While the present disclosure has been described at some length and with some particularity with respect to the several described embodiments, it is not intended that it should be limited to any such particulars or embodiments or any particular embodiment, but it is to be construed with references to the appended claims so as to provide the broadest possible interpretation of such claims in view of the prior art and, therefore, to effectively encompass the intended scope of the disclosure.

CLAIMS

1. An AAV capsid protein comprising (i) a parent VP1 amino acid sequence selected from the group consisting of SEQ ID NO: 2 or SEQ ID NO: 3, and (ii) at least one targeting peptide inserted into the parent VP1 amino acid sequence of (i), wherein the targeting peptide is selected from any member of the group consisting of SEQ ID NO: 4-14326 and any member of the group consisting of SEQ ID NO: 42973-42999.

2. The AAV capsid protein of claim 1, wherein the parent VP1 amino acid sequence comprises a VP2 region and/or a VP3 region.

3. The AAV capsid protein of claim 2, wherein the targeting peptide is inserted within the VP2 region of the parent VP1 amino acid sequence.

4. The AAV capsid protein of claim 2, wherein the targeting peptide is inserted within the VP3 region of the parent VP1 amino acid sequence.

5. The AAV capsid protein of claim 1, wherein the targeting peptide is inserted at any amino acid position between amino acids 586-592, inclusive, of the parent VP1 amino acid sequence.

6. The AAV capsid protein of claim 1, wherein the targeting peptide is inserted between amino acids 588-589 of the parent VP1 amino acid sequence.

7. A peptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 4-14326 and SEQ ID NO: 42973-42999.

8. A nucleic acid sequence encoding the peptide of claim 7, selected from the group consisting of SEQ ID NO: 14327-42972 and SEQ ID NO: 4300-43053.

9. An AAV particle comprising an AAV capsid protein of any of claims 1-8 and a viral genome.

10. The AAV particle of claim 9, wherein the viral genome comprises a nucleic acid

sequence encoding a payload.

11. The AAV particle of claim 10, wherein the payload is an RNAi agent.

12. The AAV particle of claim 11, wherein the RNAi agent is selected from the group consisting of dsRNA, siRNA, shRNA, pre-miRNA, pri-miRNA, miRNA, stRNA, lncRNA, piRNA, or snoRNA.

13. The AAV particle of claim 11, wherein the RNAi agent, when expressed, inhibits or suppresses the expression of a gene of interest in a cell, wherein the gene of interest is selected from the group consisting of SOD1, MAPT, APOE, HTT, C9ORF72, TDP-43, APP, BACE, SNCA, ATXN1, ATXN2, ATXN3, ATXN7, SCN1A-SCN5A, or SCN8A-SCN11A.

14. The AAV particle of claim 10, wherein the payload is a polypeptide.

15. The AAV particle of claim 14, wherein the polypeptide is selected from the group consisting of an antibody, aromatic L-amino acid decarboxylase (AADC), survival motor neuron 1 (SMN1), frataxin (FXN), ApoE2, GBA1, GRN, ASPA, CLN2, GLB1, SGSH, NAGLU, IDS, NPC1, or GAN.

16. A pharmaceutical composition comprising the AAV particle of any of claims 9-15 and a pharmaceutically acceptable excipient.

17. A method of treating a disease in a subject by administering the pharmaceutical composition of claim 16 to said subject.

18. The method of claim 17, wherein the disease is Huntington's Disease.

19. The method of claim 17, wherein the disease is Amyotrophic Lateral Sclerosis.

20. The method of claim 17, wherein the disease is Friedreich's Ataxia.

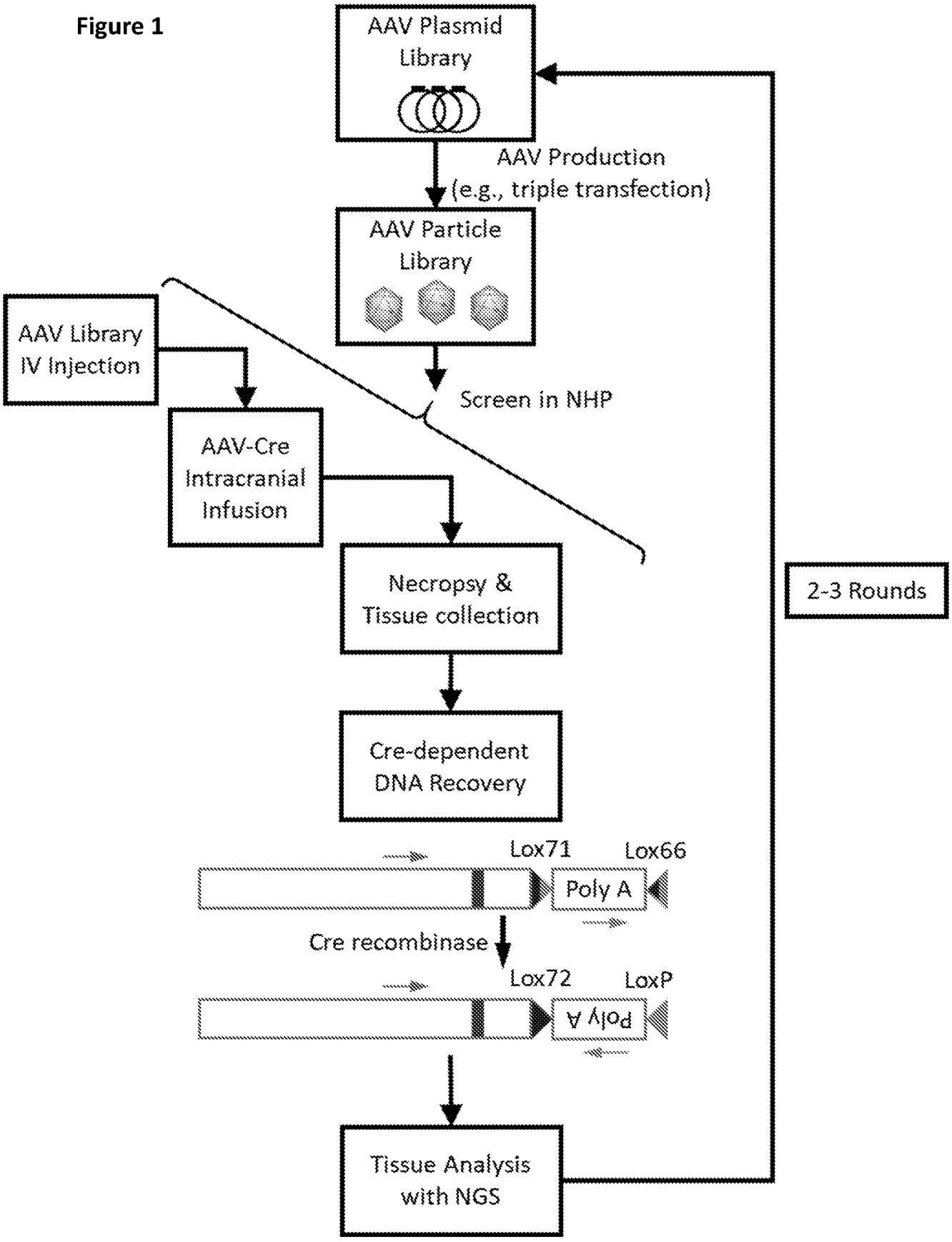
21. The method of claim 17, wherein the disease is Parkinson's Disease.

22. The method of claim 17, wherein the disease is Alzheimer's Disease.

23. The method of claim 17, wherein the disease is a tauopathy.

24. The method of claim 17, wherein the disease is neuropathic pain.

Figure 1


AAV Plasmid Library
AAV Production (e.g., triple transfection)
AAV Particle Library
AAV Library IV Injection
Screen in NHP
AAV-Cre Intracranial Infusion
Necropsy & Tissue collection
2-3 Rounds
Cre-dependent DNA Recovery
Lox71
Lox66
Poly A
Cre recombinase
Lox72
LoxP
Poly A
Tissue Analysis with NGS